

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 26, 2005, 06:03:27 ; Search time 45 Seconds
(without alignments)
1592.513 Million cell updates/sec

Title: US-10-039-073-1
Perfect score: 5052
Sequence: 1 MFHSSAMVNSHRKPMFNIHR.....NIKWLXNLPFLRTWLMVNT 960

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pgp:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pgp:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pgp:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pgp:*
5: /cgn2_6/ptodata/1/iaa/ECTUS_COMB.pgp:*
6: /cgn2_6/ptodata/1/iaa/backfiles.pgp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5052	100.0	960	US-09-345-650-1	Sequence 1, Appli
2	2507.5	49.6	948	US-09-620-312D-1105	Sequence 1105, Ap
3	2027	40.1	1025	US-08-530-792D-23	Sequence 23, Appl
4	2016.5	39.9	1026	US-08-530-792D-22	Sequence 22, Appl
5	1444	28.6	957	US-09-949-016-6154	Sequence 6154, Ap
6	1440	28.5	964	US-09-949-016-7431	Sequence 7431, Ap
7	1264.5	25.0	967	US-09-139-802-201	Sequence 201, App
8	1264.5	25.0	967	US-09-659-786-201	Sequence 201, App
9	1125	24.2	919	US-09-919-039-222	Sequence 222, App
10	1165	23.1	977	US-08-335-844A-22	Sequence 22, Appl
11	1165	23.1	977	US-09-129-366-22	Sequence 22, Appl
12	1117	22.1	972	US-08-335-844A-24	Sequence 24, Appl
13	1117	22.1	972	US-09-129-366-24	Sequence 24, Appl
14	1100	21.8	972	US-08-335-844A-23	Sequence 23, Appl
15	1100	21.8	972	US-09-129-366-23	Sequence 23, Appl
16	1083	21.4	699	US-09-270-767-45507	Sequence 45507, A
17	986	19.5	593	US-08-637-670-38	Sequence 38, Appl
18	908	18.0	608	US-08-637-670-36	Sequence 36, Appl
19	884	17.5	850	US-09-902-540-10199	Sequence 10199, A
20	868	17.2	990	US-09-657-931A-11	Sequence 11, Appl
21	867	17.2	848	US-09-583-110-2738	Sequence 2738, Ap
22	863	17.1	995	US-09-657-931A-1	Sequence 1, Appli
23	844	16.7	815	US-09-107-433-5059	Sequence 5059, Ap
24	841.5	16.7	946	US-09-657-931A-10	Sequence 10, Appl
25	820	16.2	1009	US-09-657-931A-13	Sequence 13, Appl
26	818.5	16.2	986	US-09-657-931A-12	Sequence 12, Appl
27	785.5	15.5	942	US-09-657-931A-9	Sequence 9, Appli

28	711.5	14.1	616	4	US-08-637-670-26	Sequence 26, Appl
29	709	14.0	620	4	US-08-637-670-40	Sequence 40, Appl
30	693.5	13.7	616	4	US-08-637-670-28	Sequence 28, Appl
31	692.5	13.7	917	4	US-09-902-540-12845	Sequence 12845, A
32	679.5	13.5	923	4	US-09-328-352-4371	Sequence 4371, Ap
33	659	13.0	528	4	US-08-637-670-27	Sequence 27, Appl
34	647	12.8	912	4	US-09-902-540-16181	Sequence 16181, A
35	543	10.7	582	4	US-09-270-767-45532	Sequence 45532, A
36	482	9.5	386	4	US-08-637-670-24	Sequence 24, Appl
37	477.5	9.5	346	4	US-08-637-670-35	Sequence 35, Appl
38	466	9.2	362	4	US-08-637-670-37	Sequence 37, Appl
39	460.5	9.1	359	4	US-08-637-670-39	Sequence 39, Appl
40	459	9.1	350	4	US-08-637-670-25	Sequence 25, Appl
41	458	9.1	350	4	US-09-902-540-11278	Sequence 11278, A
42	440	8.7	680	4	US-09-602-777A-104	Sequence 104, App
43	391	7.5	867	4	US-09-248-796A-18160	Sequence 18160, A
44	379.5	7.5	242	4	US-09-270-767-44186	Sequence 44186, A
45	364.5	7.2	380	4	US-09-270-767-44186	Sequence 44186, A

ALIGNMENTS

RESULT 1
US-09-345-650-1
; Sequence 1, Application US/09345650
; Patent No. 6362324
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: 17867, A No. 6362324el Human Amino peptidase
; FILE REFERENCE: 5800-36
; CURRENT APPLICATION NUMBER: US/09/345.650
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 960
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-345-650-1

Query Match	100.0%;	Score	5052;	DB	3;	Length	960;
Best Local Similarity	100.0%;	Pred. No.	0;				
Matches	960;	Conservative	0;	Mismatches	0;	Indels	0;
						Gaps	0;
Qy	1	MFHSSAMVNSHRKPMFNIHRGFCYCLTALPOICQSFSPSSVHYFTEDPGAFPVATNGE	60				
Db	1	MFHSSAMVNSHRKPMFNIHRGFCYCLTALPOICQSFSPSSVHYFTEDPGAFPVATNGE	60				
Qy	61	RFPQQLRLPSVVIPLHYDLFVHPNLTSDFVASEKIEVLVSNATQFTILHSKOLEITNA	120				
Db	61	RFPQQLRLPSVVIPLHYDLFVHPNLTSDFVASEKIEVLVSNATQFTILHSKOLEITNA	120				
Qy	121	TLOSEEDSRYPKPKELKVLSPAEQIALVPEKLTPLHLYVYVAMDFQAKLGDGEGFY	180				
Db	121	TLOSEEDSRYPKPKELKVLSPAEQIALVPEKLTPLHLYVYVAMDFQAKLGDGEGFY	180				
Qy	181	KSTYRTLGGETRIILAVTDFTQARMAPPCDEPLFANFISIKIRRESRHIALSNMPKVK	240				
Db	181	KSTYRTLGGETRIILAVTDFTQARMAPPCDEPLFANFISIKIRRESRHIALSNMPKVK	240				
Qy	241	TIELEGGLEDHFTTVMSTYLVAIYVCDPHSLSGFTSGGVKSVIYASPKRNQTHVAL	300				
Db	241	TIELEGGLEDHFTTVMSTYLVAIYVCDPHSLSGFTSGGVKSVIYASPKRNQTHVAL	300				
Qy	301	QASIKLIDFYBKFDIYYPLSKLDLIAIPDPAPGAMENWGLIITYRETSLLPDKPTSSASD	360				
Db	301	QASIKLIDFYBKFDIYYPLSKLDLIAIPDPAPGAMENWGLIITYRETSLLPDKPTSSASD	360				
Qy	361	KLWTRVIAHSLAHQWFGNLTVMEMWMDIWLKEGFAKYMELIAVNATYPELQFDDYFLNV	420				
Db	361	KLWTRVIAHSLAHQWFGNLTVMEMWMDIWLKEGFAKYMELIAVNATYPELQFDDYFLNV	420				

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Qy 421 CFEVITKDSNSSRPIISKPAETPTQIOEMFDEVSYNKGACILANMLKDFLGEEKFOKGIQ 480
Db 421 CFEVITKDSNSSRPIISKPAETPTQIOEMFDEVSYNKGACILANMLKDFLGEEKFOKGIQ 480
Qy 481 YLKKFSYRNAKNDLWSLSNSCLESDFTSQGVCHSDPKMTSNMLAFIGNAEVKEKMTT 540
Db 481 YLKKFSYRNAKNDLWSLSNSCLESDFTSQGVCHSDPKMTSNMLAFIGNAEVKEKMTT 540
Qy 541 WTLOKGIPLLVKQDGCSRLRQBRFLQGVFQEDPEWRALQERYLWHPITUTYSTSSNVI 600
Db 541 WTLOKGIPLLVKQDGCSRLRQBRFLQGVFQEDPEWRALQERYLWHPITUTYSTSSNVI 600
Qy 601 HRHLKSKTDLDPKTSWKFVNSNGYIVHVEGHGWDOLITQLNQNHLLRPKDRV 660
Db 601 HRHLKSKTDLDPKTSWKFVNSNGYIVHVEGHGWDOLITQLNQNHLLRPKDRV 660
Qy 661 GLIHDVQLVAGRLTLDKALDMTYYLQHETSSPALLEGSLYLSFYHMDRRNISISE 720
Db 661 GLIHDVQLVAGRLTLDKALDMTYYLQHETSSPALLEGSLYLSFYHMDRRNISISE 720
Qy 721 NLKRYLQYFKPVIDRQSWSDKGSWDRMLRSALLKLACDLNHAPCIQKAELFSQWMS 780
Db 721 NLKRYLQYFKPVIDRQSWSDKGSWDRMLRSALLKLACDLNHAPCIQKAELFSQWMS 780
Qy 781 SGKLNIPDVLKIVYSGAQTACGNVYLLEYELSSSAEQNKLYALSTSKHOKLLKL 840
Db 781 SGKLNIPDVLKIVYSGAQTACGNVYLLEYELSSSAEQNKLYALSTSKHOKLLKL 840
Qy 841 IELGMEGVKIKTONLAALLHAIARRPKQQQLAWDFVRENTHLLKXFDLGSYDIRMIISG 900
Db 841 IELGMEGVKIKTONLAALLHAIARRPKQQQLAWDFVRENTHLLKXFDLGSYDIRMIISG 900
Qy 901 TTAHFSKDKLOEVKLPFESLEAGSHLDIFQTVLETITKNIKWLEKNLPTLRTWLVMT 960
Db 901 TTAHFSKDKLOEVKLPFESLEAGSHLDIFQTVLETITKNIKWLEKNLPTLRTWLVMT 960
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RESULT 2

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US-09-620-312D-1105
; Sequence 1105, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunqing
; APPLICANT: Wang, Duanrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 1105
; LENGTH: 948
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-620-312D-1105

Query Match 49.6%; Score 2507.5; DB 4; Length 948;
Best Local Similarity 50.9%; Pred. No. 1.7e-230;
Matches 476; Conservative 173; Mismatches 268; Indels 19; Gaps 7;

Qy 23 YCLTALPQICICQSPVSSYHFTEDPGAPVATNGERPFWOELRLPSVVIPLHYDLFV 82
Db 15 FLSSLLALTAV---STPSWCQSTE---ASPRKSDGTPEPMKIRLPEYVIPVHYDILI 67
Qy 83 HPNLTSLDFVASKEIVLSNATQFILHSKDLIEITNATLQSEEDSYMKPGKELKVS 142
Db 68 HANLTTLTFTWGTTKVITASOPTSTIILSHHLLQISRAILRKAGAGELSE--BPLQVLEH 125
Qy 143 PAHEQIALLVPEKLTPLHYVAMDFOAKLGDGFEFYKSTYRTLGGETRILAVTDPEPT 202
Db 126 PQEQIALLAPEPLLVGLPYTVVIHVAGNLSETFHGFYKSTYRTKEGELRILASTQPEPT 185
Qy 203 QARMAPCDEPLFKANFSIKIRRESRHIALSNMPKVKTIEGGLLEDHFETTVKMSY 262
Db 186 AARMAPCDEPLFKANFSIKIRRESRHIALSNMPKVKTIEGGLLEDHFETTVKMSY 245
Qy 263 LVAYIVCDPHSLSGTSSGVKSVIYASPKRNOYHALQALSLKLLDFEYKVFDIYPLSK 322
Db 246 LVAFIISDFESVSKITKSGVKSVYAVPKINQADYALDANVTLLLEFYEDYFIPPLPK 305
Qy 323 LDLIAPDPFAPGAWENGLITYRETSLLFPDKTSSASDKLWVTVRIAHELAHQWFGNLVT 382
Db 306 QDLAALPDPFQSGAWENGLITYRESALLFPAEKSSASSKLGITVTVAHELAHQWFGNLVT 365
Qy 383 MEWMDIWLKEGAKYKMWELIANNATYBELQFDYFLNVCFEVITKDSNSSRIPSKPAET 442
Db 366 MEWMDLWLNEGFAKMFVSVTHPELVGDFYFPGKCFDANMEVDALNSHSPVSTEVEN 425
Qy 443 PTQIQEMFDEVSYNKGACILANMLKDFLGEEKFOKGIQYLKFSYRNAKNDLWSLSNS 502
Db 426 PAQIREMFDVSYDKGACILANMLREYLSADAFKSGIVQYLKHSYKNTKKNEDLWDSNASI 485
Qy 503 CLESDFTSQ--GVCHSDPKMTSNMLAFIGNAEVKEKMTTWTLOKGIPLLVKQDGCSLR 560
Db 486 C-PTDGVKGMGDFC-SRSQHSSSSSHHWQGVGVKTMNTWTTLQRGFPPLITITVRGRNVH 543
Qy 561 LQOERFLQGVFQEDPEWRALQERYLWHPITUTYSTSSNVIHRLHILKSKTDLDPKETS 620
Db 544 MKOEHYMKG-----SDGAPDTGYLWHPVPLTFTITSKDMVHRFLKTKTDVLILPEVEW 597
Qy 621 VKFNVDNGYIIVHVEGHGWDOLITQLNQNHLLRPRKDRVGLIHDVQLVAGRLTLDKA 680
Db 598 IKFNVMNGYIIVHVEDDGDWDSLTGLLKGTHTAVSSNDRASLINNAFQLVSIKLSIEKA 657
Qy 681 LDMTYLQHETSSPALLEGSLYLSFYHMDRRNISIDISENLKRYLQYFKPVIDRQSW 740
Db 658 LDLSLYLKHETEIMPVFOGELNELIPMYKLMKEKDMNEVEVTFQKAFILRLDLIDKQWT 717
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Db 718 DEGSVSEQMLRSELLLLACVHNTPQCVQRAEGYFRKWKESNGNLSLPVDVTLAVFAVGAQ 777
Qy 801 TTAGMNYLLEQVELSSSAEQNKLYALSTSKHOKLLKLIELGMEGVKIKTONLAALLH 860
Db 778 STEGWDPLYSKYQFSLSTESKSIQIEFALCFTQNKELQLWLLDSSFKGDKIKTQEFQILT 837
Qy 861 AIARRPKQOQLAWDFVRENTHLLKXFDLGSYDIRMIISGTTAHPFSKDKLOEVKLPFES 920
Db 838 LIGRNPVGYPLAWQFLRKKNWKLQVQFELGSSSIAHVMVMTGTTNQFSTRTRLEEVKGFSS 897
Qy 921 LEAQSGSHLDIFQTVLETITKNIKWLEKNLPTLRTWL 956
Db 898 LKENGSQLRCVQQTITETIENIGMDKNFDKIRWL 933
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```
RESULT 3
US-08-530-792D-23
; Sequence 23, Application US/08530792D
; Patent No. 5972680
; GENERAL INFORMATION:
; APPLICANT: Knowles, W. J.; Guralaki, D.; Haigh, W.; Letsinger, J. T.;
; APPLICANT: Clairmont, K.; and Hart, J.
; TITLE OF INVENTION: Glucose Transporter Vesicle Amino-peptidase
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bayer Corporation
; STREET: 400 Morgan Lane
; CITY: West Haven
; STATE: Connecticut
; COUNTRY: U.S.A.
; ZIP: 06516
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" diskette, 1.44 Mb Storage
; COMPUTER: Dell Windows 95 PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/530,792D
; FILING DATE: 09/19/95
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/309,232
; FILING DATE: 09/20/94
; ATTORNEY/AGENT INFORMATION:
; NAME: Brewer, Alice A.
; REGISTRATION NUMBER: 32888
; REFERENCE/DOCKET NUMBER: MMH 323P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 812-2705
; TELEFAX: (203) 812-5492
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1025 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein;
; ORIGINAL SOURCE:
; ORGANISM: Rattus norvegicus
; STRAIN: Sprague-Dawley
; DEVELOPMENTAL STAGE: adult
; TISSUE TYPE: skeletal muscle
; IMMEDIATE SOURCE:
; LIBRARY: Clontech rat skeletal muscle cDNA library in lambda
; LIBRARY: gt11 and mRNA isolated from rat skeletal muscle
; CLONE: 12.1 (from lambda gt11 library), PCR product clones 5,
; CLONE: 334, and KC44.
; FEATURE:
; NAME/KEY: complete amino acid sequence for GTVap, long version
; IDENTIFICATION METHOD: translation from cDNA
US-08-530-792D-23
Query Match 40.1%; Score 2027; DB 2; Length 1025;
Best Local Similarity 44.4%; Pred. No. 2.2e-184;
Matches 402; Conservative 158; Mismatches 310; Indels 36; Gaps 5;
QY 54 PVATNGERFPWOELRPLSVIPLHYDLFVHPNLTSLDFVASEKIEVLVSNATQFIILHSK 113
DB 153 PIATNGKVPFPAQIRLPTAIIPQRYELSLHPNLTSMTRGVSITSLQALQDTRDILLAST 212
QY 114 DLEIYNATLQSEEDRYNPKGKLVLSYPAHEQIALLVPEKLTPLHLYKYVAMDPOAKLG 173
DB 213 GHNISVTFMSAVSSQ----ERQVEILEYVPVHEQIAVAPESLITGHNITLKIEYSANIS 268
QY 174 DGEFEGYKSTYTLGGETRIILAVTDFEPTQARMAPCEDEPLFKANFSIKIRRESHTAL 233
DB 269 NSYGYFGYITTDKSNKKNAATQFEPPLAARSAPPCDFEPAFKATFIKITRDEHHTAL 328
QY 234 SNMPKVTIIEGGLLEDHPFTTVMSTYLVAYIVCDFHSLSGFTSSGKVIYASPDKR 293
DB 329 SNMPKSSVPTTEGLIQDEFSESVMSTYLVAFIVGEMRNLSQ-DVNGTLYSVAVPDKI 387
QY 294 NOTHYALQASLKLDIFYEKYFDIYIPLSKLDLIAIPDFAPGAMENWGLITVRETSLFLDP 353
DB 388 DOYHALDTVTVKLLEFYQNYFEIQYPLKLDLVAIPDFEAGAMENWGLITFREETLLVDN 447
QY 354 KTSSASDKLVWTRVIAHELAHQWFGNLTVMWMDIWLKEGFAKYKMEILIAVNAVYPELOF 413
DB 448 ATSSVADKLVTKIIAHELAHQWFGNLTVMWMDLWLNIEGFATFMEYFSEKIFKELNS 507
QY 414 DDYFLNVCFEVITKDSLNSSRPISKPAETPOIOMEDFVSNKGACILNMLKDFLGBEK 473
DB 508 YEDFLDARFKTRKXDSLNSSHPITSSVSQSEIQIEEMFDSLSYFKGASLLMLKSYLSBDV 567
QY 474 FQKGIIOYLLKFKFSYRNAKNDLWSSLSNSCLESFTSGGVCHSDPKMTSNMLAFGENAE 533
DB 568 FQHAILLYLNHSYAAIQSDDLWDSFNE-----VTGKTLD 602
QY 534 VKEMMTTTLQKGIPLLVKQDGCRLQOBERFLQGVFQEDPEWRALQERYLMHIPLYS 593
DB 603 VKKMKTTTLQKGFPLVTQKGTGTELLLOQBERPPFSM---QPEIQDSDTSLHWHIPISYV 659
QY 594 TSSSNVTHRH---ILKSKTDTLDLPEKTSVWKNVDSNGYIIVHYEGHWDQLITQLNQN 650
DB 660 TGRNYSYRSVSLDKKSDVINLTQVQWVKVNTNMTGYIVHYAHGMAALINQLKRN 719
QY 651 HTLLRPKDRVGLIHDVOLFQVAGRLTLDKALDMTYIYLQHETSSPALLEGLSYFSFYHMM 710
DB 720 PYLSDKDRANLINNIIFELAGLGKVPLOMAPDLIDYLRNETHAPITALEFQTDLIYNLL 779
QY 711 DRNIDISENLKRYLLQYFKPVIDRQSWSDKSGVWDRMLRSALLKLACDLNHPACIOKA 770
DB 780 EKLGHMDLSSRLVTRVHKLLQNLQOQTQOQTTWDEGTPSMRELASALLEFACASLENCTWA 839
QY 771 AELFSQWMESSGKUNIPDVLKIVYSGAQTGANNYLLQEYELSMSAEONKILYALST 830
DB 840 TKLFDGWMASNGTQSLPTDVTMTTVFKVGARTEKGLFLFSYSSMGSAEKDKILEALAS 899
QY 831 SKHQEKLLKLIELGMEGVKIKTONLAALLHAIARRPKQQLAWDFVRENWTHLLKFPDLG 890
DB 900 SADAHKLYWLMKSSLDGDIIRTKQLSLIIRTVGRQFPFGLHLLANDFVRENWTHLLKFPDLG 959
QY 891 SYDIRMIISGTTAHHFSSKDKLQEVKLFESLEAGSHLDIFQTVLETITKNIKWLKXLP 950
DB 960 SYTIQSIVAGSTHFLSTKTHLSEVQEFFENQSEATLQRCVQEAPEVIELNIQWMAKLNK 1019
QY 951 TLRTWL 956
DB 1020 TLTWL 1025
RESULT 4
US-08-530-792D-22
; Sequence 22, Application US/08530792D
; Patent No. 5972680
; GENERAL INFORMATION:
; APPLICANT: Knowles, W. J.; Guralaki, D.; Haigh, W.; Letsinger, J. T.;
; APPLICANT: Clairmont, K.; and Hart, J.
; TITLE OF INVENTION: Glucose Transporter Vesicle Amino-peptidase
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bayer Corporation
; STREET: 400 Morgan Lane
; CITY: West Haven
; STATE: Connecticut
; COUNTRY: U.S.A.
; ZIP: 06516
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" diskette, 1.44 Mb Storage
; COMPUTER: Dell Windows 95 PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows 95
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/530,792D
; FILING DATE: 09/19/95
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/309,232
; FILING DATE: 09/20/94
; ATTORNEY/AGENT INFORMATION:
; NAME: Brewer, Alice A.
; REGISTRATION NUMBER: 32888
; REFERENCE/DOCKET NUMBER: MMH 323P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 812-2705
; TELEFAX: (203) 812-5492
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1025 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein;
; ORIGINAL SOURCE:
; ORGANISM: Rattus norvegicus
; STRAIN: Sprague-Dawley
; DEVELOPMENTAL STAGE: adult
; TISSUE TYPE: skeletal muscle
; IMMEDIATE SOURCE:
; LIBRARY: Clontech rat skeletal muscle cDNA library in lambda
; LIBRARY: gt11 and mRNA isolated from rat skeletal muscle
; CLONE: 12.1 (from lambda gt11 library), PCR product clones 5,
; CLONE: 334, and KC44.
; FEATURE:
; NAME/KEY: complete amino acid sequence for GTVap, long version
; IDENTIFICATION METHOD: translation from cDNA
US-08-530-792D-23
Query Match 40.1%; Score 2027; DB 2; Length 1025;
Best Local Similarity 44.4%; Pred. No. 2.2e-184;
Matches 402; Conservative 158; Mismatches 310; Indels 36; Gaps 5;
QY 54 PVATNGERFPWOELRPLSVIPLHYDLFVHPNLTSLDFVASEKIEVLVSNATQFIILHSK 113
DB 153 PIATNGKVPFPAQIRLPTAIIPQRYELSLHPNLTSMTRGVSITSLQALQDTRDILLAST 212
QY 114 DLEIYNATLQSEEDRYNPKGKLVLSYPAHEQIALLVPEKLTPLHLYKYVAMDPOAKLG 173
DB 213 GHNISVTFMSAVSSQ----ERQVEILEYVPVHEQIAVAPESLITGHNITLKIEYSANIS 268
QY 174 DGEFEGYKSTYTLGGETRIILAVTDFEPTQARMAPCEDEPLFKANFSIKIRRESHTAL 233
DB 269 NSYGYFGYITTDKSNKKNAATQFEPPLAARSAPPCDFEPAFKATFIKITRDEHHTAL 328
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Qy	206	MATPCFDEPLFKANFSIKIRRSRIHALSNMPKVKTIELBGGLLEHDIFETTVKQSYLVA	265
Db	229	KSFPCEDEPNKATYITISITHPKYGALSNMPVAKESVDKWTTRTTTFEKSVPMTSYLVC	288
Qy	266	YIIVCDPHSISGGFTSSGVKYSIYASPDKENQTHYALQASLKLKLLDFEYKFDIYYIPLSKLDL	325
Db	289	FAVHQFDSVKRISNSGKPUTIYVPEQKHQTAEBYAAANITKSVDYFEBYFAMNYSLPKLOK	348
Qy	326	IAIPDFAPGAMENWGLITVRETSLLFDPKTSSASDKLWTVTVIAHELHQAOWFGNLTMEW	385
Db	349	IAIPDFGCTGAMENWGLITVRETNLIYDPEKASASSNQORVATVVAHELWHQWFGNIVTMDW	408
Qy	386	WNDIWLKEGFAYKMELIAVNATYIPELQF--DDYFLNVCFEVTIKDSLNSRRSPISKPAETPT	444
Db	409	WEDLWLNIEGFASFEFLGVNHAETDQWRDQWLLLEDVLPQVEDDSLMSHPHIVTVITPD	468
Qy	445	QIOEMFDEYSYNGKACILNMLKDFLGEKBFQKGIQYLKFSYNAKNQDLSLNSLNSCL	504
Db	469	EITSVPDGISYSGKSSILRMLBDMTKPNFQKQGMVLEKYQFNKAKTSDFWAALBEA--	526
Qy	505	ESDFTSGGVCHSDPKWTSNMLAFLGENAEVEMWTTWTLQKIPLLVVKDGGCSLRLQE	564
Db	527	-----SRILPVEKVMWDTWTRQMGYPVLNV--NGVK-NITQK	558
Qy	565	RFQGVGFQBDPEWRALQE----RYLWHIPLATY---STSSSNVIRHILKSKTIDLDPK	617
Db	559	RFL-----DPRANFSQPPSDIGYTNVLPVKWTEDNITSSVLFNRSEKEGITLNSNPSG	613
Qy	618	TSVKNFVDSNGYIYVHVBEGHWQDLITQLNQNHITLRLPKDRVGLIHDFVQLVAGRLTL	677
Db	614	NAFLKINPDHIGFYRVNYEVATWDSIATLSLNKHTFSSADRASLIDDAFALARAQLLDY	673
Qy	678	DKALONTYYILOHETSS---PALLEGLSYLESGFYHMDRRNISDIENLKYLYLOYPKPIV	734
Db	674	KVALNLTLYLKREENPLPQWRVISAVTVIISWF-----EDDKELYPMIEEYFQGVKPIA	728
Qy	735	DROSWDKGSVDWDRMLRSALLKLACDLNHAFCIOKAALFQWMESSGKLNIPDVLKIV	794
Db	729	DSLGWMDAGDHVTKLRRSSVLGFACMGKGDREALNNASLSFEQWIL--NGTYSFVNRLIIV	786
Qy	795	YSYGAOTTA--GWNYYLEQYELSSSAEONKILVALSTSKHQBKLKLKJELGMEGVKIK	851
Db	787	YRYGMQNSGNEISWNTLEEQYKTSIAGQEKELIYGLASVKNVTLBRYLDLKLKOTNLIK	846
Qy	852	TQMLAALLHAIARRPKGOQLAWDFVRENTWTHLLKAKKFDLGSYDIRMIISGTTAHFFSKDKL	911
Db	847	TQDVFVIRIYSVNSYGNKMANWVQLNWDYLVNRYTLNRRNLGRIVT-IAEFPNTELQJL	905
Qy	912	QEVKLPFESLEAQQSHLDFIQTVLETTITIKNIKWLEKNLPLTRTW	955
Db	906	WOMESFFAKYPOAGAGEKPREOVLSTVKNNIELWIKOHRNITREW	949

RESULT 6

US-09-949-016-7431
; Sequence 7431, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0

Db 560 TLSQEHFLL-----DPDSNVTSPSEPNVYVPIITSIRDRGQQQDWLIDVRAQNDLFSFT 611

Qy 595 SSSNVIRHILKSKTDTLDPKTSNVKFNVDNSGYIIVHYEGHGWQDLITQLNQNHLL 654

Db 615 SGN-----EWLLNLNVTCYRVYNDENWRKTIQTQLQORDHSAI 653

Qy 655 RPKDRVGLIHDVPQVAGRLTDLKALDMYTYLQHTETSSPALLEGISYLESPYHMDRRN 714

Db 654 PVINRAQIINDAFNLASAHKVPVTLALNNTLFLIBERQYMPWEAALSSLSYFKLMFDR-- 711

Qy 715 ISDISENKXYLLQYFKPVI-----DRQSWSD-KGSVWDRMLRSALLKLADLNHAPCIQ 768

Db 712 -SEVYGPKNYLKKQVTPLFIFHRNNTNNRREIPENLMDQYSEVNAISTACNSGVPECEE 770

Qy 769 KAAELFSQWMESSGKLNIPITDVLKIVY--SVGAQTTAGNYYLLEQYELSMSSAEQNKILY 826

Db 771 MYSGLFQWQWENPNPNPIHPNLRSTVYCNAIAQGESEWDPAWEQFRNATLVNEADKLRA 830

Qy 827 ALSTSKHQBLKLJELGMEGVKIKTONLAALLHAIARRPKGQQLAWDFVRNTHLLKK 886

Db 831 ALACSKELWILNRYLSYTLNPLIRKQDATSTIISITNNVIGQGLVWDFVQSNMVKLFND 890

Qy 887 FDLGSDYDIRMIIISGTTAHPSSKDKQEVKLPPESLEAQ--GSHLDIFQTVLETITNKKM 944

Db 891 YGGGSEFSFNLIQAVTRFSTYEYLOQEQFKDNEETFGSGGTRALSOALEKTKANIKW 950

Qy 945 LEKNLPTLRITLWMVNT 960

Db 951 VKENKEVLQWFTENS 966

RESULT 8

US-09-659-786-201

; Sequence 201, Application US/09659786

; Patent No. 6491894

; GENERAL INFORMATION:

; APPLICANT: Ruoslahti, Erkki

; APPLICANT: Pasqualini, Renata

; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing

; TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using

; TITLE OF INVENTION: Same

; FILE REFERENCE: P-LJ 3203

; CURRENT APPLICATION NUMBER: US/09/659,786

; CURRENT FILING DATE: 2000-09-11

; PRIOR APPLICATION NUMBER: 08/926,914

; PRIOR FILING DATE: 1997-09-10

; PRIOR APPLICATION NUMBER: 08/710,067

; PRIOR FILING DATE: 1996-09-10

; NUMBER OF SEQ ID NOS: 226

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 201

; LENGTH: 967

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-659-786-201

Query Match 25.0%; Score 1264.5; DB 3; Length 967;

Best Local Similarity 31.4%; Pred. No. 2.2e-111;

Matches 325; Conservative 158; Mismatches 386; Indels 167; Gaps 26;

Qy 20 RGYFCULTAI-----LPQICICSFSPSSYHFTEDPGAPVVA----- 56

Db 3 KGFYISKSGILGILLGVAACVTIIALSVVYQEKKNANSSPVASTTSPASATTNPASA 62

Qy 57 -TNGERFPQWELRLSPVPLHLVPLVHNLTSLD-----FVASKIEVLVSNATQFIIL 110

Db 63 TTLDSQKAMNRYRLNPLKPDYSQVTLRPLYTPNDRGLYVFKGSSVTRFTCKEATDVIII 122

Qy 111 HSKOLEITNATLQSEDSRYMKPGKELVLSY-----PAHEQIALLVP-EKLTPLHK-- 161

Db 123 HSKLNYT-----LSQGRHVLRVGGSGQPPDIIDKTELVEFTEYLVVHLKGS 170

Qy 162 -----YVAMDFQAKLGDGFGFYKSTYRTLTGGETRIILAVTDFEPTQARMAFFCPDEPLF 216

Db 171 VKDSQYEMDSEFEGELADDLAGFYRSEYME-GNVRKVATTQMOAADARKSPCFDEPAM 229

Qy 217 KANFSTKIRRESHIALSNM-PKVKTIELEGGLLED-----HFETTVMNSTYLVAIVTC 269

Db 230 KAEFNITLIHPKDLTALSNNLKPGRPTLP-----EDPNMNVTEFHTTPKMSTYLLAFIVS 285

Qy 270 DFHSLSGFTSSGVKSVIYASDPKKNQTH--YALQASLKLDFEYKYFDIYVPLSKLDLIA 327

Db 286 EFDYVSKQASNGVLIIRIWARPSAIAAGHDYALNVTGPIINFAGHYDTPPLPKSDQIG 345

Qy 328 IPDFAPGAMENWGLIYRTSLFLDPKTSASDKLWTVRIAHELAWHGFNGLVMTMEWN 387

Db 346 LPDFNAGAMENWGLIYRNSLLFDPKSSSSNKERVTVVIAHELAWHGFNGLVMTMEWN 405

Qy 388 DIWLKGGFKAKMELIANNATYPELOPDDYF-LNVCFEVTIKDLSNLRSPISKPA---ETP 443

Db 406 DLWNEGFASYEVLGADYAEPTNWLKOLWLNVDVRYMAVDALASSHPLSTPASEINTP 465

Qy 444 TOIQEMFEVSNKGACILNMLKDFGESEKFGKIIOYLKFSYRNKNDLWLSL----- 499

Db 466 AQISELFDAYSISKSGASVLRMLSSFLSEDFVFKGLASLYLHTFAYQNTIYTLNWLHQB 525

Qy 500 SNSCLESDFTSGGVCHSDPKMTSNMLAFLEGNAEYKEMTWTTLQKGIPLVWQDGCGL 559

Db 526 NNRSIQLPIT-----VRDINRWTLQMGFEVITV--DTSTG 559

Qy 560 RLOQERFLQGVFOEDPE---WRALQRYLWHIPLT-----YST 594

US-09-139-802-201

Query Match 25.0%; Score 1264.5; DB 3; Length 967;

Best Local Similarity 31.4%; Pred. No. 2.2e-111;

Matches 325; Conservative 158; Mismatches 386; Indels 167; Gaps 26;

Qy 20 RGYFCULTAI-----LPQICICSFSPSSYHFTEDPGAPVVA----- 56

Db 3 KGFYISKSGILGILLGVAACVTIIALSVVYQEKKNANSSPVASTTSPASATTNPASA 62

Qy 57 -TNGERFPQWELRLSPVPLHLVPLVHNLTSLD-----FVASKIEVLVSNATQFIIL 110

Db 63 TTLDSQKAMNRYRLNPLKPDYSQVTLRPLYTPNDRGLYVFKGSSVTRFTCKEATDVIII 122

Qy 111 HSKOLEITNATLQSEDSRYMKPGKELVLSY-----PAHEQIALLVP-EKLTPLHK-- 161

Db 123 HSKLNYT-----LSQGRHVLRVGGSGQPPDIIDKTELVEFTEYLVVHLKGS 170

Qy 162 -----YVAMDFQAKLGDGFGFYKSTYRTLTGGETRIILAVTDFEPTQARMAFFCPDEPLF 216

Db 171 VKDSQYEMDSEFEGELADDLAGFYRSEYME-GNVRKVATTQMOAADARKSPCFDEPAM 229

Qy 217 KANFSTKIRRESHIALSNM-PKVKTIELEGGLLED-----HFETTVMNSTYLVAIVTC 269

Db 230 KAEFNITLIHPKDLTALSNNLKPGRPTLP-----EDPNMNVTEFHTTPKMSTYLLAFIVS 285

Qy 270 DFHSLSGFTSSGVKSVIYASDPKKNQTH--YALQASLKLDFEYKYFDIYVPLSKLDLIA 327

Db 286 EFDYVSKQASNGVLIIRIWARPSAIAAGHDYALNVTGPIINFAGHYDTPPLPKSDQIG 345

Qy 328 IPDFAPGAMENWGLIYRTSLFLDPKTSASDKLWTVRIAHELAWHGFNGLVMTMEWN 387

Db 346 LPDFNAGAMENWGLIYRNSLLFDPKSSSSNKERVTVVIAHELAWHGFNGLVMTMEWN 405

Qy 388 DIWLKGGFKAKMELIANNATYPELOPDDYF-LNVCFEVTIKDLSNLRSPISKPA---ETP 443

Db 406 DLWNEGFASYEVLGADYAEPTNWLKOLWLNVDVRYMAVDALASSHPLSTPASEINTP 465

Qy 444 TOIQEMFEVSNKGACILNMLKDFGESEKFGKIIOYLKFSYRNKNDLWLSL----- 499

Db 466 AQISELFDAYSISKSGASVLRMLSSFLSEDFVFKGLASLYLHTFAYQNTIYTLNWLHQB 525

Qy 500 SNSCLESDFTSGGVCHSDPKMTSNMLAFLEGNAEYKEMTWTTLQKGIPLVWQDGCGL 559

Db 526 NNRSIQLPIT-----VRDINRWTLQMGFEVITV--DTSTG 559

Qy 560 RLOQERFLQGVFOEDPE---WRALQRYLWHIPLT-----YST 594

US-09-139-802-201

Query Match 25.0%; Score 1264.5; DB 3; Length 967;

Best Local Similarity 31.4%; Pred. No. 2.2e-111;

Matches 325; Conservative 158; Mismatches 386; Indels 167; Gaps 26;

Qy 20 RGYFCULTAI-----LPQICICSFSPSSYHFTEDPGAPVVA----- 56

Db 3 KGFYISKSGILGILLGVAACVTIIALSVVYQEKKNANSSPVASTTSPASATTNPASA 62

Qy 57 -TNGERFPQWELRLSPVPLHLVPLVHNLTSLD-----FVASKIEVLVSNATQFIIL 110

Db 63 TTLDSQKAMNRYRLNPLKPDYSQVTLRPLYTPNDRGLYVFKGSSVTRFTCKEATDVIII 122

Qy 111 HSKOLEITNATLQSEDSRYMKPGKELVLSY-----PAHEQIALLVP-EKLTPLHK-- 161

Db 123 HSKLNYT-----LSQGRHVLRVGGSGQPPDIIDKTELVEFTEYLVVHLKGS 170

Qy 162 -----YVAMDFQAKLGDGFGFYKSTYRTLTGGETRIILAVTDFEPTQARMAFFCPDEPLF 216

Db 171 VKDSQYEMDSEFEGELADDLAGFYRSEYME-GNVRKVATTQMOAADARKSPCFDEPAM 229

Qy 217 KANFSTKIRRESHIALSNM-PKVKTIELEGGLLED-----HFETTVMNSTYLVAIVTC 269

Db 230 KAEFNITLIHPKDLTALSNNLKPGRPTLP-----EDPNMNVTEFHTTPKMSTYLLAFIVS 285

Qy 270 DFHSLSGFTSSGVKSVIYASDPKKNQTH--YALQASLKLDFEYKYFDIYVPLSKLDLIA 327

Db 286 EFDYVSKQASNGVLIIRIWARPSAIAAGHDYALNVTGPIINFAGHYDTPPLPKSDQIG 345

Qy 328 IPDFAPGAMENWGLIYRTSLFLDPKTSASDKLWTVRIAHELAWHGFNGLVMTMEWN 387

Db 346 LPDFNAGAMENWGLIYRNSLLFDPKSSSSNKERVTVVIAHELAWHGFNGLVMTMEWN 405

Qy 388 DIWLKGGFKAKMELIANNATYPELOPDDYF-LNVCFEVTIKDLSNLRSPISKPA---ETP 4

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Db 171 VKDSQYEMDSEPEGELADDLAFGYSEYME-GNVRKVATTQMQAADARKFPFCDEPAM 229
Qy 217 KANFIFIKIRRESRHIALSNM-PKVTIELEGGLD-----HFETTVMSTYLVAYIVC 269
Db 230 KAENFNIILHPKDLTALSNMLPKGSTPLP-----EDPNWVTEFHTTPKMSTYLLAFIVS 285
Qy 270 DPHLSUGFTSSGVKSVISVASDPKRNQTH--YALQASLKLLDFYKYFYDIYVPLSKLDLIA 327
Db 286 EFDYVEKQASNGVLIRIWARPSAIAAGHGDIYALNVTGPIILNFFAGHYDTPYLPKSDQIG 345
Qy 328 IPDFAPGAMENWGLTYRETSLLDPKTSASDKLWTRVIAHELAWHGFNLVTMEWN 387
Db 346 LPDFNAGAMENWGLTYRENSLLDFPLSSSSNKERVVTVIAHELAWHGFNLVTIEWN 405
Qy 388 DIWLKEGFAKYMELAVNATPELQDDYF-LNVCFEVTIKDLSNRRPISGKPA---ETP 443
Db 406 DLMLNEGFAVYVYLGADYAEFTWNLKDLWLVNDVYRVWADALASSHPLSTPASEINTP 465
Qy 444 TQIQEMFDEVSNKGACILNMLKDFLGBEKFQKGIQYKFKPSYRNKNDLWSSL----- 499
Db 466 AQISELFAISYSGASVLRMLSSFLSBDVFKGLASYLHTFAYQNTIYLNLDHQLQBAV 525
Qy 500 SNSCLESDFTSQGVCHSDPKMTSNMLAFLGENAEVKENMTWTLOKGIPLLVKODGCSL 559
Db 526 NNRISQLPTT-----VRDIMNRWTLQMGPFVITV--DTSTG 559
Qy 560 RLQQRERFQGVQEDPE---WRALQERYLWHIPLT-----YST 594
Db 560 TLSQEHFLL-----DPDSNVTRPSEFNWVIVPITSIRDRGQQQDYMLDVRAQNDLFST 614
Qy 595 SSSNVHHRHILKSKTDLTLPEKTSWVKFNVDNSGYIIVHYEGHGWQDLITQLNQNHTLL 654
Db 615 SGN-----EWLLNLNVGYRVNYDEENWRKIQTQLQRDHSAI 653
Qy 655 RPKRVGLIHDVQLVGAGRLTLDKALDMTYYLQHETSSPALLEGSLYLESFYHMMDRN 714
Db 654 PVINRAQINDAFNLASAHKVPVTLANTLFLIEERQYMPWEAALSSLSYFKLMPDR-- 711
Qy 715 ISDISENLKRYLQYFKPVI-----DROSWD-KGSVWDRMLRSALLKLACDLNHAPCIQ 768
Db 712 -SEVYGPKNYLLKKQVTLFLHFRNTNNWREIPENLMDQYSEVNAISTACNGVPECEE 770
Qy 769 KAAELFSQWMESSGKINLPTDVLKIV--SVGAQTTAGNNYLLQYELSMSAEQNKILY 826
Db 771 MVSGLFKQWENPNPNPIHPNLRSTVYCNATAQGGEEEDFAWEQFRNATLVNEADKLRA 830
Qy 827 ALSTSKHQEKLKLIELGHEGKVIKTONLAALLHAIARRPKQOQLAWDFVRENWTHLKK 886
Db 831 ALACSKELWILNRYLSYTLNPLIRKQDATSTIISITNNVIGQGLVWDFVQSNMKKLPND 890
Qy 887 FDLGSDYRMIISGTTAHFSSKDLQEVKLPFESLEAQ--GSHLDIFOTVLETITKNIKW 944
Db 891 YGGGSFSSNLQIQTARFSTFEYELQLEQFKQKNEETGFGSGTALQALEKTKANIKW 950
Qy 945 LEKNLPTLRTWLMVNT 960
Db 951 VKENKEVVQLWFTENS 966
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RESULT 9

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US-09-919-039-222
; Sequence 222, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
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; SOFTWARE: PERL Program
; SEQ ID NO 222
; LENGTH: 919
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6727066 2278688CD1
US-09-919-039-222
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Query Match

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24.2%; Score 1225; DB 4; Length 919;
Best Local Similarity 32.6%; Pred. No. 1.2e-107; Indels 126; Gaps 26;
Matches 309; Conservative 163; Mismatches 351;
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Qy 55 VATGERFPQBELRPSVVIPLHYDLFVHPNLTSLDFVASEKIEVL--VSNATQFIILHS 112
Db 42 LAAMPEKRPEE--RLPADVSPINCSLCKPDL--LDFTFECKLEAAAQVRQATNQIVMNC 97
Qy 113 KDLBITNATLQSEDSRYMKPG-----KELKVLSTYPAHEQIALLVPEKLTPLHKYVYAM 166
Db 98 ADIDIITASYAPEGDEBEIHATGFNYQNEDEKVTLSFPSTLQTG-----TGTLLK----I 146
Qy 167 DFOAKLGDGPEGFYKSTYRTLGGETRILAVTDFPPTOARMAPPFCDFDEPLKXANFSIKIRR 226
Db 147 DFGELNDKMGKFRSKYTTSPSGEVRYAANTQPEATDARRAFPCWDEPAIKATPDISLVV 206
Qy 227 ESRHIALSNMPKV--KTIELEGGLEDHFETTVKMYSTYLVAYIVCDFHSLSGFTSSGVKV 284
Db 207 PKDRVALSNMVIDRKVPDDENLVEVKFARTVMSTYLVAFVVGVEYDFVETRSDKGVCV 266
Qy 285 SIYASPKRQNTYHALQASLKLLDFYKYFYDIYVPLSKLDLIAIPDFAPGAMENWGLTY 344
Db 267 RVTYTPVGAEGKQFALVAAKTLPFYKDYFNVPYPLPKIDLIAIADFAAGAMENWGLVTV 326
Qy 345 RETSLLDPKTSASDKLWTRVIAHELAWHGFNLVTMEWNNDIWLKEGFAKYMELIAY 404
Db 327 RETALLDPKNSCSSQWVALVGHCHLAHGFNLVTMEWHTLWLNNEGFAWIEYLCV 386
Qy 405 NATYPELQFDDYFLNVCFEVTIK--DSLNSRRPISKPAETPTQIQEMFDEVSNKGACILN 463
Db 387 DHCPEYDIWTFVYSADYTRAQELDALDNSHPIEVSVGHPEVDEIFDAISYSGASVIR 446
Qy 464 MLKDFLEBEPKGIQIYKFKPSYRNKNDLWLSNLSLESDFTSQGVCHSDPKMTSN 523
Db 447 MLHDYIGKDFPKGKNMYLTKFQKNAATEDLWESLENA----- 485
Qy 524 MLAFLGENAEEVEMMTWTLOKGIPLLVK--ODGCSRLQOBERPLOG--VFQEDPE 576
Db 486 -----SGKPIAAVNTWTQMGFFLIYVEAEQVEDDLRLLSQKFCAGSYVGEDCPQ 539
Qy 577 WRALQERYLWHIPLTYSTSSS-NVIHRHILKSKTD---TLDLPEKTSWVKFNVDNSGYI 632
Db 540 WM-----VPITISTSEDPNQAKLKILMDKPEMNVVLKNVVPDQWVKLNLGTGVFYR 590
Qy 633 VHYEGHGWQDLITQLNQNHTLLRPKDRVGLIHDVQLVGAGRLTLDKALDMTYYLQHETS 692
Db 591 TQYSSAMLESLLPGIRD--LSLPEVDRLGLQNDLFLSARAGII----- 631
Qy 693 SPALLEGSLYLESFYHMMDRNRNIDIS-----ENLKRYLLQYKPKFVIDR 736
Db 632 --STVEYKWNFAFNPEPNYTVWSDLSNGLSTLSLHTDFYEEIQEFVKDVFSPIGER 689
Qy 737 QSWSDK--GSVWDRMLRSALLKLACDLNHAPCIQKAAELFSQWMESSGKINLPTDVLKI 793
Db 690 LGWDPKPEGHL--DALLRGLVLGKLGAGHKATLEEARRRPKDHVE--GKQILSADLRSP 746
Qy 794 VYSV----GAQTTAGNNYLLQYELSMSAEONKILYALSTSKHQEKLKLIELGMEKV 849
Db 747 VYLTVLKHGDTTL--DIMLKLHKQADMQEBEKNRIERVGLATLPLDLTKQLVLTFALESSEV 804
Qy 850 IKTONLAALLHAIARRPK-GOQLAWDFVRENWTHLKKFGLDGSYDIRMIISGTTAHFSSK 908
Db 805 -RPQDTVSVIGGVAGGSKHGRKAANKFIKDNWEELYNRYQ--GGFLISRLIKLSVEGFAVD 862
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QY 909 DKLOEVKLFPSLEAQGSHLDIFOTVLETTITKNIKWLEKNLPTLRTWLM 957
DB 863 KMAEVAKAFESHAPSARTI-QCCENILLNANLKRDAESHQYLL 910

RESULT 10
US-08-335-844A-22
; Sequence 22, Application US/08335844A
; Patent No. 6066503
; GENERAL INFORMATION:
; APPLICANT: GRAHAM, MARGARET
; APPLICANT: SMITH, TREVOR STANLEY
; APPLICANT: MUNN, EDWARD ALBERT
; APPLICANT: KNOX, DAVID PATRICK
; APPLICANT: OLIVER, JOANNA JANE
; APPLICANT: NEWTON, SUSAN ELIZABETH
; TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING
; TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE
; TITLE OF INVENTION: VACCINES AGAINST HELMINTH INFECTIONS
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz
; STREET: Suite 701-E, 555 Thirteenth St., N.W
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/335,844A
; FILING DATE: 09-JAN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB PCT/GB93/00943
; FILING DATE: 06-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9209936
; FILING DATE: 08-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: WALKER, Barbara W.
; REGISTRATION NUMBER: 35,400
; REFERENCE/DOCKET NUMBER: 1181-223A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)783-6040
; TELEFAX: (202)783-6031
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 977 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-335-844A-22

Query Match 23.1%; Score 1165; DB 3; Length 977;
Best Local Similarity 29.2%; Pred. No. 7.7e-102;
Matches 280; Conservative 192; Mismatches 411; Indels 76; Gaps 21;

QY 39 SVPSYHT-----EDGAPVATNGRFPWQELRPSVPIPLHYDLFVH---PNL 86
DB 41 SIGLYTFYTRKAFDTGTGNGGQDPVDDNSPSA-BELRLPTTKPLTYDLIVITKLPNY 99
QY 87 TSL-----VFSEKIEVLVSNATQFIILHSDLEITNATLQSEDSRYMKPGK 135
DB 100 VNYPEKDFADGTGVIAEVVE-----PTKSIVLNSKNIPV--IAQCELFSSNNQKLDI 152
QY 136 ELKVLSPAHQIALLVPEKUTPHLYKYVAMDQAKLGDGEGFYKSTYRTLGGETILA 195
DB 153 E-KVVDQPRLEKVEFLVKKLKNQKITLKIIVYIGLINDMLGGLYRTYTTDKDGTAKIAA 211

QY 196 VTDPEPTQARMAPCPDEPLFKANFSIKIRRSRRIALSNNPKVKTTELGGLLEHPEF 255
DB 212 CTWEPDARLWVCPDEPTFKANVTVIHPKGTSAVNGIEKGEVSGDWTTTFDP 271
QY 256 TVRMSTYLVAYIVCDPHSLSGFTSSGVKVSIIYASPKRQNTHYALQASLKLDPYKYFD 315
DB 272 TRMPSYLIJALVISSEPKYIENYTKSGVRPPIPARPEAMKMTYAMIAIGICLDYVEFPF 331
QY 316 IYPLSKLDLIAJDPDPAGAMENGLITYRETSLLPDPKTTSSASDKLWTRVTAHELAHQ 375
DB 332 IKFPLPKQDMVALPDFSSGAMENGLITYREGSVLYDENLYGPMNKERVAEVIHAELAQ 391
QY 376 WFGNLVTMEWMDIWLKEGFAKYMELIAVNATYPEL-QFDDYFLNVCF-EVITKDSNSS 433
DB 392 WFGNLVTMKWMDNLWLNNEGPAFVEYIGADFISDGLWEMKDFLLAPYTTSGITADAVASS 451
QY 434 RPISKPAETQIQEMFDEVSYNKGACILNMLKDFLGBEKFQKGIIOYLKFSYRNAKND 493
DB 452 HPLSPRIDKAADVSEAFDDITYRKGAQVQLMNLNLVGDENFKQSVSRYLKFSYDAAA 511
QY 494 DLWSSLSNSCLESDFTSGGVCHSDPKWTSNMLAFGENAEVEMMTTWTLOKGIPLLVK 553
DB 512 DLWAAF-----DETVOGI--TCPN-----GGPLKMSFAPQWTTQMGFPVLTV 553
QY 554 Q-DGCSLRLQOERFLOGVFOEDPE-WRALQERYLWHIPLTYSTSSSNVIHRHLKSKTDT 611
DB 554 SVNATTLKVTKYRQNKDAKEPEKYRHPYTGKWDVPLWYQDEQQVKETLWKREPLY 613
QY 612 LDLPEKTSWYKFNVDNNGYIVHYEGHGWDPOLITQLNQNHLLRPKDRVGLIHDVQLVG 671
DB 614 FHVSNSDSSVVNAERRAPCRSNYDANGWRNIMRLKQNHKVYGPRTNALISDAFAAAA 673
QY 672 AGRITLDKALDMTYILOHETSSPALLEGSLYSFHYHMDRNRISDISENLKRYLLQYFK 731
DB 674 VEEMNYETVEMLKYTVKEEDYLPWKBAIS---GFNTILDFGSEPESEWASEYMRKLMK 730
QY 732 PVIDROS-----WSDKGSVMDRLRSALLKLACDLNHAPCIQKAAELFSQ-----W 777
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QY 778 MESSGKLNIPTDLKIVYVGAQT--TAGWNYLLEQYELSMSSAAQNKILYALSTSKHQE 835
DB 791 QOATDCVKVTAPLRKTVYCYGVQEGDEAFDKVMELYNAREQVLEKDSREALGCHKDVT 850
QY 836 KLIKLELQME--GKVIKTONLAALHAIARRPKGOOLANDFVRENWTHLLKKFDLGSYD 893
DB 851 ALKGLMLALDRNSSFVRLQDAHDVFNIVSRNPVGNELFNFLTERMEEILESIRHRS 910
QY 894 IRMTISGTTAHSKDKLOEVKLFPSLEAQGSHLDIFOTVLETTITKNIKWLEKNLPTL 952
DB 911 VDRVIKACTRLRSREQVQLKNLYKN-DKAREYGNAGAIERSEHRVKNIEKHFKL 968

RESULT 11
US-09-129-366-22
; Sequence 22, Application US/09129366
; Patent No. 6534638
; GENERAL INFORMATION:
; APPLICANT: GRAHAM, MARGARET
; APPLICANT: SMITH, TREVOR STANLEY
; APPLICANT: MUNN, EDWARD ALBERT
; APPLICANT: KNOX, DAVID PATRICK
; APPLICANT: OLIVER, JOANNA JANE
; APPLICANT: NEWTON, SUSAN ELIZABETH
; TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING
; TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE
; TITLE OF INVENTION: VACCINES AGAINST HELMINTH INFECTIONS
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz
; STREET: Suite 701-E, 555 Thirteenth St., N.W
; CITY: Washington

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STATE: D. C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/129.366
FILING DATE: 05-AUG-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/335,844
FILING DATE: 09-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB PCT/GB93/00943
FILING DATE: 06-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9209936
FILING DATE: 08-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, Barbara G.
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1181-241A
TELEPHONE: (202)783-6040
TELEFAX: (202)783-6031
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 977 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-129-366-22

Query Match 23.1%; Score 1165; DB 4; Length 977;
Beat Local Similarity 29.2%; Pred. No. 7.7e-102;
Matches 280; Conservative 192; Mismatches 411; Indels 76; Gaps 21;

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QY 87 TSL-----VASEKIEVLVSNAQPIILHSKDLITNATLQSEEDSRVMPKPK 135
DB 100 VNPPEKDAIDGTGVIAEVE-----PTKSLVLSKNIPV--IADQCELFNNQKLDI 152
QY 136 ELKVLSPAEHQIALLVPEKLTPLHLYVYVAMPQAKLGGPEGFYKSTYRILGGETRILA 195
DB 153 E-KVVDQPRLEKVEFLVKKLEKQKITLKIYVIGLINDMLGGLYRTTYTDKDGTTKIAA 211
QY 196 VTDEPTQARMAFCFDEPLKANKFSIKIRRESRIHALSNMPKVTIELEGLLDHFET 255
DB 212 CTHMEPTARLMPVCFDEPTFKANVTVIHPKGTSAVNSGIEKGEVSGDWVTTREDP 271
QY 256 TVKMSYLVAVYICVDFHSLGTSVSGVKVSIYASPDKRNQTHYALQASIKLIDFYEKYFD 315
DB 272 TPRMPSYIALVISEFKYIENYKSGVRFPARPPEAMKWTEYAMIGIKCLDYEDFG 331
QY 316 IYPLSKLIDLTAIPDPAFAGAMENWGLITYRFTSLFPDKPTSASDKLWTRVIAHELAHQ 375
DB 332 IKFPLPKQDMVALPDPSSGAMENWGLITYREGSVLYDENLYGPMNKERVAEIVIAHELAHQ 391
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QY 434 RPIKPAETPTQIQBMFVEVSNYKACILNMLKDFLGEKFKQGIQYLVKFSYRNAKND 493
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QY 494 DLWSSLSNCSLESDFTSQGVCHSDPKMTSNMLAFLGENAEVKEMMTTWTLOKGIPLLVK 553

;
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/335,844
; FILING DATE: 09-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB PCT/GB93/00943
; FILING DATE: 06-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9209936
; FILING DATE: 08-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, Barbara G.
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1181-241A
; TELEPHONE: (202)783-6040
; TELEFAX: (202)783-6031
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 977 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-335-844-24
; Sequence 24, Application US/08335844A
; Patent No. 6065503
; GENERAL INFORMATION:
; APPLICANT: GRAHAM, MARGARET
; APPLICANT: SMITH, TREVOR STANLEY
; APPLICANT: MUNN, EDWARD ALBERT
; APPLICANT: KNOX, DAVID PATRICK
; APPLICANT: OLIVER, JOANNA JANE
; APPLICANT: NEWTON, SUSAN ELIZABETH
; TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING
; TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE PREPARATION OF
; TITLE OF INVENTION: VACCINES AGAINST HELMINTH INFECTIONS
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz
; STREET: Suite 701-E, 555 Thirteenth St., N.W
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/335,844A
; FILING DATE: 09-JAN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB PCT/GB93/00943
; FILING DATE: 06-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9209936
; FILING DATE: 08-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: WALKER, Barbara W.
; REGISTRATION NUMBER: 35,400
; REFERENCE/DOCKET NUMBER: 1181-223A
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QY 845 MEGKVIKTONLAALLHATARRPKGOQLANDPVRENWTHLLKKFDLGSYDIRMIIISGTTAH 904

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Job time : 49 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
OM protein - protein search, using sw model
Run on: September 26, 2005, 06:03:27 ; Search time 1880 Seconds
(without alignments)
207.843 Million cell updates/sec

Title: US-10-039-073-1
Perfect score: 5052
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1826554 seqs, 407025358 residues

Total number of hits satisfying chosen parameters: 1826554

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5052	100.0	960	13 US-10-039-073-1	Sequence 1, Appli
2	5052	100.0	960	14 US-10-168-475-6	Sequence 6, Appli
3	4141	82.0	785	15 US-10-363-616-459	Sequence 459, App
4	3799	75.2	728	9 US-09-764-853-646	Sequence 646, App
5	3770	74.6	722	9 US-09-764-853-819	Sequence 819, App
6	2516.5	49.8	941	15 US-10-220-443-2	Sequence 2, Appli
7	2515.5	49.8	941	15 US-10-264-237-2723	Sequence 2723, App
8	2515.5	49.8	941	18 US-10-472-533-329	Sequence 329, App
9	2515.5	49.8	944	14 US-10-106-698-6381	Sequence 6381, Ap
10	2512.5	49.7	941	9 US-09-989-722-353	Sequence 353, App
11	2512.5	49.7	941	9 US-09-989-723-353	Sequence 353, App

12	2512.5	49.7	941	9	US-09-989-279-353	Sequence 353, App
13	2512.5	49.7	941	9	US-09-989-727-353	Sequence 353, App
14	2512.5	49.7	941	9	US-09-989-731-353	Sequence 353, App
15	2512.5	49.7	941	9	US-09-989-732-353	Sequence 353, App
16	2512.5	49.7	941	9	US-09-991-073-353	Sequence 353, App
17	2512.5	49.7	941	9	US-09-990-442-353	Sequence 353, App
18	2512.5	49.7	941	9	US-09-991-163-353	Sequence 353, App
19	2512.5	49.7	941	9	US-09-993-604-353	Sequence 353, App
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21	2512.5	49.7	941	9	US-09-989-721-353	Sequence 353, App
22	2512.5	49.7	941	9	US-09-992-598-353	Sequence 353, App
23	2512.5	49.7	941	9	US-09-989-293A-353	Sequence 353, App
24	2512.5	49.7	941	9	US-09-989-735-353	Sequence 353, App
25	2512.5	49.7	941	9	US-09-990-444-353	Sequence 353, App
26	2512.5	49.7	941	9	US-09-991-181-353	Sequence 353, App
27	2512.5	49.7	941	9	US-09-989-730-353	Sequence 353, App
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33	2512.5	49.7	941	10	US-09-989-728-353	Sequence 353, App
34	2512.5	49.7	941	10	US-09-990-441-353	Sequence 353, App
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36	2512.5	49.7	941	10	US-09-997-428-353	Sequence 353, App
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38	2512.5	49.7	941	10	US-09-990-438-353	Sequence 353, App
39	2512.5	49.7	941	10	US-09-990-562-353	Sequence 353, App
40	2512.5	49.7	941	10	US-09-990-711-353	Sequence 353, App
41	2512.5	49.7	941	10	US-09-989-726-353	Sequence 353, App
42	2512.5	49.7	941	10	US-09-998-156-353	Sequence 353, App
43	2512.5	49.7	941	10	US-09-990-437-353	Sequence 353, App
44	2512.5	49.7	941	10	US-09-991-157-353	Sequence 353, App
45	2512.5	49.7	941	10	US-09-997-514-353	Sequence 353, App

ALIGNMENTS

RESULT 1
US-10-039-073-1
; Sequence 1, Application US/10039073
; Publication No. US20020098177A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: 17867, A No. US20020098177A1el Human Aminopeptidase
; FILE REFERENCE: 35800/240749(5800-36
; CURRENT APPLICATION NUMBER: US/10/039,073
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 09/345,650
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 960
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-073-1

Query Match 100.0%; Score 5052; DB 13; Length 960;
Best Local Similarity 100.0%; Pred. No. 0;
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Db 121 TLQSEEDSRYPKPGKELKVLSPYAHEQIALLVPEKLTPLHKYVYVAMDFQAKLGDGFGFY 180
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Qy 241 TIELEGGLEDHFFETTVKMSYLVAYIVCDPHSLSGFTSSGVKVSIVASDPKRNQTHYAL 300
Db 241 TIELEGGLEDHFFETTVKMSYLVAYIVCDPHSLSGFTSSGVKVSIVASDPKRNQTHYAL 300
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Qy 421 CFEVITKDSLNSRRPISKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGEKEFKGIIQ 480
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RESULT 2

US-10-168-425-6
; Sequence 6, Application US/10168425
; Publication No. US20030124706A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YANG, Junning
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: BURFORD, Neil
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: REDDY, Roopa
; APPLICANT: YUE, Henry
; APPLICANT: NGUYEN, Dannie B.
; APPLICANT: TANG, Y. Tom
; APPLICANT: YAO, Monique G.
; APPLICANT: LAL, Preeti

; TITLE OF INVENTION: PROTEASES
; FILE REFERENCE: PI-0003 PCT
; CURRENT APPLICATION NUMBER: US/10/168,425
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/172,055; 60/177,334; 60/178,884; 60/179,903
; PRIOR FILING DATE: 1999-12-23; 2000-01-21; 2000-01-28; 2000-02-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PERL Program
; SEQ ID NO 6
; LENGTH: 960
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030124706A1 60116897CD1
US-10-168-425-6

Query Match 100.0%; Score 5052; DB 14; Length 960;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 960; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MFHSSAMVNSHRKPMNIHRGFYCLTAILPOICICQSFSPSSVYHFTEDPGAPVATNGE 60
Db 1 MFHSSAMVNSHRKPMNIHRGFYCLTAILPOICICQSFSPSSVYHFTEDPGAPVATNGE 60
Qy 61 RFPWQELRLPSVVIPLHYDLFVHPNLTSLDFVASEKIEVLVSNATQFIILHSDKLEITNA 120
Db 61 RFPWQELRLPSVVIPLHYDLFVHPNLTSLDFVASEKIEVLVSNATQFIILHSDKLEITNA 120
Qy 121 TLQSEEDSRYPKPGKELKVLSPYAHEQIALLVPEKLTPLHKYVYVAMDFQAKLGDGFGFY 180
Db 121 TLQSEEDSRYPKPGKELKVLSPYAHEQIALLVPEKLTPLHKYVYVAMDFQAKLGDGFGFY 180
Qy 181 KSTYRTLGGETRIILAVTDPEFTQARMAPCDEPLFKANFISIKIRRESRHIALSNMPPVK 240
Db 181 KSTYRTLGGETRIILAVTDPEFTQARMAPCDEPLFKANFISIKIRRESRHIALSNMPPVK 240
Qy 241 TIELEGGLEDHFFETTVKMSYLVAYIVCDPHSLSGFTSSGVKVSIVASDPKRNQTHYAL 300
Db 241 TIELEGGLEDHFFETTVKMSYLVAYIVCDPHSLSGFTSSGVKVSIVASDPKRNQTHYAL 300
Qy 301 QASLKLDLFYKYFDIYYPLSKLDLIAIPDPAPGAMENWGLITYRETSLLFPDKTSSASD 360
Db 301 QASLKLDLFYKYFDIYYPLSKLDLIAIPDPAPGAMENWGLITYRETSLLFPDKTSSASD 360
Qy 361 KLWTRVIAHSLAHQWFGNLTVMWMDIWLKEGFAKYMELIAVNATYPELQPDYFLNV 420
Db 361 KLWTRVIAHSLAHQWFGNLTVMWMDIWLKEGFAKYMELIAVNATYPELQPDYFLNV 420
Qy 421 CFEVITKDSLNSRRPISKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGEKEFKGIIQ 480
Db 421 CFEVITKDSLNSRRPISKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGEKEFKGIIQ 480
Qy 481 YLKKFSYRNKNDLWSSLNSCLESDFTSGGVCHSDPKMTSNMLAFGENAEVKEMWTT 540
Db 481 YLKKFSYRNKNDLWSSLNSCLESDFTSGGVCHSDPKMTSNMLAFGENAEVKEMWTT 540
Qy 541 WTLQKGIPLLVKQDGCSSLRLQOERFLQGVQEDPEWRALQERYLWHIPLTYSTSSNVI 600
Db 541 WTLQKGIPLLVKQDGCSSLRLQOERFLQGVQEDPEWRALQERYLWHIPLTYSTSSNVI 600
Qy 601 HRHILKSKTDTLDLPEKTSWVKFNVDNSNGYIYVHVEGHGWDLITQLNQNHLLRPKDRV 660
Db 601 HRHILKSKTDTLDLPEKTSWVKFNVDNSNGYIYVHVEGHGWDLITQLNQNHLLRPKDRV 660
Qy 661 GLIHDVFLQVAGRLTLDKALDMTYYLQHETSSPALLEGLSYLESFYHMDRRNISDI 720
Db 661 GLIHDVFLQVAGRLTLDKALDMTYYLQHETSSPALLEGLSYLESFYHMDRRNISDI 720
Qy 721 NLKRYLLOQYFKPVIDROSWSKGSVWDRMLRSALLKLACDLNHAPCIQKAELFSQWMS 780
Db 721 NLKRYLLOQYFKPVIDROSWSKGSVWDRMLRSALLKLACDLNHAPCIQKAELFSQWMS 780

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QY 781 SGKLNPTDVLKIVSVGAQTAGWNLYLLEQVELSMSSAEONKILYALSTSHQKLLKL 840
DB 781 SGKLNPTDVLKIVSVGAQTAGWNLYLLEQVELSMSSAEONKILYALSTSHQKLLKL 840
QY 841 IELHMEGKVIKTONLAALHAJARPKGOOLAWDFVRENWTHLLKKFDLGSYDIRMIISG 900
DB 841 IELHMEGKVIKTONLAALHAJARPKGOOLAWDFVRENWTHLLKKFDLGSYDIRMIISG 900
QY 901 TTAFFSSKDKLQEVKLFPFESLAQSGSHLDIFQTVLETTITKNIKLEKNLPTLRTWLWMT 960
DB 901 TTAFFSSKDKLQEVKLFPFESLAQSGSHLDIFQTVLETTITKNIKLEKNLPTLRTWLWMT 960

RESULT 3
US-10-363-616-459
; Sequence 459, Application US/10363616
; Publication No. US20040044181A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-113 (793)
; CURRENT APPLICATION NUMBER: US/10/363,616
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 09/654,935
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 490
; SEQ ID NO 459
; LENGTH: 785
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-616-459

Query Match 82.0%; Score 4141; DB 15; Length 785;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 782; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFHSSAMVNSHRKPMFNHHRGYCYCTAILPQICISQFSVPSSYHFTDPCGAPPVATNGE 60
DB 1 MFHSSAMVNSHRKPMFNHHRGYCYCTAILPQICISQFSVPSSYHFTDPCGAPPVATNGE 60
QY 61 RPPWQELRLPSVVIPLHYDLFVHPNLTSLDFVASEKIEVLVSNATQFIILHKSQLEITNA 120
DB 61 RPPWQELRLPSVVIPLHYDLFVHPNLTSLDFVASEKIEVLVSNATQFIILHKSQLEITNA 120
QY 121 TIQSEDSRYMKPGKELVLSYPAHEQIALLVPEKLTPLHLYVAMDFQAKLGDGEGFY 180
DB 121 TIQSEDSRYMKPGKELVLSYPAHEQIALLVPEKLTPLHLYVAMDFQAKLGDGEGFY 180
QY 181 KSTYRTLGETRILAVTDPPTQARMAPCPDEPLFKANFSIKIRRESRHIALSNMPKVK 240
DB 181 KSTYRTLGETRILAVTDPPTQARMAPCPDEPLFKANFSIKIRRESRHIALSNMPKVK 240
QY 241 TIEEGGLLEDFHFTTVKMSTYLVAYIVCDPHSLSGFTSSGVKVIYASPKRNQTHYAL 300
DB 241 TIEEGGLLEDFHFTTVKMSTYLVAYIVCDPHSLSGFTSSGVKVIYASPKRNQTHYAL 300
QY 301 QASLKLLDPYEKYFDIYYPLSKLDLIAIPDFAPGAMENWGLITYRETSLLFPDKTSSASD 360
DB 301 QASLKLLDPYEKYFDIYYPLSKLDLIAIPDFAPGAMENWGLITYRETSLLFPDKTSSASD 360
QY 361 KLWVTRVIAHELAHQWFGNLTVMWVNDIWLKEGPAKYMELIAVNATYPELQDDYFLNV 420
DB 361 KLWVTRVIAHELAHQWFGNLTVMWVNDIWLKEGPAKYMELIAVNATYPELQDDYFLNV 420
QY 421 CFEVITKDSLSNRPIKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGEKFKQGI 480
DB 421 CFEVITKDSLSNRPIKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGEKFKQGI 480
QY 481 YLKKEFSYRNAKNDLLWSSLSNSCLESDFTSGGVCHSDPKMTSNMLAFGENAEVKEKMTT 540
DB 481 YLKKEFSYRNAKNDLLWSSLSNSCLESDFTSGGVCHSDPKMTSNMLAFGENAEVKEKMTT 540
QY 541 WTLQKGIPLLVVKQDGCSSLRLOQERFLQGVFQEDPEWRALQERYLWHIPLTYSTSSNNVI 600
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DB 541 WTLQKGIPLLVVKQDGCSSLRLOQERFLQGVFQEDPEWRALQERYLWHIPLTYSTSSNNVI 600
QY 601 HRHILKSKTDTLDLPEKTSWVKFNVDNGYIIVHYEGHWDQLITQLNQNHHTLLRPKDRV 660
DB 601 HRHILKSKTDTLDLPEKTSWVKFNVDNGYIIVHYEGHWDQLITQLNQNHHTLLRPKDRV 660
QY 661 GLIHDVFLQVAGRLTLDKALDMTYIYLOHETSSPALLEGSLYLSFYHMDRRNISDISE 720
DB 661 GLIHDVFLQVAGRLTLDKALDMTYIYLOHETSSPALLEGSLYLSFYHMDRRNISDISE 720
QY 721 NLKRYLQYKPKVTDROSWSKGSVMDRMLRSALLKLACDLNHAAPCIQKAAELFSQWMS 780
DB 721 NLKRYLQYKPKVTDROSWSKGSVMDRMLRSALLKLACDLNHAAPCIQKAAELFSQWMS 780
QY 781 SGKL 784
DB 781 SGKL 784

RESULT 4
US-09-764-853-646
; Sequence 646, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P0206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 646
; LENGTH: 728
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-853-646

Query Match 75.2%; Score 3799; DB 9; Length 728;
Best Local Similarity 100.0%; Pred. No. 2,1e-295;
Matches 722; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 239 VKTIEGGLLEDFHFTTVKMSTYLVAYIVCDPHSLSGFTSSGVKVIYASPKRNQTHY 298
DB 7 VKTIEGGLLEDFHFTTVKMSTYLVAYIVCDPHSLSGFTSSGVKVIYASPKRNQTHY 66
QY 299 ALQASLKLLDPYEKYFDIYYPLSKLDLIAIPDFAPGAMENWGLITYRETSLLFPDKTSSA 358
DB 67 ALQASLKLLDPYEKYFDIYYPLSKLDLIAIPDFAPGAMENWGLITYRETSLLFPDKTSSA 126
QY 359 SDKLWVTRVIAHELAHQWFGNLTVMWVNDIWLKEGPAKYMELIAVNATYPELQDDYFL 418
DB 127 SDKLWVTRVIAHELAHQWFGNLTVMWVNDIWLKEGPAKYMELIAVNATYPELQDDYFL 186
QY 419 NVCPEVITKDSLSNRPIKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGEKFKQGI 478
DB 187 NVCPEVITKDSLSNRPIKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGEKFKQGI 246
QY 479 IQYLKKEFSYRNAKNDLLWSSLSNSCLESDFTSGGVCHSDPKMTSNMLAFGENAEVKEKMM 538
DB 247 IQYLKKEFSYRNAKNDLLWSSLSNSCLESDFTSGGVCHSDPKMTSNMLAFGENAEVKEKMM 306
QY 539 TTWTLQKGIPLLVVKQDGCSSLRLOQERFLQGVFQEDPEWRALQERYLWHIPLTYSTSSNN 598
DB 307 TTWTLQKGIPLLVVKQDGCSSLRLOQERFLQGVFQEDPEWRALQERYLWHIPLTYSTSSNN 366
QY 599 VIHRLKSKTDTLDLPEKTSWVKFNVDNGYIIVHYEGHWDQLITQLNQNHHTLLRPK 658
DB 367 VIHRLKSKTDTLDLPEKTSWVKFNVDNGYIIVHYEGHWDQLITQLNQNHHTLLRPK 426
QY 659 RVGLIHDVFLQVAGRLTLDKALDMTYIYLOHETSSPALLEGSLYLSFYHMDRRNISDI 718
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Db 427 RVGLIHDVFLVGVGRLTLDKALDWTYYLQHTSSPALLGLEGLSYLESFYHMMDRRNISDI 486
Qy 719 SENLKRYLLQYFKPVIDRQSWSDKGSVWDRMLRSALLKLACDLNHAPCIQKAAELFSQWM 778
Db 487 SENLKRYLLQYFKPVIDRQSWSDKGSVWDRMLRSALLKLACDLNHAPCIQKAAELFSQWM 546
Qy 779 ESSGKLNIPDVLKIVYSGVGAQTAGWNYLLEQYELSMSSAEQNKILYALSTSKHQEKLL 838
Db 547 ESSGKLNIPDVLKIVYSGVGAQTAGWNYLLEQYELSMSSAEQNKILYALSTSKHQEKLL 606
Qy 839 KLIELGMEGVKIKTONLAALLHAIARRPKGQQLAWDFVRENWTHLLKKFDLGSYDIRMII 898
Db 607 KLIELGMEGVKIKTONLAALLHAIARRPKGQQLAWDFVRENWTHLLKKFDLGSYDIRMII 666
Qy 899 SGTTAHFSSKDKLOEVKLPFESLEAQGSHLDIFQTVLETTITKNIKWLEKNLPTLRTWLMV 958
Db 667 SGTTAHFSSKDKLOEVKLPFESLEAQGSHLDIFQTVLETTITKNIKWLEKNLPTLRTWLMV 726
Qy 959 NT 960
Db 727 NT 728

RESULT 5
US-09-764-853-819
; Sequence 819, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 819
; LENGTH: 722
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (237)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (296)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (719)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (720)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (721)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-853-819

Query Match 74.6%; Score 3770; DB 9; Length 722;
Best Local Similarity 99.3%; Pred. No. 4.3e-293;
Matches 717; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 239 VKTIELEGGLEDHFETTVKMTSLVYVIVCDPHSLGFTSSGVKVSIVYASPDKRNOTHY 298
Db 1 VKTIELEGGLEDHFETTVKMTSLVYVIVCDPHSLGFTSSGVKVSIVYASPDKRNOTHY 60
Qy 299 ALQASLKLLDFEYKFDIYYPLSKLDLIAIPDFAPGAMENWGLITYRETSLFPDKTSSA 358
Db 61 ALQASLKLLDFEYKFDIYYPLSKLDLIAIPDFAPGAMENWGLITYRETSLFPDKTSSA 120
Qy 359 SDKLVWTRVIAHELAHQWFGNLVMEWWDNIWLKEGFAKYMELIAVNAATPELOFDDYFL 418
Db 121 SDKLVWTRVIAHELAHQWFGNLVMEWWDNIWLKEGFAKYMELIAVNAATPELOFDDYFL 180
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Qy 419 NVCFEVITKDSLNSRRPIKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGBEKFQKGI 478
Db 181 NVCFEVITKDSLNSRRPIKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGBEKFQKGI 240
Qy 479 IOYLKXFSYRNAKNDLWSSLSNCSLESDFTSQGVCHSDPKMTSNMLAFLGENAEVKEMM 538
Db 241 IOYLKXFSYRNAKNDLWSSLSNCSLESDFTSQGVCHSDPKMTSNMLAFLGENAEVKEMM 300
Qy 539 TTWTLOKGIPLLVKQDGCSLRLQOERFLOQVQEDPEWRALQERYLWHIPLTYSTSSN 598
Db 301 TTWTLOKGIPLLVKQDGCSLRLQOERFLOQVQEDPEWRALQERYLWHIPLTYSTSSN 360
Qy 599 VIHRHILKSKTDTLDLPEKTSWVKFNVDNSGYIVHYEGHGWDLITQLNQNHLLRPKD 658
Db 361 VIHRHILKSKTDTLDLPEKTSWVKFNVDNSGYIVHYEGHGWDLITQLNQNHLLRPKD 420
Qy 659 RVGLIHDVFLVGVGRLTLDKALDWTYYLQHTSSPALLGLEGLSYLESFYHMMDRRNISDI 718
Db 421 RVGLIHDVFLVGVGRLTLDKALDWTYYLQHTSSPALLGLEGLSYLESFYHMMDRRNISDI 480
Qy 719 SENLKRYLLQYFKPVIDRQSWSDKGSVWDRMLRSALLKLACDLNHAPCIQKAAELFSQWM 778
Db 481 SENLKRYLLQYFKPVIDRQSWSDKGSVWDRMLRSALLKLACDLNHAPCIQKAAELFSQWM 540
Qy 779 ESSGKLNIPDVLKIVYSGVGAQTAGWNYLLEQYELSMSSAEQNKILYALSTSKHQEKLL 838
Db 541 ESSGKLNIPDVLKIVYSGVGAQTAGWNYLLEQYELSMSSAEQNKILYALSTSKHQEKLL 600
Qy 839 KLIELGMEGVKIKTONLAALLHAIARRPKGQQLAWDFVRENWTHLLKKFDLGSYDIRMII 898
Db 601 KLIELGMEGVKIKTONLAALLHAIARRPKGQQLAWDFVRENWTHLLKKFDLGSYDIRMII 660
Qy 899 SGTTAHFSSKDKLOEVKLPFESLEAQGSHLDIFQTVLETTITKNIKWLEKNLPTLRTWLMV 958
Db 661 SGTTAHFSSKDKLOEVKLPFESLEAQGSHLDIFQTVLETTITKNIKWLEKNLPTLRTWLMV 720
Qy 959 NT 960
Db 721 XT 722

RESULT 6
US-10-220-443-2
; Sequence 2, Application US/10220443
; Publication No. US20030215820A1
; GENERAL INFORMATION:
; APPLICANT: Levine, Stewart
; TITLE OF INVENTION: REGULATORS OF TYPE-1 TUMOR NECROSIS FACTOR RECEPTOR AND OTHER CYTOKINES
; TITLE OF INVENTION: RECEPTOR SHEDDING
; FILE REFERENCE: 218732
; CURRENT APPLICATION NUMBER: US/10/220,443
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06464
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/185,586
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 2
; LENGTH: 941
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-220-443-2

Query Match 49.8%; Score 2516.5; DB 15; Length 941;
Best Local Similarity 51.1%; Pred. No. 2.4e-192;
Matches 478; Conservative 171; Mismatches 268; Indels 19; Gaps 7;

Qy 23 YCITAILPQICISQFSPSSHYFTDPGAFPPVATNGERPPQOELRLPSVVIPLHYDLFV 82
Db 15 FLUSLLALLTV----STPSWCQSTE---ASPKRSQGTGTPPPMKNKIRLPEVIPHYVDLLI 67
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Qy	921	LEAGSHLDIQTVLETTIKNWKLEKMLPTLRWL	956
Dd	898	LKENGSQLRCVQQTIETIEENIGMWDKNFDRVWL	933
 RESULT 8 US-10-472-533-329			
; Sequence 329, Application US/10472533			
; Publication No. US20050197285A1			
; GENERAL INFORMATION:			
; APPLICANT: Human Genome Sciences, Inc.			
; TITLE OF INVENTION: Human Secreted Proteins			
; FILE REFERENCE: PS906PCT			
; CURRENT APPLICATION NUMBER: US/10/472,533			
; CURRENT FILING DATE: 2003-09-20			
; PRIOR APPLICATION NUMBER: US 60/331,287			
; PRIOR FILING DATE: 2001-11-13			
; PRIOR APPLICATION NUMBER: US 60/306,171			
; PRIOR FILING DATE: 2001-07-19			
; PRIOR APPLICATION NUMBER: US 60/277,340			
; PRIOR FILING DATE: 2001-03-21			
; NUMBER OF SEQ ID NOS: 650			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 329			
; LENGTH: 941			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-472-533-329			
 Query Match 49.8%; Score 2515.5; DB 18; Length 941;			
Best Local Similarity 51.0%; Pred. No. 2.9e-192;			
Matches 477; Conservative 172; Mismatches 268; Indels 19; Gaps 7;			
Qy	23	YCLTAIPLQICISQFSVPSSYHTEDEGAFVATNGSRFPWQELRLPSVVIPHYDLFV	82
Dd	15	FLSSLLALLIV---STPSNCQSTE---ASPKRSDGTFFPNKKIRLPEYVIPHYDILLI	67
Qy	83	HPNLTSLDIFVASEKIEVLVSUNATOFIIILHSKDLEITNATLOSEBDSRWKPGKEIKULSY	142
Dd	68	HANEUTLTTFWGVTTKVEITASOPTSTIILSHHLQISRATLRKGAGERLSE--EPLQVLEH	125
Qy	143	PAHQIALLVPEKLTPHLKYVVMDFQAKLGDFEGFYKSYRTLGGTRILAVTDREPT	202
Dd	126	PQEQIALLAEPLLVGLPYTVTHYAGLSLSETFHGFYSKSYRWEGBRLRLASTQFEPT	185
Qy	203	QARMAFPCEDEPLFKANFSIKIRRESRHIALSNMPKVKTILEGGLLEDHFETTVMNSTY	262
Dd	186	AARMAFPCEDEPAFKASFISKIRREPRLAISNMPLVKSVTVAEGLIEDHFDVTVMNSTY	245
Qy	263	LVAVICDPFSLSGFTSCGVKSIVYASDPKNQTHYALQASLKLLDFYEKYFDIYYPLSK	322
Dd	246	LVAFIISDFESVSKITKSGVKSVYAVDPKNQADYALDAATAVTLLEFYEDYFSPYLPKP	305
Qy	323	LDLIAIDPFAFGAMENWGLITYRETSLLDPKTSSASKLWTRVIAHELAHOWFNGLVT	382
Dd	306	QDLAAIDPFQSGAMENWGLITYREGALLDFAEKSASSKLGITWTVAHELAHOWFNGLVT	365
Qy	383	MEWNIDLWKEGFARYKAMELIANVATYPQLQDDYFLNVCFEVIKDSLNSRPISKPAET	442
Dd	366	MEWNIDLWNSGFAKFMEFVSVSTHPELKVGDYFFGKCFDAMEVDALNSSHPVSTPVEN	425
Qy	443	PTQIQEMPDENVYNGACIILMKDXDFLGEERFKGIIOYLKFKFSRYNAKNDLWSLSNS	502
Dd	426	PAQIREMFDDVSYPDKGACILNNLREYLSADAFKGIYOYLQKHSYKNTKNEDLMSMASI	485
Qy	503	CLESDFTSG--GVCHSDPDKMTSNMLAFLGENAEVKEMMTTWTLQXGIPLLVVKQDGCSLR	560
Dd	486	C-PIDVGKMGDGFC-SRSQHSSSSSHWHQEGRVDVKTMMNTWTLQRGFPFIITVRGRNVH	543
Qy	561	LQQRFLQGVQFQEPENRALQERYLWHIPLTYSTSSSNVHIRHLKSKTDTLDLPEKTSW	620
Dd	544	MKBHYMKG-----SDCAPDTGYLHWVPLRFITFSKSDMWRHFLKTKTDVLLIPPEEVW	597

Qy	621	VKNVDSNGYIYVHYEGHWQDLITQLNQNHITLRPKDVRGLIHDVFLVGAGRLTLDKA	580
		: : : : : : : : : :	
Db	598	IKFNVMNGYIYVHYEDDGDWDLTGLLKTRHTAVSSNDRASLINNAFQLVSTIGKLSIEKA	657
		: : : : : : : : :	
Qy	681	LDMTYILQHETSSPALLEGLSYLSFVHYHMDRRNISDKRYLLQVFKPVIDRQWS	740
		: : : : : : : : :	
Db	658	LDLSLYLKHETEMPVQGLNELIPMYKLMKRDKNVEVETQFKAPLIRLLRLDIDKQWT	717
		: : : : : : : : :	
Qy	741	DKGSVDMRLRSALLKLACDLNHAPCTQKAAELFSQMMESSGKLNIPTDVLKIVYSVGAQ	800
		: : : : : : : : :	
Db	718	DEGSVSEMLRSELLLLACVHNYQCVQRAEGYFRKWKESNGNLSPDVDTLAVFAVGAQ	777
		: : : : : : : : :	
Qy	801	TTAGWNYLLFQYELSMSAEQNKLYALSTSKHQBKLLKLELHGEGKVIKTONLAALLH	860
		: : : : : : : : :	
Db	778	STEGWDFLYSKYQFSLSTESKTEQFALCRTQNKKEKLQWLDESFGDKIKTQEPQILT	837
		: : : : : : : : :	
Qy	861	AIARRPKGQQLAWDFVRENTHLLKLPDLGSYDIRMIISGTTAHFSSKDKLQEVKLPES	920
		: : : : : : : : :	
Db	838	LIGNPVGYPLAWQFLRNNWKLQKFLGSSSAHVMGNTNQFSTRLEEVKGFFSS	897
		: : : : : : : : :	
Qy	921	LEAQGSHLDIFQTVLETTITRNKLEKNLPTLRTWL	956
		: : : : : : : : :	
Db	898	LKENGSQLRCVQQTITETIENIGWKNDFKIRVWL	933
		: : : : : : : : :	
RESULT 9			
US-10-106-698-6381			
; Sequence 6381, Application US/10106698			
; Publication No. US20030109690A1			
; GENERAL INFORMATION:			
; APPLICANT: Ruben et al.			
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Peptides			
; FILE REFERENCE: PA005P1			
; CURRENT APPLICATION NUMBER: US/10/106,698			
; CURRENT FILING DATE: 2002-03-27			
; PRIOR APPLICATION NUMBER: PCT/US00/26524			
; PRIOR FILING DATE: 2000-09-28			
; PRIOR APPLICATION NUMBER: US 60/157,137			
; PRIOR FILING DATE: 1999-09-29			
; PRIOR APPLICATION NUMBER: US 60/163,280			
; PRIOR FILING DATE: 1999-11-03			
; NUMBER OF SEQ IDS: 8564			
; SOFTWARE: PatentIn Ver. 3.0			
; SEQ ID NO 6381			
; LENGTH: 944			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-106-698-6381			

best local similarity	31.0%;	Fied. NO. 4.98-194;	
Matches	477;	Conservative	172;
Mismatches	268;	Indels	19;
Gaps	7;	TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides;	
APPLICANT: RUBEN ET AL.		TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides;	

Qy	323	LDLIAIPDPFAPGAMENWGLITVRETSLAPDPKTSASDCKLWTVRIAHELAHQFNGLVTT	392
Db	309	QDUAAIPDFQSGAMENWGLITVRESALLPDAEKSASSKUGITWVAHLEAHQFNGLVTT	368
Qy	383	MEWNNDIWLKEGFYAKYMEIIAYNATYIPELQFDDYPLANVCEVITTKDSLNSRSPISPAET	442
Db	369	MEWNNDLWLNBEFAYKFMFEPVSVSVTHPELKYVDGYFFGKCFDAMEVDALNSHPVSTPEVN	428
Qy	443	PTQIQEMFDEVSYNVKGACILNNLDFLGBEEFQKGILOYLKKSRYRANKNDLWLSLNS	502
Db	429	PAQIREMFODVSYDKGACILNNMLREIYLSADAFKGI VOYLQKHSYKNTKNEIDLWDSWASI	488
Qy	503	CLESDFTSG--GVCHSDPKMTSNMLAFIAGENAEVKEMMTTWTLQKIGPLLVVQDQCSLR	560
Db	489	C-PTDGVKMGDGC-FSRSHSSSSHHMQHGVGVKTMWNTWTLQRGFPPLITITVRGRNVH	546
Qy	561	LOQERFLQGVFOEDPEWALQERYLWHIPLIYTSSSNVHRHLKSKTTDLDPKTSW	620
Db	547	MKEOEHYMKG-----SDGAPDTGYLWVHVPILFTYSKDMVHRFLKTKTDLVTLPLBEVEM	600
Qy	621	VKFNVDNSGYIYVHYEGHGWDOILITQLNQNHITLRLPKDRVGLIHDVQLVQAGRLTLDKA	680
Db	601	IKFNVMGNGYIYVHYEDDGDWSDLTGLLKGTHTAVSSNDRASLINNAFQVLSIGKLSIEKA	660
Qy	681	LDWTTYLQHETSSPALLEGLSYLSBFYHMDRRNISDIENLKYLLQYKFPVIDRQSW	740
Db	661	LDLSLYLKHETIMPVQFQGNELIPMYKLMKEKDMNEVEYTFQKAFILRLRLDILDKQTWT	720
Qy	741	DKGSVMDRLRSALLKACLADLNHAPCIQKAAELFSQWMESSGKLINPTDVLKTVYSGVQAQ	800
Db	721	DEGSVSEMLRSELLELLACVHNYQECVQABGYFRKWKESENGLSLPVDVTLAVFVGAQ	780
Qy	801	TTAGVNYLLEQVELSMSSAEQNKIYALYSTKHQEKLLKLIELGMBGKVIKTQNLAALLH	860
Db	781	STEGMDPLYSKYQFSLSSSTKSQIEFALCRTQNKELQWLDDSFQKDKIKTQFFQIILT	840
Qy	861	AIARRPKGOOLAWDFVRENWTHLLKKFDLGSYDTRMIISGTTAHFSSKDKLQBVKLPFFS	920
Db	841	LIGENPVGYPLAQFLRKNNWKLQKFLPGLSSSAHVMVMTTQGFSTRFLEEBEVKGFPS	900
Qy	921	LEAQGSHLDIQTVLVETTTKNIKWLEKNLPTLRTWL	956
Db	901	LKENGSQLRCVOQTTEIENIGWMDKNFDIRVWL	936

RESULT 10
US-09-989-722-353

; Patent No. US2002007
; GENERAL INFORMATION:

APPLICANT:	Ashkenazi, Avi J.
APPLICANT:	Baker, Kevin P.
APPLICANT:	Botstein, David
APPLICANT:	Desnoyers, Luc
APPLICANT:	Eaton, Dan L.
APPLICANT:	Ferrara, Napoleone
APPLICANT:	Fong, Sherman
APPLICANT:	Gerber, Hanspeter
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APPLICANT:	Watanabe, Colin K.
APPLICANT:	Williams, P. Mickey

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, PRIOR FILING DATE: 1998-07-09

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Query Match 49.7%; Score 2512.5; DB 9; Length 941;
Best Local Similarity 51.0%; Pred. No. 5.1e-192;
Matches 477; Conservative 172; Mismatches 268; Indels 19;

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83	QY	HNPLNSLDPVASEKIEVLVSNATOFIILHSKOLEITNATLOSEEDSRYPKPGKELKVL5Y	142
68	Db	HANLVTLLTFWGTVKVEITASOPTSTIILHSHHLOISRATLRKAGKERLSE--EPLQVLEH	125
143	QY	PAHEQIALLVPEKLTPLPHLKYYVAMDFOAKLGDGPEGFYKSTYRTLGGETRILAVTDPEPT	202
126	Db	PPQEQIALLAPEPLLVLGYPTVVHYAGNLSETHFGYKSTYRTKGEGLRLASTOQEP	185
203	QY	QARMAFFCFDDEPLFKANFSIKIRRESHIALSNMPKVTIELSGGLLEHDHFETVMKSTY	262
186	Db	AARMAFFCFDDEPAFKASEFSIKIRREPHRLAISNMLPKSVTVAEGLTIEDHFDVTVMKSTY	245
263	QY	LVAYITVCDPHSLSGFTSSGVKSVIYASPDKENOTHYALQASLKLLDPYEKYFDIYYPLSK	322
246	Db	LVAFIISDFESVSKITSGVKSVYVYVDPKINQADYALDAADAVTLLEBFYEDFYFIPYLPK	305
323	QY	LDLIAIPDFAPGAMENWGLITYRETSTLLFPDKPTSSASDKLWVTRVTAHELAHQFNGLVLT	382
306	Db	QDLAAIPDFQSGAMENWGLITYRESALLFDAEKSASSKLGITVVAHELAHQFNGLVLT	365
383	QY	MEWVNDIWLKGGPAPKYMELIAVNAITYPELODDYFLNVCFEYITKOSLNSSRPISKAET	442
366	Db	MEWVNDIWLNEGFAKFMFVSVSTHPELKVGYDFGKCFDAMEVDALNSSHPVSTPVEN	425
443	QY	PTIOEMEDFVSYNKGACILNMLKDFLGEKFKGIIQYLKKFSYRNAKNDLWSSLNS	502
426	Db	PAQIEMFDDVSYDKGACILNMLREYLSADAFKSGIVQYLOKHSYKNTKNEDLWDSMASI	485
503	QY	CLESDFSTG---GVCHSPDKMTSNMLAFLGENAEMKMTWTTLQKGIPLLVLVVKQDGC5LR	560
486	Db	C-PTDGVKMGDGF-C-SRSQHSSSSSHHQEGVDVKTMMTWTLQRGEPPLITIIVRGNVH	543
561	QY	LOQERFLQGVQEDPEWRALQERYLWHPITYUTYSTSSNVIHRHILKSKTDTLDLPEKTSW	620
544	Db	MKOEHYMKG-----SDCAPDTGYLWHPVITFTITSKNMVRFLTKTKTDVLLPLPEVSW	597

Qy	621	VKENVDSNGYIYVHVHEGCHWDOLITQIINQNHILLPKDRVCLIHDPQLVGAGRLTLDKA	580
Db	598	IKFNVMGNGYIYVHVEDDGDWLSLTGLLKGTHTVASSNDRASLINNAEQLVSIQKLSIEKA	657
Qy	681	LDMTYTLOHETSGPALLGESYLESFYHMDRRNISIDISENLKRYLLQYFKPVIDRQMS	740
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Qy	741	DGKSVDMRLRSALLKACLMDLNHAFICIKAAELFSQWMESSGKLNIPDVLKIYVSGAQ	800
Db	718	DEGSVSEQMLRSELILLACVHNYQPCVQRAEGYFRKWKESGNLSLSDVDTLAVFAVGAQ	777
Qy	801	TTAGWNYLLEQYELSNSSAEOINKILYALSTSKHQEKLKLELGMGEKVKYIKTONLAALLH	860
Db	778	STEGWDFLYSKYQFSLUSSTKSQIEFALCRTONKEKLQWLDESFKGDKIKTQEFFQIIT	837
Qy	861	ATARRPKGOQLAWDFVRENWTHLLKKFDLGSYDIRMIIISGTHAFSSKDKLQBVKLFPPES	920
Db	838	LIGRNPVGYPLAWQFLRKNWNKLVQKPELGSSTAHVMVMTTQFSTRTLEEVKGFSS	897
Qy	921	LEAQSGHLDIFQTVLETTIKNIKMLEKNPLPLRTWL	956
Db	898	KRENSQRLFCVOQTETIETIENIGWMDKNFDRVWL	933

RESULT 11

US-09-989-723-353
 ; Sequence 353, Application US/09989723
 ; Patent No. US20020072092A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Bocstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2730P1C62
 ; CURRENT APPLICATION NUMBER: US/09/989, 723
 ; PRIOR FILING DATE: 2001-11-19
 ; CURRENT APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16
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 ; PRIOR FILING DATE: 1997-10-17
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 ; PRIOR FILING DATE: 1997-11-13
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 ; PRIOR FILING DATE: 1997-11-24
 ; CURRENT APPLICATION NUMBER: 60/075945
 ; PRIOR FILING DATE: 1998-02-25
 ; CURRENT APPLICATION NUMBER: 60/078910

APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC65
CURRENT APPLICATION NUMBER: US/09/989,727
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 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 49.7%; Score 2512.5; DB 9; Length 941;
 Best Local Similarity 51.0%; Pred. No. 5.1e-192;
 Matches 477; Conservative 172; Mismatches 268; Indels 19; Gaps 7;

Qy	23	YCLTALLPOICSCQSPFSSVHYHTEPCARPVATNGEREPWQELRLPSPVPIPLHYDLFV	82
Db	15	FLUSLLAULTV-----STPWCQSTQ---ASPKRSDGTFPPWKNIRLPEYVIPHYDILLI	67
Qy	83	HNPLTSLDVEASEKIEVLVSNATQPIILHSKDLEITNATLQSEDSRYMKPKGKELKLSY	142
Db	68	HANLTTLTWGTTKVEITASQPTSTIILSHHLQISRATLRKAGERLSE--EPLQVLEH	125
Qy	143	PAHEQIALVLPKLTPLHLKYVYAMPQAKLGDGFGFYKSTYRTLGGSTRILAVTDREPT	202
Db	126	PPOEQIALLAPEPLAVGLPYTVVIHYAGNLSETFHGFYKSTYRTKEGELRLASTQPEPT	185
Qy	203	QARMAPCCDEPLFKANFSIKIRRESRHIALSNMPKVTIELEGGLLEDHETTVKXSTY	262
Db	186	AARMAPCCDEFAFKASFISIKIRREPRHLAISNPLKSVTVABGLIEDHFDVTVKXSTY	245
Qy	263	LVAYIVCDPHLSGFTSSGVKSVIYASPDKRNQTHYALQASLKILDFYKFDIYVPLSK	322
Db	246	LVAFIISDFESVKITKSGVKSVYAVDPKINQADYALDAAVTLLLEFYEDYFSPYLPK	305
Qy	323	LDLIAIPDPAGAMENWGLITVRETSLLFPDKPTSSASDKLWTRVVIHAELAHQWGNLVT	382
Db	306	QDLAAIPDFQSGAMENWGLTVYRESALLFDAEKSSASKLGITVTVHAELAHQWGNLVT	365
Qy	383	MEWNDIWLKEGFAKMWELIAYNATYPELQDDYFLNCFEVIYKDSLNSRRPISKPAET	442
Db	366	MEWNDLWLNEGFAKFMFESVSVTHPELKVGDYFFGKCFDAMEYDALNSHPHSTVEEN	425
Qy	443	PTQIQBMFDESVYKNGACILNMLKDFLGEKFKGIIOLYALKFSYRNAKNDLWSSLNS	502
Db	426	PAQIRENFDDVYDKGACILNMLRYLSADAFKSGIVYLOKHSYKNTKNEEDLWDSNASI	485
Qy	503	CLESDFTSQ--GVCHSDPKMTSNMILAFILGENAEBKEMMTTWTLOKGIPLLVYVKGDCSLR	560
Db	486	C-PTDGVKMGDGC-FRSQHSSSSSHHQEGVDVKTMTMTWTLOQGFPLIITVVRGNVH	543
Qy	561	LOQERFLQGVFQDEPWALQERYLWHIPLTYSTSSSVNIHRHLIKSKTDTLDLPEKTSW	620
Db	544	MKEQHYMKG-----SDGAPDPTGYLWHVPLFTFTSKSNMVRFLKTKTVDVLLPPEVW	597
Qy	621	VRFNVDNCGYIVHVHGEHGWDLITQLNQHPTLLRPKORVGLIHDVOLFVAGAGRLTDKA	680
Db	598	IKFNVCNGYIIVHVEDDGDWDSLTGLLKGTHTVASSNDRASLIINNAFOLVIGKLSIEKA	657
Qy	681	LDMTYVLOHETSPALLGLELSYLESFYHMDRRNISDISENKRYLLQYFKPVIDROSWS	740

[illegible]

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OM protein - protein search, using sw model

Run on: September 26, 2005, 06:03:26 ; Search time 182 Seconds
(without alignments)
2701.077 Million cell updates/sec

Title: US-10-039-073-1
Perfect score: 5052
Sequence: 1 MFHSSAMVNSHRKPMFNHR.....NIKWLKXNPLRTLWLMVNT 960

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	5052	100.0	960 2 Q9HBX2	Q9hb22 homo sapien
2	5047	99.9	960 2 Q725K1	Q725k1 homo sapien
3	4789.5	94.8	915 2 Q6P179	Q6p179 homo sapien
4	2768	54.8	532 2 Q8TD32	Q8td32 homo sapien
5	2516.5	49.8	929 1 ART1 HUMAN	Q9hz08 h adipocyte
6	2512.5	49.7	941 2 Q6UWY6	Q6uw66 homo sapien
7	2480	49.1	930 1 ART1 MOUSE	Q9eqh2 mus musculus
8	2430	48.1	930 1 ART1 RAT	Q9j222 rattus norv
9	2034	40.3	1003 2 Q6PE23	Q6pe23 brachydanio
10	2027	40.1	1025 1 LCAP RAT	P97629 r leucyl-cy
11	2022	40.0	1025 2 Q8C129	Q8c129 mus musculus
12	1999	39.6	1025 1 LCAP HUMAN	Q9uiq6 homo sapien
13	1883	37.3	694 2 Q8C9W5	Q8c9w5 mus musculus
14	1847	36.6	997 2 Q6PCG5	Q6pcg5 xenopus lae
15	1690	33.5	350 2 Q8WVJ4	Q8wvj4 homo sapien
16	1564	31.0	549 2 Q8C4S7	Q8c4s7 mus musculus
17	1455.5	28.8	942 1 AMPE PIG	Q95334 sus scrofa
18	1444	28.6	957 1 AMPE HUMAN	Q07075 homo sapien
19	1391.5	27.5	1012 2 Q9VFW7	Q9vfw7 drosophila
20	1391	27.5	945 1 AMPE RAT	P50123 rattus norv
21	1390.5	27.5	945 1 AMPE MOUSE	P16406 mus musculus
22	1389.5	27.5	1036 2 Q86P55	Q86p55 drosophila
23	1373.5	27.2	994 2 Q86N05	Q86nq5 drosophila
24	1371.5	27.1	991 2 Q7PQR3	Q7pqr3 anopheles g
25	1367	27.1	903 2 Q81NH5	Q81nh5 drosophila
26	1367	27.1	1025 2 Q81NH6	Q81nh6 drosophila
27	1361.5	26.9	988 2 Q9VFX0	Q9vfx0 drosophila
28	1343	26.6	885 2 Q81HC5	Q81hc5 drosophila
29	1340	26.5	942 2 Q9VFW9	Q9vfw9 drosophila
30	1339	26.5	885 2 Q9VFW8	Q9vfw8 drosophila
31	1329.5	26.3	691 2 Q8BZ14	Q8bz14 mus musculus

32	1329.5	26.3	862 2 Q8IGR1	Q8igr1 drosophila
33	1327	26.3	1025 1 THDE RAT	Q10836 rattus norv
34	1322	26.2	1024 2 Q6UWJ4	Q6uwj4 homo sapien
35	1320	26.1	1024 1 THDE HUMAN	Q9uku6 homo sapien
36	1312	26.0	964 1 AMPN RAT	P15684 rattus norv
37	1310	25.9	1025 1 THDE MOUSE	Q8k093 mus musculus
38	1298	25.7	965 1 AMPN FELCA	P79171 felis silve
39	1290.5	25.5	1007 2 Q9U0D1	Q9u0d1 aplysia cal
40	1280.5	25.3	866 2 Q9W0S4	Q9w0e4 drosophila
41	1280.5	25.3	1053 2 Q8IRH0	Q8irh0 drosophila
42	1280.5	25.3	1075 2 Q8IRH1	Q8irh1 drosophila
43	1275	25.2	997 2 Q7QAH5	Q7qah5 anopheles g
44	1274	25.2	965 1 AMPN RABIT	P15541 oryctolagus
45	1272.5	25.2	866 2 Q9GPG3	Q9gpg3 drosophila

ALIGNMENTS

RESULT 1
Q9HBX2 PRELIMINARY; PRT; 960 AA.
AC Q9HBX2;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Aminopeptidase.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Schomburg L.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF191545; AAG38383.1; --
DR MEROPS: M01.024; --
DR GO: GO:0004177; F:aminopeptidase activity; IEA.
DR GO: GO:0004179; F:membrane alanyl aminopeptidase activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR001930; Peptidase M1.
DR InterPro: IPR006025; Pept M Zn_BS.
DR Pfam: PF01433; Peptidase_M1; 1.
DR PRINTS: PR00756; ALADIPTASE.
DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Aminopeptidase.
SQ SEQUENCE 960 AA; 110461 MW; 261EFC06870D644E CRC64;

Query Match	100.0%;	Score 5052;	DB 2;	Length 960;
Best Local Similarity	100.0%;	Pred. No. 4.8e-291;		
Matches 960;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MFHSSAMVNSHRKPMFNHRGFCYCLTALPQICISQFSPSSVSHFTEDPGAPVATNGE	60	
Db	1	MFHSSAMVNSHRKPMFNHRGFCYCLTALPQICISQFSPSSVSHFTEDPGAPVATNGE	60	
Qy	61	RFPWOELRPLSVWITPLHYDLFVHPNLTSLDFVASEKIEVLVSNATQFTILHLSKOLEITNA	120	
Db	61	RFPWOELRPLSVWITPLHYDLFVHPNLTSLDFVASEKIEVLVSNATQFTILHLSKOLEITNA	120	
Qy	121	TQSEEDSRYMKPGKELKVLSPAEHQIALLVPEKLTPHLKYVVAMDFOAKLGDGEGFY	180	
Db	121	TQSEEDSRYMKPGKELKVLSPAEHQIALLVPEKLTPHLKYVVAMDFOAKLGDGEGFY	180	
Qy	181	KSTYRTLGGETRILAVTDFEPTQARMAFCFDEPLKAFNFSIKIRRESRHIALSNMPKVK	240	
Db	181	KSTYRTLGGETRILAVTDFEPTQARMAFCFDEPLKAFNFSIKIRRESRHIALSNMPKVK	240	
Qy	241	TIELEGGLEDHFTTVKMSYLVAVIVCDFHLSLGSFTSSGVKVSIVASPDKNQTHYAL	300	
Db	241	TIELEGGLEDHFTTVKMSYLVAVIVCDFHLSLGSFTSSGVKVSIVASPDKNQTHYAL	300	
Qy	301	QASLKLLDIFYEKYFDIYVPLSKLDLIAIPDPAPGNMWNGLIITYRETSLFDPKTSASD	360	

Db 301 QASLKLLDFYKFDIYYPLSKJLDLIAIPDFAPGAMENWGLIITYRETSLLFDPKTSASD 360
Qy 361 KLWTRVIAHIAHQWFGNLTVMWWDNIWLKEGFAKYMELIAVNATYPELQFDYFLNV 420
Db 361 KLWTRVIAHIAHQWFGNLTVMWWDNIWLKEGFAKYMELIAVNATYPELQFDYFLNV 420
Qy 421 CFEVITKDSLNSSRPISKPAETPTQIQEMFDEVSNKGACILNMLKDFLGEKEFKGIQ 480
Db 421 CFEVITKDSLNSSRPISKPAETPTQIQEMFDEVSNKGACILNMLKDFLGEKEFKGIQ 480
Qy 481 YLKKFSYRNAKNDLWSSLSNCSLESDFTSGGVCHSDPKMTSNMLAFGENAEYKEMWTT 540
Db 481 YLKKFSYRNAKNDLWSSLSNCSLESDFTSGGVCHSDPKMTSNMLAFGENAEYKEMWTT 540
Qy 541 WTLQKGIPLLVVKQDGCRLRQERFLQGVQEDPEWRALQERYLWHIPLTYSTSSNVI 600
Db 541 WTLQKGIPLLVVKQDGCRLRQERFLQGVQEDPEWRALQERYLWHIPLTYSTSSNVI 600
Qy 601 HRHILKSKTDTLDLPEKTSWVKFNVDNSNGYIYVHVEGHGWDLITQLNQHNTLLRPKDRV 660
Db 601 HRHILKSKTDTLDLPEKTSWVKFNVDNSNGYIYVHVEGHGWDLITQLNQHNTLLRPKDRV 660
Qy 661 GLIHDVQLVGAGRLTLDKALDMTYIYLQHETSSPALLEGSLYSLEYFYHMDRRNISISE 720
Db 661 GLIHDVQLVGAGRLTLDKALDMTYIYLQHETSSPALLEGSLYSLEYFYHMDRRNISISE 720
Qy 721 NLKRYLQYFKPVIDRQSWSDKGSVWDRMLRSALLKLACDLNHAPCIQKAELFSQWMS 780
Db 721 NLKRYLQYFKPVIDRQSWSDKGSVWDRMLRSALLKLACDLNHAPCIQKAELFSQWMS 780
Qy 781 SGKLNIPDVLKIVYVGAQTAGNVLLEQYELSMSSAEONKILYALSTSKHQEKLLKL 840
Db 781 SGKLNIPDVLKIVYVGAQTAGNVLLEQYELSMSSAEONKILYALSTSKHQEKLLKL 840
Qy 841 IELGMEGVKIKTONLAALLHAIARRPKGQQLAWDFVRENWTHLLKXFDLGSYDIRMIISG 900
Db 841 IELGMEGVKIKTONLAALLHAIARRPKGQQLAWDFVRENWTHLLKXFDLGSYDIRMIISG 900
Qy 901 TTAHFSSKDKLQEVKLPFESLEAQGSHLDIPQTVLETTITKNIKWLEKNLPLRTLWLMVNT 960
Db 901 TTAHFSSKDKLQEVKLPFESLEAQGSHLDIPQTVLETTITKNIKWLEKNLPLRTLWLMVNT 960

RESULT 2

Q725K1 PRELIMINARY; PRT; 960 AA.
AC Q725K1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Leukocyte-derived arginine aminopeptidase long form variant.
GN Name=1-rap;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxID=9606;
RN [1]
SEQUENCE FROM N.A.
RX PubMed=12799365; DOI=10.1074/jbc.M305076200;
RA Tanioka T., Hattori A., Masuda S., Nomura Y., Nakayama H.,
RA Mizutani S., Tsujimoto M.;
RT "Human leukocyte-derived arginine aminopeptidase:The third member of
RT the oxytocinase subfamily of aminopeptidases.";
RL J. Biol. Chem. 278:32275-32283(2003).
DR EMBL; AB109031; BAC78818.1; -;
DR MEROPS; M01.024; -;
DR GO; GO:0004177; F:aminopeptidase activity; IEA.
DR GO; GO:0004179; F:membrane alanyl aminopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001930; Peptidase_M1.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF01433; Peptidase_M1; 1.

DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Aminopeptidase.
SQ SEQUENCE 960 AA; 110447 MW; 27898FE2107E814E CRC64;
Query Match 99.9%; Score 5047; DB 2; Length 960;
Best Local Similarity 99.9%; Pred. No. 9.4e-291;
Matches 959; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MFHSSAMVNSHRKPMENIHRGFYCLTRAILPQICICSQFSPSSVSHFTEDGCAFFVATNGE 60
Db 1 MFHSSAMVNSHRKPMENIHRGFYCLTRAILPQICICSQFSPSSVSHFTEDGCAFFVATNGE 60
Qy 61 RFPWQELRLPSVPIPLHYDLFVHPNLTSLDFVASEKIEVLVSNATQFIILHSDKLEITNA 120
Db 61 RFPWQELRLPSVPIPLHYDLFVHPNLTSLDFVASEKIEVLVSNATQFIILHSDKLEITNA 120
Qy 121 TLOSEEDSRYPKPKELKVLSPYPAHEQIALLVPEKLTPHLKYVYVAMDFOAKLGDGPEGFY 180
Db 121 TLOSEEDSRYPKPKELKVLSPYPAHEQIALLVPEKLTPHLKYVYVAMDFOAKLGDGPEGFY 180
Qy 181 KSTYRTLGGETRI LAVTDFPTQARMAPCFDEPLPKANFSIKIRRESRIHALSNMFKVK 240
Db 181 KSTYRTLGGETRI LAVTDFPTQARMAPCFDEPLPKANFSIKIRRESRIHALSNMFKVK 240
Qy 241 TIELEGLLEDHPETTVMSTYLVAYIVCDPHSLSGFTSGGVKSVIYASDPKRNQTHYAL 300
Db 241 TIELEGLLEDHPETTVMSTYLVAYIVCDPHSLSGFTSGGVKSVIYASDPKRNQTHYAL 300
Qy 301 QASLKLLDFYKFDIYYPLSKJLDLIAIPDFAPGAMENWGLIITYRETSLLFDPKTSASD 360
Db 301 QASLKLLDFYKFDIYYPLSKJLDLIAIPDFAPGAMENWGLIITYRETSLLFDPKTSASD 360
Qy 361 KLWTRVIAHIAHQWFGNLTVMWWDNIWLKEGFAKYMELIAVNATYPELQFDYFLNV 420
Db 361 KLWTRVIAHIAHQWFGNLTVMWWDNIWLKEGFAKYMELIAVNATYPELQFDYFLNV 420
Qy 421 CFEVITKDSLNSSRPISKPAETPTQIQEMFDEVSNKGACILNMLKDFLGEKEFKGIQ 480
Db 421 CFEVITKDSLNSSRPISKPAETPTQIQEMFDEVSNKGACILNMLKDFLGEKEFKGIQ 480
Qy 481 YLKKFSYRNAKNDLWSSLSNCSLESDFTSGGVCHSDPKMTSNMLAFGENAEYKEMWTT 540
Db 481 YLKKFSYRNAKNDLWSSLSNCSLESDFTSGGVCHSDPKMTSNMLAFGENAEYKEMWTT 540
Qy 541 WTLQKGIPLLVVKQDGCRLRQERFLQGVQEDPEWRALQERYLWHIPLTYSTSSNVI 600
Db 541 WTLQKGIPLLVVKQDGCRLRQERFLQGVQEDPEWRALQERYLWHIPLTYSTSSNVI 600
Qy 601 HRHILKSKTDTLDLPEKTSWVKFNVDNSNGYIYVHVEGHGWDLITQLNQHNTLLRPKDRV 660
Db 601 HRHILKSKTDTLDLPEKTSWVKFNVDNSNGYIYVHVEGHGWDLITQLNQHNTLLRPKDRV 660
Qy 661 GLIHDVQLVGAGRLTLDKALDMTYIYLQHETSSPALLEGSLYSLEYFYHMDRRNISISE 720
Db 661 GLIHDVQLVGAGRLTLDKALDMTYIYLQHETSSPALLEGSLYSLEYFYHMDRRNISISE 720
Qy 721 NLKRYLQYFKPVIDRQSWSDKGSVWDRMLRSALLKLACDLNHAPCIQKAELFSQWMS 780
Db 721 NLKRYLQYFKPVIDRQSWSDKGSVWDRMLRSALLKLACDLNHAPCIQKAELFSQWMS 780
Qy 781 SGKLNIPDVLKIVYVGAQTAGNVLLEQYELSMSSAEONKILYALSTSKHQEKLLKL 840
Db 781 SGKLNIPDVLKIVYVGAQTAGNVLLEQYELSMSSAEONKILYALSTSKHQEKLLKL 840
Qy 841 IELGMEGVKIKTONLAALLHAIARRPKGQQLAWDFVRENWTHLLKXFDLGSYDIRMIISG 900
Db 841 IELGMEGVKIKTONLAALLHAIARRPKGQQLAWDFVRENWTHLLKXFDLGSYDIRMIISG 900
Qy 901 TTAHFSSKDKLQEVKLPFESLEAQGSHLDIPQTVLETTITKNIKWLEKNLPLRTLWLMVNT 960
Db 901 TTAHFSSKDKLQEVKLPFESLEAQGSHLDIPQTVLETTITKNIKWLEKNLPLRTLWLMVNT 960


```
RESULT 3
Q6P179 PRELIMINARY; PRT; 915 AA.
AC Q6P179;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE LRAP protein.
GN Name=LRAP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gricham J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC065240; AAH65240.1; -
DR GO; GO:0004179; P:membrane alanyl aminopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
SQ SEQUENCE 915 AA; 105525 MW; 10075BE1C076377F CRC64;

Query Match 94.8%; Score 4789.5; DB 2; Length 915;
Best Local Similarity 95.3%; Pred. No. 1.7e-275;
Matches 915; Conservative 0; Mismatches 0; Indels 45; Gaps 1;

Qy 1 MFHSSAMVNSHRKPNFNIHRGYPCLTALPQICICQSFVSSSYFTEDPGAFPATNGE 60
Db 1 MFHSSAMVNSHRKPNFNIHRGYPCLTALPQICICQSFVSSSYFTEDPGAFPATNGE 60

Qy 61 RPPWQELRLPSVVIPLHYDLFVHPNLTSLDFVASEKIEVLVSNATQFIILHKSLEITNA 120
Db 61 RPPWQELRLPSVVIPLHYDLFVHPNLTSLDFVASEKIEVLVSNATQFIILHKSLEITNA 120

Qy 121 TLQSEDSRYMKPGKELVLSYPAHEQIALLVPEKLTPLHLYKYVAMDFQAKLGDGEGFY 180
Db 121 TLQSEDSRYMKPGKELVLSYPAHEQIALLVPEKLTPLHLYKYVAMDFQAKLGDGEGFY 180

Qy 181 KSTYTLGGETRILAVTDPEPTQARMAPCFDEPLFKANFSIKIRSRHIALSNMPKV 240
Db 181 KSTYTLGGETRILAVTDPEPTQARMAPCFDEPLFKANFSIKIRSRHIALSNMPKV 240

Qy 241 TIEGGLLEDHEDFETTVKMTYLVAVIVCDFHSLSGFTSSGVKVIYASPKRNTHYAL 300
Db 241 TIEGGLLEDHEDFETTVKMTYLVAVIVCDFHSLSGFTSSGVKVIYASPKRNTHYAL 300

Qy 238 -----KSVIYASPKRNTHYAL 255
Db 238 -----KSVIYASPKRNTHYAL 255
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Qy 301 QASLKLLDFEYKFDIYYPLSKLDLIAIPDPAPGAMENWGLIITYRETSLLDFDPKTSASD 360
Db 256 QASLKLLDFEYKFDIYYPLSKLDLIAIPDPAPGAMENWGLIITYRETSLLDFDPKTSASD 315

Qy 361 KLWTRVIAHSLAHQWFGNLTVMWMDNIWLKEGFAKYMELIAVNATYPELQFDDYFLNV 420
Db 316 KLWTRVIAHSLAHQWFGNLTVMWMDNIWLKEGFAKYMELIAVNATYPELQFDDYFLNV 375

Qy 421 CFEVITKDSLNSSRPISKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGBEKFKGIHQ 480
Db 376 CFEVITKDSLNSSRPISKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGBEKFKGIHQ 435

Qy 481 YLKPFSTRNAKNDLWSLSNLSCLSDFTSGVCHSDPKMTSNMLAFILGNAEVEKMTT 540
Db 436 YLKPFSTRNAKNDLWSLSNLSCLSDFTSGVCHSDPKMTSNMLAFILGNAEVEKMTT 495

Qy 541 WTLQKGIPLLVKODGCSLRQQERFLQGVFOEDPEWRALQERYLWHIPLTYSTSSNNVI 600
Db 496 WTLQKGIPLLVKODGCSLRQQERFLQGVFOEDPEWRALQERYLWHIPLTYSTSSNNVI 555

Qy 601 HRHILKSKTDTLDLPEKTSWYKFNVDNSNGYIVHYEGHGWDLITQLNQNHTLLRPKDRV 660
Db 556 HRHILKSKTDTLDLPEKTSWYKFNVDNSNGYIVHYEGHGWDLITQLNQNHTLLRPKDRV 615

Qy 661 GLIHDFQLVGAGRLTLDKALDWTYYLQHETSSPALLEGSLYSFYHMDRRNITSDISE 720
Db 616 GLIHDFQLVGAGRLTLDKALDWTYYLQHETSSPALLEGSLYSFYHMDRRNITSDISE 675

Qy 721 NLKRYLLQYKPKFVTDROSWSKGSWDMRLSALLKLACDINHAPCIQKAAELFSQMWES 780
Db 676 NLKRYLLQYKPKFVTDROSWSKGSWDMRLSALLKLACDINHAPCIQKAAELFSQMWES 735

Qy 781 SGKLNIPDVLKIVYSVGAQTACAGNYLLEQYELSSSAEQNKILYALSTSKHQEKLLKL 840
Db 736 SGKLNIPDVLKIVYSVGAQTACAGNYLLEQYELSSSAEQNKILYALSTSKHQEKLLKL 795

Qy 841 IELQMEGKVIKTONLAALLHAIARRPKQQQLAWDFVRENWTHLLKKFDLGSYDIRMIISG 900
Db 796 IELQMEGKVIKTONLAALLHAIARRPKQQQLAWDFVRENWTHLLKKFDLGSYDIRMIISG 855

Qy 901 TTAHFSSKDKLQEVKLPFESLEAOGSHLDIFQTVLETITKIKWLEKKNLPLRTWLWYNT 960
Db 856 TTAHFSSKDKLQEVKLPFESLEAOGSHLDIFQTVLETITKIKWLEKKNLPLRTWLWYNT 915

RESULT 4
Q8TD32 PRELIMINARY; PRT; 532 AA.
AC Q8TD32;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Leukocyte-derived arginine aminopeptidase short form.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21374137; PubMed=11481040;
RA Hattori A., Matsumoto K., Mizutani S., Tsujimoto M.;
RT "Genomic organization of the human adipocyte-derived leucine
RT aminopeptidase gene and its relationship to the placental leucine
RT aminopeptidase/oxytocinase gene.";
RL J. Biochem. 130:235-241 (2001).
[2]
RP SEQUENCE FROM N.A.
RA Tanioka T., Hattori A., Masuda S., Nomura Y., Nakayama H.,
RA Mizutani S., Tsujimoto M.;
RT "Human leukocyte-derived arginine aminopeptidase: The third member of
RT the oxytocinase subfamily of aminopeptidases.";
RL J. Biol. Chem. 274:10033-10037 (1999).
EMBL; AY028805; AAK37776.1; -.
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DR MEROPS; M01.024; --
DR GO; GO:0004177; F:aminopeptidase activity; IEA.
DR GO; GO:0004179; P:membrane alanyl aminopeptidase activity; IEA.
DR CO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001930; Peptidase M1.
DR Pfam; PF01433; Peptidase M1.
DR PRINTS; PR00756; ALADIPTASE.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Aminopeptidase.
SQ SEQUENCE 532 AA; 60937 MW; DA0F4F00AD9E80D71 CRC64;

Query Match          54.8%; Score 2768; DB 2; Length 532;
Best Local Similarity 99.6%; Pred. No. 6.6e-156;
Matches 523; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MFHSSAMVNSHRKPMFNHRRFYCLTALPQICSCQSPSPSSVHYFTEDPGAPFVATNGE 60
Db 1 MFHSSAMVNSHRKPMFNHRRFYCLTALPQICSCQSPSPSSVHYFTEDPGAPFVATNGE 60

Qy 61 RFPQOELRPSVVIPLHYDLFVHNLTSLDFVASEKIEVLVSNATQRTIILHSDKLEITNA 120
Db 61 RFPQOELRPSVVIPLHYDLFVHNLTSLDFVASEKIEVLVSNATQRTIILHSDKLEITNA 120

Qy 121 TLQSEEDSRVYMKPGKELKVLSPAHQIALLVPEKLTPLHLKYYVAMDFQAKLGDGFEGFY 180
Db 121 TLQSEEDSRVYMKPGKELKVLSPAHQIALLVPEKLTPLHLKYYVAMDFQAKLGDGFEGFY 180

Qy 181 KSTYRTLTGGETRIILAVTDFTQARMAPPCCDEPLFKANFSIKIRRSRHIALSNMPKVK 240
Db 181 KSTYRTLTGGETRIILAVTDFTQARMAPPCCDEPLFKANFSIKIRRSRHIALSNMPKVK 240

Qy 241 TIELEGGLEDHFETVWMSYLVAYIVCDPHSLSGFTSSGVKYSIVASDPKRNQTHYAL 300
Db 241 TIELEGGLEDHFETVWMSYLVAYIVCDPHSLSGFTSSGVKYSIVASDPKRNQTHYAL 300

Qy 301 QASLKLLDFYKDYFYIYPLSKLLDIAIPDPAPGAMENWGLITYRETSLFLDPKNTSSASD 360
Db 301 QASLKLLDFYKDYFYIYPLSKLLDIAIPDPAPGAMENWGLITYRETSLFLDPKNTSSASD 360

Qy 361 KLWTRVIAHLAQHWFGLNLTWMEWNDIWLKEGFAKYMELIAVNATYPELQFDYFLNV 420
Db 361 KLWTRVIAHLAQHWFGLNLTWMEWNDIWLKEGFAKYMELIAVNATYPELQFDYFLNV 420

Qy 421 CFVITKDSLNSRPIKSPASTPTQIQEMFDEVSNKGACILNMLKDFLGEKEFKGLIQ 480
Db 421 CFVITKDSLNSRPIKSPASTPTQIQEMFDEVSNKGACILNMLKDFLGEKEFKGLIQ 480

Qy 481 YLKKSFSYRNKNDLWSSLNSCLESDFTSGGVCHSDPKMTSNML 525
Db 481 YLKKSFSYRNKNDLWSSLNSCLESDFTSGGVCHSDPKMTSNMV 525

RESULT 5
ART1 HUMAN STANDARD; PRT; 929 AA.
AC Q9NZ08; O60278; Q8NEL4; Q8TADO; Q9UHF8; Q9UKY2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Adipocyte-derived leucine aminopeptidase precursor (BC 3.4.11.-) (A-
DE LAP) (ARTS-1) (Aminopeptidase PILS) (Puromycin-insensitive leucyl-
DE specific aminopeptidase) (PILS-AP) (Type 1 tumor necrosis factor
DE receptor shedding aminopeptidase regulator).
GN Name=ARTS1; Synonyms=APPILS, KIAA0525;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUB=white adipose tissue;
RX MEDLINE=99238715; PubMed=10220586;

Hattori A., Matsumoto H., Mizutani S., Tsujimoto M.;
"Molecular cloning of adipocyte-derived leucine aminopeptidase highly
related to placental leucine aminopeptidase/oxytocinase.";
J. Biochem. 125:931-938 (1999).
[2]
RN SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUB=Leukocyte;
RX MEDLINE=21374137; PubMed=11481040;
Hattori A., Matsumoto K., Mizutani S., Tsujimoto M.;
"Genomic organization of the human adipocyte-derived leucine
aminopeptidase gene and its relationship to the placental leucine
aminopeptidase/oxytocinase gene.";
J. Biochem. 130:235-241 (2001).
[3]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RC Schomburg L.;
RX "Molecular characterization of human aminopeptidase PILS.";
Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
[4]
RN SEQUENCE FROM N.A. (ISOFORM 1).
Cui X., Alsaaty S., Lawrence M., Combs C.A., Rouhani F.N.,
Levine S.J.;
"Identification of an aminopeptidase regulator of type I tumor
necrosis factor receptor shedding.";
Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
[5]
RN SEQUENCE FROM N.A. (ISOFORM 1), AND REVISION TO 718.
Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
Nomura N., Ohara O.;
Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
[6]
RN SEQUENCE OF 62-929 FROM N.A. (ISOFORM 2).
TISSUB=Brain;
RX MEDLINE=96290545; PubMed=9628581;
Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. IX.
The complete sequences of 100 new cDNA clones from brain which can
code for large proteins in vitro.";
DNA Res. 5:31-39 (1998).
[7]
RN SEQUENCE FROM N.A. (ISOFORM 1).
TISSUB=Testis;
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Uadin T.B., Toohiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[8]
RN SEQUENCE OF 25-37, AND CHARACTERIZATION.
RX MEDLINE=20512052; PubMed=11056387;
Hattori A., Kitatani K., Matsumoto H., Miyazawa S., Rogi T.,
Tsuruoka N., Mizutani S., Natori Y., Tsujimoto M.;
"Characterization of recombinant human adipocyte-derived leucine
aminopeptidase expressed in Chinese hamster ovary cells.";
J. Biochem. 128:755-762 (2000).
CC -!- FUNCTION: May play a role in the inactivation of peptide hormones.
```

CC May be involved in the regulation of blood pressure through the
 CC inactivation of angiotensin II and/or the generation of bradykinin
 CC in the kidney.
 CC -!- CATALYTIC ACTIVITY: Release of an N-terminal amino acid, xaa-|-
 CC xbb-, in which xaa is preferably Leu, but may be other amino acids
 CC including Met, Cys and Phe.
 CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
 CC -!- SUBUNIT: Monomer.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q9NZ08-1; Sequences=Displayed;
 CC Name=2;
 CC IsoId=Q9NZ08-2; Sequences=VSP 005450;
 CC -!- TISSUE SPECIFICITY: Ubiquitous.
 CC -!- PTM: N-glycosylated.
 CC -!- SIMILARITY: Belongs to the peptidase M1 family.

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 CC or send an email to license@isb-sib.ch).

DR EMBL; AF106037; AAF07395.1; ALT INIT.
 DR EMBL; AY028806; AAK37777.1; ALT INIT.
 DR EMBL; AY028807; AAK37778.1; ALT INIT.
 DR EMBL; AF183569; AAF20384.1; ALT INIT.
 DR EMBL; AF222340; AAF34664.1; ALT INIT.
 DR EMBL; AB011097; BAA35451.2; ALT INIT.
 DR EMBL; BC030775; AAH30775.1; ALT INIT.
 DR Interact; Q9NZ08 - -
 DR MEROPS; M01.018; - -
 DR H-InvDB; HIX0005052; - -
 DR MIM; 606832; - -
 DR GO; GO:0005829; C:cytosol; NAS.
 DR GO; GO:0005783; C:endoplasmic reticulum; NAS.
 DR GO; GO:000576; C:extracellular; IDA.
 DR GO; GO:0036021; C:integral to membrane; NAS.
 DR GO; GO:0005138; F:interleukin-6 receptor binding; IPI.
 DR GO; GO:0004178; F:leucyl aminopeptidase activity; IDA.
 DR GO; GO:0004239; F:methionyl aminopeptidase activity; NAS.
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IPI.
 DR GO; GO:0008270; F;zinc ion binding; NAS.
 DR GO; GO:0045444; F:adipocyte differentiation; NAS.
 DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . .; NAS.
 DR GO; GO:0006509; P:membrane protein ectodomain proteolysis; IDA.
 DR GO; GO:0050714; P:positive regulation of protein secretion; IDA.
 DR GO; GO:0008217; P:regulation of blood pressure; NAS.
 DR GO; GO:0045088; P:regulation of innate immune response; NAS.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR InterPro; IPR001930; Peptidase_M1.
 DR Pfam; PF01433; Peptidase_M1; 1.
 DR PROSITE; PR00756; ALADIPTASE.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 KW Alternative splicing; Aminopeptidase; Direct protein sequencing;
 KW Glycoprotein; Hydrolase; Metalloprotease; Polymorphism; Protease;
 KW Signal; Zinc.
 FT SIGNAL 1 24
 FT CHAIN 1 929
 FT METAL 341 341 Adipocyte-derived leucine aminopeptidase.
 FT ACT_SITE 342 342 Zinc (catalytic) (By similarity).
 FT METAL 345 345 By similarity.
 FT METAL 464 464 Zinc (catalytic) (By similarity).
 FT ACT_SITE 426 426 Zinc (catalytic) (By similarity).
 FT CARBOHYD 58 58 Proton donor (Potential).
 FT CARBOHYD 142 142 N-linked (GlcNAc . .) (Potential).
 FT CARBOHYD 402 402 N-linked (GlcNAc . .) (Potential).
 FT CARBOHYD 748 748 N-linked (GlcNAc . .) (Potential).
 FT CARBOHYD 889 889 N-linked (GlcNAc . .) (Potential).

FT	VARSPLIC	928	929	RM -> HDPEADATG (in isoform 2). /FTId=VSP_005450. R -> P (in dbSNP:26653). /FTId=VAR_012779. I -> M (in dbSNP:26618). /FTId=VAR_012780. G -> D (in dbSNP:27895). /FTId=VAR_012781. M -> V (in dbSNP:2287987). /FTId=VAR_012782. K -> R (in dbSNP:27434). /FTId=VAR_012783. Q -> E (in dbSNP:27044). /FTId=VAR_012784. G -> R (in Ref. 3). D -> N (in Ref. 2, 5 and 6). R -> O (in Ref. 2, 5 and 6).
FT	VARIANT	115	115	
FT	VARIANT	264	264	
FT	VARIANT	334	334	
FT	VARIANT	337	337	
FT	VARIANT	516	516	
FT	VARIANT	718	718	
FT	CONFLICT	502	502	
FT	CONFLICT	563	563	
FT	CONFLICT	713	713	
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Qy		23	YCLTAILPOLICICQFSVPSSYHFTEDPGAPPVATNGERFPMQELRLPSPVVIPLHYDLFV	82
Db		3	FLLSLLALLTV-----STPSWCQST---ASPKSDGTFFPWNKIRUPEYVIPVHYDULI	55
Qy		83	HPNLTSLDFVASEKIEVLVSNAQFIILHSKDLBITNATLQSEBDSRSYMKGKELKVLVS	142
Db		56	HANUTITLFWGTTKVEITASOPTSTIILSHSHLQISRAFLKAGAGERLSE--EPLQVLEH	113
Qy		143	PAHQIALLVPEKLTPLHKYVAMDFQAKLGDGEGFYKSYRTLGGETRILAVTDPEPT	202
Db		114	PRQOIALLAPEPLLVGLPYTVVTHYAGNLSETHFGFYKSYRTKEGELRLILASQFEP	173
Qy		203	QARNAFCFDEPLEKANPSKIRRESBHIALSNMPKVTIELEGGLLEDHETTVQNSTY	262
Db		174	AARNAFCFDEPEPAFKASFISKIRREPRHLAISNPLVKSVTVAEGLIEDHFDVTVMSTY	233
Qy		263	LVAVIVCDFHSLSGFTSGVKVSIYASPKRKNQTHYALQASLKLLDFYKFDIYYPLSK	322
Db		234	LVAFIISDFESVKITKSGVKVSVYAVPDKINQADYALDAAVTILLEFVDFSPYPLPK	293
Qy		323	LDLIAIPDFAPGAMENGLITYRTSLFDPKTSASDKLVWTVIAHELAHQFNGLVLT	382
Db		294	QDLAAIPDFQSGAMENGLITYRESALLFDAEKSASSKLGITMTVAHELAHQFNGLVLT	353
Qy		383	MEWNDIWLKEGFAKYMELTAVNATYBELQDDYFLNVCPEVITKDSLSNRRPSKPAET	442
Db		354	MEWNDIWLNEGFAKFMFVSVTHPELKVGDYFFGKCPDAMEVDALNSHPVSTPVEN	413
Qy		443	PTQIEMFDEVSYNKGACILNMLKDFLGEKEFKQGIQYLLKKFYSYRNAKNDLWSSLSNS	502
Db		414	PAQIRENFDDVSVDKACILNMLREYLSADAFKSGIVQYLOKHYSYKTKNEDLWDSMASI	473
Qy		503	CLESDFTS--GVCHSDPKMTSNMFLGENAEVKEMMTTWTLQKGPLLVVVKQDGCCLR	560
Db		474	C-PTDGVKMGDGC--SRSHSSSSSHWHQEGVDVKTMMNTWTTLQKGPLLITITVRGNVH	531
Qy		561	LOQERFLQGVFOEDPEWRALQERYLWHIPLTYSTSSSNVIHRHILKSTDTDLDPKTSW	620
Db		532	MKQEHYMKG-----SDGAPDPTGYLWHVPLTFTSKSDMVHRFLTKTKTDLVLIPEEVW	585
Qy		621	VKPNVDSNGYIVHYEGHGDQLITQLNQNHLLRPKDRVGLIHDVQLVQAGRLTLDKA	680
Db		586	IKFNVGNGYIVHYVEDDGDWDSLTGLKGTHTAVSSNDRASLINNAQLVSGIKLSIEKA	645
Qy		681	LDMTYYLOHETSSPALLEGSYLESFYHMDRRNISDISENLKYLYQYFKPVTDORSWS	740
Db		646	LDLSLYLKHETEMPVFGNLNELIPMYKLMEKRDMEVETQFKAFILRLRLDLIDKQWT	705
Qy		741	DKGSVWDRMLRSALLKLACDLNHPACTQKAELFSQNMESSGKLNIPDVLKVIYVCAQ	800

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Db 706 DEGSVSRMLRSQLLALLACVHYQPCVQRAEGYFRKWKESNGLSLPPDVTTLAVFAVGAQ 765
Qy 801 TTAGNYYLLEQYELSMSSAEONKILYALSTSKHOKLLKLIELGMEGVKIKTONLAALLH 860
Db 766 STEGWDFLYSKYQSLSTESQSEFALCRTQNKKEKQWLDESEFGDKIKITQFPQLT 825
Qy 861 AIARRPKGOQLAWDFVRENWTHLLKFDGLSGYDIRMIISGTTAHSFKDKLOEYKLPFES 920
Db 826 LIGRPVGYPLAWQFLRKNWKLQKPELGSSIAHVMGTGTFSTRTRLEEVKGFSS 885
Qy 921 LEAGSHLDIFQTVLETTIKNIKLEKNLPLRTWL 956
Db 886 LKENGSQLRCVQQTETIEENIGWMDKNFKIRVWL 921

RESULT 6
Q6UWY6 PRELIMINARY; PRT; 941 AA.
AC Q6UWY6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE ARTS-1.
GN ORFNames=UNQ584;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RA "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment."
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358590; AAQ8953.1; -.
DR GO; GO:0004179; F:membrane alanyl aminopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001930; Peptidase_M1.
DR Pfam; PF01433; Peptidase_M1.
DR PRINTS; PR00756; ALADIPTASE.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
SQ SEQUENCE 941 AA; 107143 MW; C3DC8ACFCF5B8CC CRC64;

Query Match 49.7%; Score 2512.5; DB 2; Length 941;
Best Local Similarity 51.0%; Pred. No. 2.1e-140;
Matches 477; Conservative 172; Mismatches 268; Indels 19; Gaps 7;

Qy 23 YCLTAILPQICISQFSVPSSHYHTEDPGAPPVATNGERFPWQBLRPLPSVVIPLHYDLFV 82
Db 15 FLSSLLALLTV-----STPSWCQSTE---ASPKRSDGTFPPFNKIRLPEYVIPVHYDILLI 67
Qy 83 HPNLTSLDFVASEKIEVLVSNATQFIILHSKDLBITNATLQSEDSRYMPGKELKVLVS 142
Db 68 HANLITLTFWCTTKVEITASOPTTIIILSHLQISRATLRKGAERLSE--EPLQVLEH 125
Qy 143 PAHEQIALLVEKLTPHLKYVYVAMDFOAKLGDGEGFYKSTYRTLTGGETRILAVTDEPT 202
Db 126 PPQEQIALLAPELLVGLPYTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFPT 185
Qy 203 QARNAFCDFEPLKANKFSIKIRRESHIALSNPNKVKTELEGGLLEDHFETVVKVSTY 262
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Qy 263 LVAVIVCDRHSLSGFTSSGKVSIVYASPDKRNOTHYALQASLKLLDFEYKVFYIYPLSK 322
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Qy 323 LDJIAIPDFAPGAVENWGLITYRETSLLFPDKPTSSASDKLWTRVIAHELAHQWFGNLVT 382
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Db 366 MEWNNDLWLNKEGFAKMEFVSVSTPELKVGDYFFGKCFDAMEVDALNSHPVSTVEN 425
Qy 443 PTOIQEMFDEVSNKGACILNMLKDFLGEKFKQGIQYLLKFSYRNKAKNDLWSSLSNS 502
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Qy 503 CLESDFTS--GVCHSDPKMTSNMLAFGLGNAEVEKEMTTWTTLQKGPLVLVVKDGCGLR 560
Db 486 C-PTDGVKGMDFC-SRSQHSSSSSHHWQEGVDVKTMMNTWTTLQRGFPPLITITVRGRNVH 543
Qy 561 LQOERFLOGVFQSDPEWRALQERYLWHIPLTYSTSSNVIRHLKSKTDTLDLPEKTSW 620
Db 544 MKQEHYMKG-----SDGAPDTGYLWHVPLTFTITSKSNMVHRLTKTQDVLILPEEVEW 597
Qy 621 VKFNVDNSGYIIVHYEGHGWDLITOLNQNHLLRPKDRVGLIHVDVQLVGAGRLTLDKA 680
Db 598 IKFNVGNGYIIVHYEDDGWDSLTGLKGTHTAVSSNDRASLINNAFQVLSIGKLSIEKA 657
Qy 681 LDMTYILOHETSSPALLEGSLYSLEFVHMDDRNISDISENLKRYLQYKPKVIDRQSW 740
Db 658 LDLSLYLKHEITEMPVFOGLNELIPMYKLMKEKMDMNEVEQFKAFLIRLLRDLIDKQWT 717
Qy 741 DKGSVDRMLRSALLKLACDLNAPCIQKAAELFSQWMESSGKLNPTDVLKTVYSVGAQ 800
Db 718 DEGSVSEQMLRSELLLLACVHNYPQCVQRAEGYFRKWKESNGLSLPPDVTTLAVFAVGAQ 777
Qy 801 TTAGNYYLLEQYELSMSSAEONKILYALSTSKHOKLLKLIELGMEGVKIKTONLAALLH 860
Db 778 STEGWDFLYSKYQSLSTESQSEFALCRTQNKKEKQWLDESEFGDKIKITQFPQLT 837
Qy 861 AIARRPKGOQLAWDFVRENWTHLLKFDGLSGYDIRMIISGTTAHSFKDKLOEYKLPFES 920
Db 838 LIGRPVGYPLAWQFLRKNWKLQKPELGSSIAHVMGTGTFSTRTRLEEVKGFSS 897
Qy 921 LEAGSHLDIFQTVLETTIKNIKLEKNLPLRTWL 956
Db 898 LKENGSQLRCVQQTETIEENIGWMDKNFKIRVWL 933

RESULT 7
ART1_MOUSE
ID ART1_MOUSE STANDARD; PRT; 930 AA.
AC Q9EQH2; Q9ET63;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Adipocyte-derived leucine aminopeptidase precursor (EC 3.4.11.-) (A-LAP) (ARTS-1) (Aminopeptidase Pfls) (Puromycin-insensitive leucyl-specific aminopeptidase) (PILS-AP) (VEGF induced aminopeptidase).
GN Name=Artal; Synonyms=Appils;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Hattori A., Kitatani K., Matsumoto H., Mizutani S., Tsujimoto M.;
RT "Molecular cloning of murine adipocyte-derived leucine aminopeptidase and its expression in adipocyte cell line, 3T3-L1 cells."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RP [2]
RP SEQUENCE FROM N.A.
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QY 887 FDLGSYDIRMIISGTTAHSKDKLOEVLPFESLEAQSGLDIFQTVLETTIKNIKWLE 946
DB 853 FELGSSSIAHVMYGTGPNSTRARLEEVKGFPSLSKQNGSQLRCVQQTIIETIENIRWMD 912
QY 947 KNLPTLRTWL 956
DB 913 KNFDKIRLWL 922

RESULT 9
Q6PE23
ID ID6PE23 PRELIMINARY; PRT; 1003 AA.
AC Q6PE23;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE Hypothetical protein zgc:66103.
CN ORFName=zgc:66103;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]_TaxID=7955;
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.J., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC059317, RAH59317.1; -;
DR ZFIN, ZDB-GENE-030131-1534; zgc:66103.
DR GO, GO:0004179; F:membrane alanyl aminopeptidase activity; IEA.
DR GO, GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro, IPR001930; Peptidase M1.
DR InterPro, IPR006025; Pept M Zn_BS.
DR Pfam, PF01433; Peptidase_M1_1.
DR PRINTS, PR00756; ALADIPTASE.
DR PROSITE, PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 1003 AA; 114373 MW; E2209CE4B753E978 CRC64;

Query Match 40.3%; Score 2034; DB 2; Length 1003;
Best Local Similarity 43.8%; Pred. No. 5.5e-112;
Matches 407; Conservative 170; Mismatches 293; Indels 60; Gaps 10;

QY 33 CICQSFSVPSSVHYFTEDGCAFPVATNGERFFPQELPSVPLHYDLFVPHNLTSLOFV 92
DB 128 CQKSNSSMSISY-----PISISGELFPWTDRLPVSVPVHYVNSLHPLDLSMTFQ 178
QY 93 ASEKIEVLSNATQFIILHSKDLEITNATLQSEEDSRVYMKPGKELKVLSPYPAHEQIALLV 152

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DB 179 GNVSIVLVWHETKNIVLHSSDMNIIVKTFDD-----KEYRFLEYKPMQOIAIKF 228
QY 153 PEKLTPLHKYVAMDFQAKLDGDFEGFYKSTYRTLGGETRILAVTDFDEPTQARMAFPCFD 212
DB 229 PEDLKKG-QYVLKFSYKANLSYDGFYNSSVDTAGTKRVLAATQFPEPLAARAFPCFD 287
QY 213 EPLFKANFSIKIRRESRHIALSNMPKVTIBL-EGGLEDHPETTVKMSYLVVAIVCDF 271
DB 288 EPAPKSTFVVRWNTREKYISLSNMPKIKTTDLNENGLQEDFEFSSVKMSYLVVAIVAEF 347
QY 272 HSLSGFTSSGVKSVIYASPKRNOTHYALQASLKLDPYKVFYDIYYPLSKLDLIAIPDF 331
DB 348 SSHSKNVSK-TTVSVIYAVDPKKQVHALETACKLLKFYNTFFEEYPLSKLDLVIAIPDF 406
QY 332 APGAMENWGLITYRETSLLFPDKTSSASDKLWTVRIAHELAHQWFGNLVMEWMDIWL 391
DB 407 LAGAMENWGLITFRETTLLVG-NQSSRFDKQLVTSVIAHELAHQWFGNLVTRWMDLWL 465
QY 392 KEGFAKYMELIYAVNATYPELQFDYFYNVCEPVITKOSLNSRSPISKPAETPTQIQEHPD 451
DB 466 NEGFAITYQMYSIENVPDLIDIEFLNVRFKALAKOALNSSHPVSTFVSTPEQVEEMFD 525
QY 452 EVSYNKGACILNMLKDFLGEKFKOGIIQYLKFSYRNAKNDLWSSLSNCSLCSDFTS 511
DB 526 SVSYEKGASILLNLNATLDGEPHKGVIEYQNTNLSNTEKSKDLWNSLSQVSKS----- 580
QY 512 GVCHSDPKMTSNMLAFGLGNAEVEKEMTTWTLOKGIPLLVVVKQDGCSLRLQOERFLOGVF 571
DB 581 -----LNVSEMNWNTVTHKGFPLTVKRNQGPQVTLQSEHFLNLA- 619
QY 572 QEDPEWALQORYLWHLPTVYSTSSNVIHR-----HILKSKTDTLDLPEKTSVWKNVD 626
DB 620 -----ENGTDSDSLWHLPLTVYVNDSCSVLRSCQVFF-LKDKEATLQLPGQVKNLKNFR 673
QY 627 SNGYVIHYEHGHDQILITQLNQNHLLRPDRVGLIHDVQLVQAGARLTLDKALDMTY 686
DB 674 SDGYVIHYDHQGSDDLISALKVDVNVLPSEDKAALINNI FALSRGKVSFRQVJNLMDY 733
QY 687 LQHTSSPALLEGSLYESFYHMMDRRINISBNLKRYLLQYKPKVPIDROSWSKGVW 746
DB 734 IRNETEAPLTEALSQGLQYIYLLDKRDLNASSMTTYIESHFGSLMESQSWETSVS 793
QY 747 DRMLRSALLKACDLNHAPCTOKAAELFSQWMSGKLNIPITDVLKVIYVGAQTACWN 806
DB 794 KWTLSALLEATACALNRPCTTQARRLPDOWLASNKTLQIPSDLMRTVFKVAAKTDEGS 853
QY 807 YLLEQYELSSSAEQNKILYALSTSKEQELKLKLELGMGKVIKTONLAALLHAIARRP 866
DB 854 KLGSKHSIYDTEKRWLEALASTQDVRKIWIWLQKSLDGEIQNGEPFLIVHTVCRDF 913
QY 867 KGQQLAWDFVRENWTHLLKFDLGSYDIRMIISGTTAHSKDKLOEVLPFESLEAQS 926
DB 914 AGLYVAMDFMKNENKIKTQEPGIPGSPALQSIITSTTSQFSTKTHLAEVQNFSSLGKGS 973
QY 927 HLDIFQTVLETTIKNIKWLEKQLPLRTWL 956
DB 974 QMRIVQEALETIKHNRWMEKNLTLQSWL 1003

RESULT 10
LCAP_RAT
ID LCAP_RAT STANDARD; PRT; 1025 AA.
AC P97629; Q11009;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Leucyl-cystinyl aminopeptidase (EC 3.4.11.3) (Cystinyl aminopeptidase)
DE (Oxytocinase) (Otaase) (Insulin-regulated membrane aminopeptidase)
DE (Insulin-responsive aminopeptidase) (IRAP) (Placental leucine
aminopeptidase) (P-IAP) (Vesicle protein of 165 kDa) (Vp165) (GP160).
GN Name=Lmpep; Synonyms=Irap, Otaase;
OS Rattus norvegicus (Rat).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC STRAIN=Sprague-Dawley; TISSUE=Adipocyte;
 RA MEDLINE=96007507; PubMed=7559527; DOI=10.1074/jbc.270.40.23612;
 RA Keller S.R., Scott H.M., Mastick C.C., Abersold R., Lienhard G.E.,
 RT "Cloning and characterization of a novel insulin-regulated membrane
 RT aminopeptidase from Glut4 vesicles.",
 RL J. Biol. Chem. 270:23612-23618(1995).
 RL [2]
 RN SEQUENCE OF 168-176; 387-399; 731-740 AND 893-905.
 RP MEDLINE=94164972; PubMed=8119954;
 RA Mastick C.C., Abersold R., Lienhard G.E.,
 RT "Characterization of a major protein in GLUT4 vesicles. Concentration
 RT in the vesicles and insulin-stimulated translocation to the plasma
 RT membrane.",
 RL J. Biol. Chem. 269:6089-6092(1994).
 CC -!- FUNCTION: Release of an N-terminal amino acid, cleave before
 CC cysteine, leucine as well as other amino acids, degrades peptide
 CC hormones such as oxytocin, vasopressin and angiotensin III, and
 CC plays a role in maintaining homeostasis during pregnancy. May be
 CC involved in the inactivation of neuronal peptides in the brain.
 CC Cleaves Met-enkephalin and dynorphin. Binds angiotensin IV and may
 CC be the angiotensin IV receptor in the brain (By similarity).
 CC -!- CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Cys-|-
 CC Xaa, in which the half-cysteine residue is involved in a disulfide
 CC loop, notably in oxytocin and vasopressin.
 CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
 CC -!- SUBUNIT: Homodimer. Binds tankyrases 1 and 2 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Localized mainly
 CC in intracellular vesicles together with GLUT4. Relocalizes to the
 CC plasma membrane in response to insulin. The dileucine
 CC internalization motif and/or the interaction with tankyrases may
 CC be involved in intracellular sequestration.
 CC -!- TISSUE SPECIFICITY: Highly expressed in heart, brain, spleen,
 CC lung, kidney and white adipose tissue. Detected at lower levels in
 CC skeletal muscle and liver.
 CC -!- PTM: N-glycosylated.
 CC -!- SIMILARITY: Belongs to the peptidase M1 family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>
 CC or send an email to license@ebi.ac.uk).

FT METAL 468 468 Zinc (catalytic) (By similarity).
 FT METAL 487 487 Zinc (catalytic) (By similarity).
 FT CARBOHYD 145 145 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 184 184 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 215 215 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 256 256 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 266 266 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 368 368 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 374 374 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 447 447 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 525 525 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 578 578 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 664 664 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 682 682 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 695 695 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 758 758 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 834 834 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 850 850 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 989 989 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 909 916 LMKSSLDG -> YGTTQRAW (in Ref. 1;
 FT AAB38021).
 FT CONFLICT 916 1025 Missing (in Ref. 1; AAB38021).
 SQ SEQUENCE 1025 AA; 117201 MW; 8AD3BA3A46PB5EF CRC64;
 Query Match 40.1%; Score 2027; DB 1; Length 1025;
 Best Local Similarity 44.4%; Pred. No. 1.5e-111;
 Matches 402; Conservative 158; Mismatches 310; Indels 36; Gaps 5;
 Qy 54 PVATNGRFPQWELRLPSVIVPLHYDLFVHPNLTSLDFVASEKIEVLVSNTQPIILHSK 113
 Db 153 PIATNGKVFVPAQIRLPTAIIPQRYELSLHPNLTSMTRGVSITISLQALQDTRDIILHST 212
 Qy 114 DLEITWATLQSEDSRVMKPGKELKVLSPAHQIALLVPEKLTPLHKLKYYVAMDFOAKLG 173
 Db 213 GHNISSVTFMSVSSQ-----EKQVEILEYYPHQIIVAVAPESLLTGHNYLKIEYSANIS 268
 Qy 174 DGPEGFYKTYRTLGGETRILAVTDFEPTQARMAFCDFEPLFKANFSIKIRRESRHIAL 233
 Db 269 NSYVGFYGITVTDKSNKKNFAATQPEPLAARSAFPCDFEPKATFIKITRDEHHTAL 328
 Qy 234 SNMPKVTIELEGLLEDHFTTVKMSLYLVAIVCDPHSLSGFTSGGKSVIYASPKR 293
 Db 329 SNMPKSSVPTTEGLIQDEFSESVKMSLYLVAIVGEMRNLSQ-DVNGTLVSVYAVPEKI 387
 Qy 294 NQTHYALQASLKLLDFEYKYFDIYVPLSKLDLTAIPDFAPGAMENWGLIITYRTSLFLDP 353
 Db 388 DQYHALDTTVKLEFFQNYFEIQYPLKLDLVAIPDFEAGAMENWGLITFRETLIDYN 447
 Qy 354 KTSASDKLVTRVIAHELAHQWFGNLTVMWMDIWLKEGPAKYMELIAVNATYPQLQF 413
 Db 448 ATSSVADRKLVTKIIAHELAHQWFGNLTVMQWMDLWLNFGFATFMFVPSVEKIFKELNS 507
 Qy 414 DDYFLAVCFEVIYKDSLSNSRPISKPAETPTQIEMFDEVSYNKGACILNMLKDFLEEK 473
 Db 508 YEDFLDARFETMRKDSLSNSHPISSSVSQSESEQEEMFDSLSYFKGASLLMLKSYLSEDV 567
 Qy 474 FQKGIQYLLKFKSVRNKNDLWSSLSNSCLSEDFTSGGVCHSDPKMKTNNLAPLFGNAE 533
 Db 568 FQHAIIYLHNHSAIAQSDDLWDSFNE-----VTGKTL 602
 Qy 534 VKEMMTWTTLQKGIPLLVKQDCSLRLQQLQERFLQGVQEDPEWRALQERYLHPIUTYS 593
 Db 603 VKXMKMTWTTLQKGFPLVTQKGTLELLQQRFFPSM---QPEIQSDSTSLHPIPIYSV 659
 Qy 594 TSSSNVTHRH---ILSKTDTLDELPEKTSWVKVNDVNSGYIVHYEGHGDQILITOLNQN 650
 Db 660 TDGRNYSYSESVSLLDKKSVDVNLTEQVQVQVKNVNTMTGYIIVHYAHGDGAALINQKRN 719
 Qy 651 HTLLRPKDRVGLIHVDVQLVGAGRLTLDKALDMTYTLQHEHTSSPALLEGSLYESFYHMM 710
 Db 720 PYVLSDKORANLNNIPFELAGLCKVPLQMAFDLIDYLRNETHAPTITEALFQTDLIYNLL 779
 Qy 711 DRNIDSISENLKRYLLQYFKPVIDRQSWSDKSGSVMDRLMRSALLKLACDLNHAPCIQKA 770


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Db 780 EKLGHMDLSRLVTRVHKLQNOIQOQWTWDEGTSFMRRLRSGALLFEFACAHLENCTTWA 839
Qy 771 AELFSOMESSGKLIPTDVLKIVSVGAQTAGNWNLYLEQYELSSSAEQNKILYALST 830
Db 840 TKLFDGWMASNGTQSLPTDVTMTTVFKVGARTKGLFLFSMYSSMGSEAEKDKILEALAS 899
Qy 831 SXHQEKLKLIELGHEGKVIKTONLAALLHATARPCKGOQLAWDFVRENWTHLLKKFDLG 890
Db 900 SADAHLKYLWMSKSLDGIIRTKLSLIIRTVGRQPPGHLLAWDFVKNWNKLVHKPHLG 959
Qy 891 SYDIRMISGTTAHFSSKDKLEVKLFRESLEAQSHLDIFOTVLETTIKNWKLEKNLP 950
Db 960 STIOSIVAGSTHLFSSTKTHLSEVQEFENQSEATLQRCVQAEFVIELNQLQWARNLK 1019
Qy 951 TLRTWL 956
Db 1020 TLTLWL 1025

RESULT 11
Q8C129 PRELIMINARY; PRT; 1025 AA.
AC Q8C129
DT 01-WAR-2003 (Tremblrel. 23, Created)
DT 01-WAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-WAR-2004 (Tremblrel. 26, Last annotation update)
DE Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched
DE library, clone:4732490P18 product:INSULIN-REGULATED MEMBRANE
DE AMINOPEPTIDASE IRAP homolog.
GN Name=Lmep;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:683-690(2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kusunai T., Tashiro H., Itoh M.,
RA Sumi N., Ighii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

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RA Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imocani K., Ighii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK029094; BAC26293.1; --
DR MEROPS: M01.011; --
DR MGD: MGI:2387123; Impep.
DR GO: GO:0005624; C:membrane fraction; IMP.
DR GO: GO:0004177; F:aminopeptidase activity; IMP.
DR GO: GO:0030163; P:protein catabolism; IMP.
DR InterPro: IPR000150; Hypothet cof.
DR InterPro: IPR001930; Peptidase_M1.
DR InterPro: IPR006025; Pept_M_Zn_BS.
DR Pfam: PF01433; Peptidase_M1; 1.
DR PRINTS: PR00756; ALADIPTASE.
DR PROSITE: PS01228; COF 1; UNKNOWN 1.
DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN 1.
KW Amino-peptidase.
SQ SEQUENCE 1025 AA; 117303 MW; AD6F98196EBA683B CRC64;

Query Match 40.0%; Score 2022; DB 2; Length 1025;
Best Local Similarity 44.7%; Pred. No. 2.9e-111;
Matches 405; Conservative 153; Mismatches 312; Indels 36; Gaps 6;

Qy 54 PVATNGERFPWOELRPSVVIPLHYDLFVHNLSLDVASEKIEVLVSNAQTQIILHSK 113
Db 153 PVATNGKVPWPAQIRLPTAIIPLCYELSLHNLNLSMTFRGSVTISLQALQDTRDILHST 212
Qy 114 DLEITNATLQSEDSRYMKPKELVLSYPAHEQIALVPEKLTPLHLYVYVAMDFOAKLG 173
Db 213 GHNLSRVTFMSAVSSQ-----EKQVEILEYFHEQIAVVAPEPLLTGCHNYTLKIEYSANIS 268

Qy 174 DGFEGFYKSTYRTLGGTRILAVTDPEPTQARMAPPCFDEPLPKANFISKIRRESRHIAL 233
Db 269 NSYGYGYGITVTDKSNKKYPAATQFEPPLAARSAPPCFDEPAFKATFIKITRNEHHTAL 328

Qy 234 SNMPKVTIELEGGLLEDHFTTVMSTYLVAYIVCDPHSLSGFTSSGKVIYSIYASPKR 293
Db 329 SNMPKSSVPAEGLIQIDEFSESVKMSYLVAFIVGEMRNLSQ-DVNGTLVSVVAVPEKI 387

Qy 294 NOTHVALQASLKLDDFEYKEDIYVPLSKLDLIAIPDPAPGAMENWGLITVRETSLLFDP 353
Db 388 GQVHRLDOTTIKLEFYQTYFEIQYPLKLDLVAIPDFEAGAMENWGLTTFREETLLLYDN 447

Qy 354 KTSSASDKLWTRVIAHELAHQWFGNLTVMWMDIMLKEGFAKYMELIAYNATYPELQF 413
Db 448 ATSSVADKLVTKIIAHELAHQWFGNLTVMWMDIMLNEGFATFMEYFSEKIFKELNS 507

Qy 414 DDYFLNVCFEVITKDSLNSSRPISKPAETPTQIEMDFEVSYNKACILMLKDFLGEEK 473
Db 508 YEDELDFARFKTRKDSLNSSHPISSSVQSSQISEMFDSLSYFKGASLLMLKYSLSDV 567

Qy 474 FOKGIIQYKKFSYRNKNDLWSSLNSCLESDFSTSGVCHSDPKMTSNMLAFGENAE 533
Db 568 FRHAVILYLNHNSYAAIQSDDLWDSFN-----EVTDKTL-----D 602

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Qy 831 SKHQEKLKLIELGMEGVKVIKTONLAALLHAIARRPKGQQLAWDFVRENWTHLLKKFDLG 890
Db 900 SEDYRKLYWKMSSINGDNFRTQKLSFIIRVGRHFPCHLLAWDFVENWNLVQKPEPLG 959
Qy 891 SYDRMIISGTAHFSSKDKLOEVKLPFESLEAOGSHLDIPQTVLEITRNKIKWLEKNLP 950
Db 960 SYTIQNIWAGSTYLFSTKTHLSEVQAFPEQNSEATFRLRCVQEALEVIQLNIQWMEKNLK 1019
Qy 951 TLRTWL 956
Db 1020 SLTWL 1025

RESULT 13
Q8C9W5 PRELIMINARY; PRT; 694 AA.
AC Q8C9W5
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched
DE library, clone:A430088E13 product: type 1 tumor necrosis factor
DE receptor shedding aminopeptidase regulator, full insert sequence.
DE (Fragment).
GN Name=Arts1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishi Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";

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RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozawa T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno N., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK040350; BAC30569.1; -.
DR MGD; MGI:1933403; Arts1.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0004178; F:leucyl aminopeptidase activity; IDA.
DR GO; GO:0004339; F:methionyl aminopeptidase activity; IDA.
DR GO; GO:0045766; P:positive regulation of angiogenesis; IMP.
DR InterPro; IPR001930; Peptidase_M1.
DR InterPro; IPR006025; Pept M_Zn_BS.
DR Pfam; PF01433; Peptidase_M1; 1.
DR PRINTS; PR00756; ALADIPTASE.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Aminopeptidase; Receptor.
FT NON TER 1
SQ SEQUENCE 694 AA; 80186 MW; B1EA3680BBC60BCB CRC64;
Query Match 37.3%; Score 1883; DB 2; Length 694;
Best Local Similarity 50.2%; Pred. No. 3e-103;
Matches 348; Conservative 134; Mismatches 203; Indels 8; Gaps 3;
Qy 265 AYIVCDPFLSLSGFTSSGKVIYASDPKRNQTHYALQASLKLDIFYEKYDIYPLSKLD 324
Db 1 AFIISDPKSVSKMTKSGVKSVAVPDKINQADYALDAATLLEFYEDYENIPPLPKQD 60
Qy 325 LIAIPDPAGAMENWGLITYRETSLFLDPDKTSASDKLWTRVIAHIAHLOWFNGLVME 384
Db 61 LAAIPDPQSGAMENWGLITYRESLLYDKESASSKLGITMTIVSHELAWQWFGNGLVME 120
Qy 385 WNDIWLKGFYKMYELIYVATYPELOPDYFLNCFEVIYTKDSLNSRSPISKPAETPT 444
Db 121 WNDLMLNBFYKMFYFVTVTHPELKYEDYFPGKCFNAMEVDALNSSHVPVTPENPA 180
Qy 445 QIQEMFDEVSYNGACILANMLKDFLGEKFKQGIQYIKKFSYRNNAKNDLWSLSNSC- 503
Db 181 QIREMFDVSYEGACILANMLRDYLSADTFKGIYQYLOKYSYKNTQNDLWNSMHICP 240
Qy 504 LESDFTSGGVCHSDPKWTSNMLAFGENAEVKEKMTTWTLOKGIPLLVVQDGSRLQO 563
Db 241 TDGTQTMDGFC-SRSQHSSTSHWRQEVVDVKTMMNTWTLOKGFPLITITVSGRNVHMQ 299
Qy 564 ERLQGVQFQEDPEWALQERLWHIPLTYSTSSNVTHRLKSKTDTLPEKTSWVKF 623
Db 300 EHWKMG-----SERFPETGYLWHVPLTFITSSDSVQRFLLTKTKTDLVLPEAVQWIKF 353
Qy 624 NVDSNGYIYVHYEGHGWDLITQLNQNHLLRDKPRVGLIHDFVQLVAGRLTLDKALDM 683
Db 354 NVGMNGYIYVHYADDGWASLSGLLKEAHTTISNDRASLINNAFQVLSIEKLSKALDL 413
Qy 684 TTYLQHTSSPALLEGSLYSLESYHMDRRNISIENLKRYLLOYPKVPIDRQSWDKG 743
Db 414 TLYLQNETEIMPFOALNELIPMYKLMEKEDMIEVETQFQKDFLLKLDIKQTDWDEG 473
Qy 744 SVWDRMLRSALLKADLNHAPCIQKAAELFSQWMESSGKLNIPDVLKIVSYVGAOTTA 803
Db 474 SVSERMLRSQLLLLACVRNTPQCVQRAERYFRWKKSGNSGNNISPIDTFLAVFAVGAQNT 533
Qy 804 GWNLYLLEQVLSMSSAEQNKILYALSTSKHQEKLKLIELGMEGVKVIKTONLAALLHAI 863

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Db 534 GNDFLYKYSQSSSTKESQIFSLCTSDPKLQWLLDQSKFGIITKQEPHILTLIG 593
Qy 864 RRPQGOQLAWDFVRENWTHLLKKFDLGSYDIRMIISGTTAHPFSKDKLQEVKLPFFESLEA 923
Db 594 RNPVGYPALAKFLRENWKLQVKFELGSSSIAHWYMGTTDQFSTRALVEEVKGFSSSLKE 653
Qy 924 QSHLDIFQTVLETTITKYNKLEKLPTRLTWL 956
Db 654 NGSQRLRCVQOOTIETIENIRWMDKNPKIRLWL 686

RESULT 14

ID Q6PCG5 PRELIMINARY; PRT; 997 AA.
AC Q6PCG5;
DT 05-JUL-2004 (trEMBLrel. 27, Created)
DT 05-JUL-2004 (trEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (trEMBLrel. 27, Last annotation update)
DE MGC69084 protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=1247932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahay J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Klein S., Strausberg R.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC059334; RAH59334.1; -
DR GO, GO:0004179; F-membrane alanyl aminopeptidase activity; IEA.
DR GO, GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro, IPR001930; Peptidase M1.
DR InterPro, IPR006025; Pept M Zn Bs.
DR Pfam, PF01433; Peptidase M1; 1.
DR PRINTS, PR00756; ALADIPTASE;
DR PROSITE, PS00142; ZINC_PROTEASE; UNKNOWN 1.
SQ SEQUENCE 997 AA; 113619 MW; 460E0EC895D0A14 CRC64;

Query Match 36.6%; Score 1847; DB 2; Length 997;
Best Local Similarity 41.7%; Pred. No. 6.8e-101; Indels 88; Gaps 16;
Matches 383; Conservative 161; Mismatches 287;
Qy 53 PPVATNGSRFPQELRLPSVVPIHLDFVHPNLTSLDFVASEKIEVLVSNAQPIIILHS 112
Db 150 YPIARNGKVFPAWLSRLPNSIKPIHYILTLHPNMTMSFTGTQVQINLNTARSKNVLHS 209
Qy 113 KDLBITNATLQSEBDSRYMKPG---KELKVLVSYPABEQIALLVPEKLPKLPKLYVYVAMDFQ 169
Db 210 SDLRITKANV-----LVPGGTTMDAEVLEYPREFEIAIISPESL-PKGNCLLTIEYT 260
Qy 170 AKLGDGEGEYKSTYRTLGGETRILAVTDPTQARMAPPCGDEPLFKANESIK-IRRES 228
Db 261 SNFSSSYGFYKIDYMDKGSK-RSLAATQFEPFAARKAPPCDEPAFKSTQINIRKDE 319
Qy 229 RHIALSNMPKVTTELEGGLDEHPETTVKASTVLVAVIVCDPHSLSGFTSSGVKVSIVA 288
Db 320 SMISLSNMPKAKSTTNDGLLDDFSTSVKMSVILVAFIVGDIKNTTRETNDTL-VSVYT 378
Qy 289 SPDKNQTHYALQASLKLLDFEYKDYFYIYPLSKLDLIAIPDFAPGAMENGLIITYRETS 348
Db 379 VPEKTDQVKYALDSAVKLLDFSYNYGKYPLEKLDLVAIPDFQAAAAMENGLITFRETS 438
Qy 349 LLPDPKTTSSASDKLWTVRVIAHELAHQFGLNVTMEWMDNLWKEGFAKYMELIAVNATY 408
Db 439 LLYNEDSSSIKDKQTITIAIAHELTHQWFGNLVTMEWMDNLWNEGFATMYEYFVSLLF 498
Qy 409 PELQFDDYFLNVCPEVITKDSLSRSPISKAPETPTQIEMFDEVSYNKGACILNMLKDF 468
Db 499 PELNSENFLQRPWALKKDSLSNASHPLSTDIRPEQIEEMFNDLSYKASILLMLKTF 558
Qy 469 LGEKFKQGIQIYLKFKFSYRNAKNDLWSSLSNCSLESDFTSGGVCHSDPKMNTSNLAFL 528
Db 559 LSEDMEHLIRSLSHQSHQYGGTSDSLWDSL------VVT 593
Qy 529 GENAEVKEMTTWILQKIPILLVQKDCSLRLOQERFLQGVQFQDPPEWALQERYLWHI 588
Db 594 KENPNVNMKMTQKAGYPLVTALRKGEETVRQERFLRST---KPD-HATNASTVWHI 649
Qy 599 PLTVSTSSSVIHR-----HILKSKTDTLDLPEKTSWVKFNVDNSNGYIVHVEGHGWDOL 643
Db 650 PLTVTKKCGVDPDCDKVYLKAPGTGTINVSSEFPWVKFNVMNTGYIIVDYGADWDAL 709
Qy 644 ITQLNQNTLARPDRVGLIHDVFLQVAGRLTLDKALDMTYIYLQHETSSPALLGLSYL 703
Db 710 IEQLHRDHTVLHSSDRANLIHDIPLWAGVGVPLAKAPKLLGLVNETDSAPIQA--L 766
Qy 704 ESFTH---MDDRNISDISENLKRYLQYFKPVDTRQSWSDKGSVWDRMLRSALLKLACD 760
Db 767 HQFYHIRGILLKRGDLDDLSKLMERGLDNLNNTLIKQTKDEGLTAEERLRTSLDDPACS 826
Qy 761 LNHAPCLOKAAELFSQWMESSGKLNIPTDVLKIVYVGAQTITAGWNVILEOVELSSMAE 820
Db 827 NGVNLCDRLATREFNSW--RNETRIPSDVINIVFKVGTKTTEGTFLRRRYDSSIIYSE 884
Qy 821 QNKILYALSTSKHQEKLLKLIELGNEGKVIKTONLAALLHAIARRPKQQLAWDFVRENW 880
Db 885 KSKILEALASTDNAKDLQGLMQESLAGGSIRSQELPNVISFCIRSPGVLLAWNPKQNW 944
Qy 881 THLLKKFDLGSYDIRMIISGTTAHP---SSKOKLOEVKLPFESLEAQGSHLDIFQVLETI 938
Db 945 NLITQKL-----LHFFNSTKEKSRVWYVKEA-----LETI 975
Qy 939 TKNIKWLKELNPLTLRTWLM 957
Db 976 KLINIKWMKNLSDLSKTWLL 994

RESULT 15

Q8WVJ4
ID Q8WVJ4 PRT; 350 AA.
AC Q8WVJ4;

Search completed: September 26, 2005, 06:10:34
Job time : 188 secs

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DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE LRAP protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smalus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC017927; AAH17927.1; -.
DR MEROPS; M01.024; -.
DR GO; GO:0004179; F:membrane alanyl aminopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR PRINTS; PR00756; ALADIPTASE.
SQ SEQUENCE 350 AA; 4060 MW; 5234F40276A81253 CRC64;

Query Match          33.5%; Score 1690; DB 2; Length 350;
Best Local Similarity 99.1%; Pred. No. 3.3e-92;
Matches 322; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFHSSAMVNSHRKPMFNIRHGFYCLTALPQICICQSFSPSSYHFTDPGAFPVATNGE 60
Db 1 MFHSSAMVNSHRKPMFNIRHGFYCLTALPQICICQSFSPSSYHFTDPGAFPVATNGE 60

QY 61 RPPQQLRLPSVPLHYDLFVHPNLTSLDFVASEKIEVLVSNATQFIILHSKOLEITNA 120
Db 61 RPPQQLRLPSVPLHYDLFVHPNLTSLDFVASEKIEVLVSNATQFIILHSKOLEITNA 120

QY 121 TLQSEEDSRKMPKGLKVLSPAEHQIALVPEKLTPLHLYVYVAMDFOAKLGDGEGFY 180
Db 121 TLQSEEDSRKMPKGLKVLSPAEHQIALVPEKLTPLHLYVYVAMDFOAKLGDGEGFY 180

QY 181 KSTYRTLGGTRILAVTDPEPTQARMAPPCDEPLFKANFSIKIRRESRHIALSNMPKVK 240
Db 181 KSTYRTLGGTRILAVTDPEPTQARMAPPCDEPLFKANFSIKIRRESRHIALSNMPKVK 240

QY 241 TIEEGGLLEHFFETVVKMSTYLVAIIVCDFHSLSGFTSSGKYSIYASPKRNQTHYAL 300
Db 241 TIEEGGLLEHFFETVVKMSTYLVAIIVCDFHSLSGFTSSGKYSIYASPKRNQTHYAL 300

QY 301 QASLKLLDFYKYFDIYYPLSKLDL 325
Db 301 QASLKLLDFYKYFDIYYPLSKLGM 325
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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: September 26, 2005, 06:03:26 ; Search time 170 Seconds
(without alignments)
2184.059 Million cell updates/sec

Title: US-10-039-073-1
Perfect score: 5052
Sequence: 1 MFHSSAMVNSHRKPNFNIHR.....NIKWLKRLPTLRTWLMVNT 960

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5052	100.0	960	4	AAB60299 Human ami
2	5052	100.0	960	4	AAB60299 Human pro
3	5048	99.9	960	5	Abp69122 Human pol
4	4141	82.0	785	5	Abp63022 Human pol
5	3799	75.2	728	4	Abb10338 Human CDN
6	3799	75.2	728	5	Abp66925 Human pol
7	3770	74.6	722	4	Aau22999 Novel hum
8	3770	74.6	722	4	Abb10511 Human CDN
9	3770	74.6	722	5	Abp67098 Human pol
10	3763	74.5	722	5	Adr41453 Human CD-
11	2516.5	49.8	941	5	Aau07829 Human ART
12	2515.5	49.8	941	5	Abh90347 Human pol
13	2515.5	49.8	941	6	Adh56820 Human sec
14	2515.5	49.8	941	6	Abp67098 Human sec
15	2515.5	49.8	941	6	Abp67098 Human gen
16	2515.5	49.8	941	7	Abp67098 Human sec
17	2515.5	49.8	941	7	Adc74064 Human sec
18	2515.5	49.8	941	7	Adh37852 Human sec
19	2515.5	49.8	941	4	Aag75607 Human col
20	2515.5	49.7	941	3	Aay66736 Membrane-
21	2512.5	49.7	941	3	AAB24422 Human PRO
22	2512.5	49.7	941	4	Aau12403 Human PRO
23	2512.5	49.7	941	4	Aau12403 Human PRO
24	2512.5	49.7	941	4	Abh52529 Human PRO
25	2512.5	49.7	941	6	Abu58074 Human PRO
				6	Abu59152 Novel hum

26	2512.5	49.7	941	6	ABU82664	Human sec
27	2512.5	49.7	941	6	ABU17847	Novel hum
28	2512.5	49.7	941	6	ABU60583	Human sec
29	2512.5	49.7	941	6	ABU13965	Human PRO
30	2512.5	49.7	941	6	ABU81101	Human PRO
31	2512.5	49.7	941	6	ABU72550	Novel hum
32	2512.5	49.7	941	6	ABU66801	Human PRO
33	2512.5	49.7	941	6	ABU59882	Novel sec
34	2512.5	49.7	941	6	ABU59299	Human sec
35	2512.5	49.7	941	6	ABO25996	Human PRO
36	2512.5	49.7	941	6	ABO25072	Human sec
37	2512.5	49.7	941	6	ABU59005	Human sec
38	2512.5	49.7	941	6	ABU92383	Novel hum
39	2512.5	49.7	941	6	ABU59448	Novel hum
40	2512.5	49.7	941	6	ABU67077	Human sec
41	2512.5	49.7	941	6	ABU92214	Novel hum
42	2512.5	49.7	941	6	ABU10920	Human PRO
43	2512.5	49.7	941	6	ABU81672	Novel hum
44	2512.5	49.7	941	6	ABU88611	Human sec
45	2512.5	49.7	941	6	ABO34125	Human PRO

ALIGNMENTS

RESULT 1
AAB60299
ID AAB60299 standard; protein; 960 AA.

AC AAB60299;

DT 06-APR-2001 (first entry)

DE Human aminopeptidase 17867.

KW Human aminopeptidase 17867; neutral zinc metalloproteinase;

KW zinc-binding region; M1 aminopeptidase family; lung disorder;

KW colon disorder; lung cancer; colon cancer; breast cancer; tumour;

KW squamous cell carcinoma; insulin-related disorder; diabetes;

KW drug screening.

OS Homo sapiens.

PN WO200100811-A2.

PD 04-JAN-2001.

PF 30-JUN-2000; 2000WO-US018250.

PR 30-JUN-1999; 99US-00345650.

PA (MILL-) MILLENNIUM PHARM INC.

PI Kapeller-Libermann R, Williamson M;

DR WPI; 2001-137953/14.

DR N-ESDB; AAF27148.

PT Novel human aminopeptidase polypeptide and polynucleotide useful as target for diagnosis and treatment in aminopeptidase-related disorders and for identifying modulators of therapeutic use.

XX Claim 9; Fig 1; 92pp; English.

CC The invention relates to a novel human aminopeptidase, designated aminopeptidase 17867 (AAB60299) and to cDNA encoding aminopeptidase 17867 (AAF27148). Human aminopeptidase 17867 contains a neutral zinc metalloproteinase zinc-binding region signature motif at residues 367-376, and an M1 aminopeptidase signature motif at residues 334-338. The invention also relates to host cells comprising human aminopeptidase 17867 DNA, the preparation of the protein, an antibody which binds to the protein, methods of detection of the protein, methods of modulating activity of the protein, and methods of identifying modulators of protein

CC atherosclerosis, vasculitis; autoimmune/inflammatory disorder such as
CC acquired immune deficiency syndrome (AIDS), asthma; cell proliferative
CC disorder such as actinic keratosis, cirrhosis; developmental disorder
CC such as epilepsy, anaemia; epithelial disorder such as allergic contact
CC dermatitis, eczema; neurological disorder such as Alzheimer's disease,
CC dementia and reproductive disorder such as infertility and teratogenesis.
CC PRS DNA is useful for creating 'knockin' humanised animals (pigs) or
CC transgenic animals (mice or rats) to model human disease. PRS DNA is
CC also useful in gene therapy. PRS and its immunogenic fragments are
CC useful for screening libraries of compounds in several drug screening
CC assays. PRS is useful for analysing the proteome of a tissue or cell
CC type
XX
SQ Sequence 960 AA;
Query Match 100.0%; Score 5052; DB 4; Length 960;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 960; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MFHSAMVNSHRKPMFNTHRGFYCLTALPQICISQSPVSSVYHFTBDDGAPVATNGE 60
Db 1 MFHSAMVNSHRKPMFNTHRGFYCLTALPQICISQSPVSSVYHFTBDDGAPVATNGE 60
Qy 61 RPPQELRLPSVVIPLHYDLFVHPNLTSLDFVASEKIEVLVSNATQFIILHKSQLEITNA 120
Db 61 RPPQELRLPSVVIPLHYDLFVHPNLTSLDFVASEKIEVLVSNATQFIILHKSQLEITNA 120
Qy 121 TQSEEDSRYPKPKELVSLYPANHEQIALVPEKLTPLHLYVYVAMDFQAKLGDFEGFY 180
Db 121 TQSEEDSRYPKPKELVSLYPANHEQIALVPEKLTPLHLYVYVAMDFQAKLGDFEGFY 180
Qy 181 KSTVTLGGETRILAVTDFEPTQARMAPPCDEPLFKANFSIKIRRESRHIALSNMPVK 240
Db 181 KSTVTLGGETRILAVTDFEPTQARMAPPCDEPLFKANFSIKIRRESRHIALSNMPVK 240
Qy 241 TIELEGGILLEHFEFTVKNSTYLVAYIVCDPHSLSGFTSSGVKYSIYASPKRNQTHVAL 300
Db 241 TIELEGGILLEHFEFTVKNSTYLVAYIVCDPHSLSGFTSSGVKYSIYASPKRNQTHVAL 300
Qy 301 QASKLDFEYKFDIYYPLSKLDLIAIPDPAPGAMENWGLITTYRETSLLFPDKTSSASD 360
Db 301 QASKLDFEYKFDIYYPLSKLDLIAIPDPAPGAMENWGLITTYRETSLLFPDKTSSASD 360
Qy 361 KLWTRVIAHELAWQFNLVTMEWNDIWLKEGFAKYMELIANVATYPELQFDYFLNV 420
Db 361 KLWTRVIAHELAWQFNLVTMEWNDIWLKEGFAKYMELIANVATYPELQFDYFLNV 420
Qy 421 CFEVITKDSLSRRPISKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGEKFKGLIQ 480
Db 421 CFEVITKDSLSRRPISKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGEKFKGLIQ 480
Qy 481 YLKXPSYRNKNDLWSSLSNCSLESDFTSQGVCHSDPKMTSNMLAFLGNAEVKEMMTT 540
Db 481 YLKXPSYRNKNDLWSSLSNCSLESDFTSQGVCHSDPKMTSNMLAFLGNAEVKEMMTT 540
Qy 541 WTLQKIPLLVVKQDGSRLRQERFLQGVQEDPEWALQERYLWHIPLTYSTSSNVI 600
Db 541 WTLQKIPLLVVKQDGSRLRQERFLQGVQEDPEWALQERYLWHIPLTYSTSSNVI 600
Qy 601 HRHILKSTDTLDELPEKTSWKFNVDNGYIVVHYEGHWQDITOLNQNHTLLRPKDRV 660
Db 601 HRHILKSTDTLDELPEKTSWKFNVDNGYIVVHYEGHWQDITOLNQNHTLLRPKDRV 660
Qy 661 GLIHDFVQLVAGRITLTKALDMTYLQHEYSPPALLEGLSYLESFYHMDRRNISDISE 720
Db 661 GLIHDFVQLVAGRITLTKALDMTYLQHEYSPPALLEGLSYLESFYHMDRRNISDISE 720
Qy 721 NLKRYLLQYFKPVIDRQSWKSGSVWDRMLRSALLKLACDLNHPACIQKAAELFSQWMS 780
Db 721 NLKRYLLQYFKPVIDRQSWKSGSVWDRMLRSALLKLACDLNHPACIQKAAELFSQWMS 780
Qy 781 SGKLNIPDVLKIVYVSGAQTAGNVLLEQYELSMSSAQNKILYALSTSKHQEKLKL 840
Db 781 SGKLNIPDVLKIVYVSGAQTAGNVLLEQYELSMSSAQNKILYALSTSKHQEKLKL 840

Db 781 SGKLNIPDVLKIVYVSGAQTAGNVLLEQYELSMSSAQNKILYALSTSKHQEKLKL 840
Qy 841 IELGMEGVKIKTQNLALALHAIARRPKGQQLANDFVRENWTHLLKKFPLDLSYDIRMIISG 900
Db 841 IELGMEGVKIKTQNLALALHAIARRPKGQQLANDFVRENWTHLLKKFPLDLSYDIRMIISG 900
Qy 901 TTAHFSSKDKLOEVKLPFESLEAGSHLDIFQTVLETITKNIKWLEKNLPLRTLWLMVNT 960
Db 901 TTAHFSSKDKLOEVKLPFESLEAGSHLDIFQTVLETITKNIKWLEKNLPLRTLWLMVNT 960
RESULT 3
ABP69122
ID ABP69122 standard; protein; 960 AA.
XX
AC ABP69122;
XX AC
DT 20-JAN-2003 (first entry)
XX
XX Human polypeptide SEQ ID NO 1169.
DE Human; genome mapping; gene therapy; food supplement; virus; fungus;
XX cell-proliferative disorder; neurodegenerative disease; bacterial;
XX Parkinson's disease; Alzheimer's disease; autoimmune disease;
KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
KW arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
KW haemostatic; vulnary; fungicide; antibacterial; virucide; protozoacide;
XX antiarthritic.
XX Homo sapiens.
XX WO200270539-A2.
XX
XX 12-SEP-2002.
XX
XX 05-MAR-2002; 2002WO-US005095.
XX
XX 05-MAR-2001; 2001US-00799451.
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
XX Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
XX Wehrman T, Wang J, Wang D, Drmanac RT;
XX
XX WPI: 2002-759812/82.
XX N-PSDB; ABZ11339.
XX
XX New polynucleotides comprising sequences assembled from expressed
XX sequence tags (ESTs), useful for treating cell-proliferative,
XX neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
XX or coagulation disorders.
XX
XX Claim 9; SEQ ID NO 1169; 1012pp + Sequence Listing; English.
XX
XX The invention relates to an isolated polynucleotide (I) comprising a
XX nucleotide sequence selected from any of 948 sequences (ABZ1111-
XX ABZ12066) or their mature protein coding portion, active domain coding
XX protein or complementary sequences. The polynucleotides are useful for
XX identifying expressed genes or for physical mapping of human genome. The
XX encoded polypeptides (ABP68902-ABP68949) are useful as molecular weight
XX markers, as a food supplement, for generating antibodies, in medical
XX imaging, screening and diagnostic assays and for treating cell-
XX proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
XX or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
XX diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
XX platelet or coagulation disorders, wound, burns, incision, ulcers, liver
XX or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
XX arthritis, etc. Note: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

QY	181	KSTYRTLGGETRILAVTDEPTQARMAPCPDEPLFKANFSIKIRRESRHIALSNMPKVK	240	PR	17-MAR-2000;	2000US-0190076P.
Db	181			PR	18-APR-2000;	2000US-0198123P.
QY	241	TTEEGGLEDHFETVKMSTYLVAYIVCDFHSLSGFTSSGVKVIYASPKRKNOTHVAL	300	PR	19-MAY-2000;	2000US-0205515P.
Db	241			PR	27-JUN-2000;	2000US-0209467P.
QY	301	QASLKLLDPYKFIYIYPLSKLDLIAIPDFAPGAMENGLITYRETSLLFPDKTSSASD	360	PR	28-JUN-2000;	2000US-0214886P.
Db	301			PR	30-JUN-2000;	2000US-0215135P.
QY	361	KLWTRVIAHELAHQFGLNVTMEWNNDIWLKEGFAKYMELIAVNATYPELQFDYFLNV	420	PR	07-JUL-2000;	2000US-0216647P.
Db	361			PR	07-JUL-2000;	2000US-0216647P.
QY	421	CPKVITKDSLSNRSPISKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGEKFKGIIQ	480	PR	07-JUL-2000;	2000US-0216880P.
Db	421			PR	11-JUL-2000;	2000US-0217487P.
QY	481	YLKFSYRNANNDLWSSLSNCSLSDFTSGGVCHSDPKMTSNMLAFLGENAEVKEMWTT	540	PR	14-JUL-2000;	2000US-0217496P.
Db	481			PR	14-JUL-2000;	2000US-0218290P.
QY	541	WTLOKGIPLLVKQDGSRLQOERFLOQVFOEDPEWRALQERYLWHIPLTYSTSSNVI	600	PR	26-JUL-2000;	2000US-0220963P.
Db	541			PR	26-JUL-2000;	2000US-0220964P.
QY	601	HRHILKSKTDTLDLPEKTSWKFNVDSNGYIIVHYEGHGDOLITQLNQNHTLLRPKRV	660	PR	14-AUG-2000;	2000US-0224518P.
Db	601			PR	14-AUG-2000;	2000US-0224519P.
QY	661	GLIHDFVQLVAGRLTLDKALDMTYLQHETSSPALLEGLSYLESFYHMDRRNIDISE	720	PR	14-AUG-2000;	2000US-0225213P.
Db	661			PR	14-AUG-2000;	2000US-0225214P.
QY	721	NLKRYLQYFKPVIDRQSWDKGSVWDRMLRSALLKLACDLNHAPCIQKAAELFPQWMS	780	PR	14-AUG-2000;	2000US-0225266P.
Db	721			PR	14-AUG-2000;	2000US-0225267P.
QY	781	SGKL 784		PR	14-AUG-2000;	2000US-0225268P.
Db	781			PR	14-AUG-2000;	2000US-0225268P.
RESULT 5					14-AUG-2000;	2000US-0225757P.
ID	ABB10338	standard; protein; 728 AA.				2000US-0225758P.
AC	ABB10338;					2000US-0225759P.
DT	10-JAN-2002 (first entry)					2000US-0226279P.
DE	Human cDNA SEQ ID NO: 646.					2000US-0226681P.
KW	Human; gene therapy; neural disorder; immune system disorder;					2000US-0226686P.
KW	muscular disorder; reproductive disorder; gastrointestinal disorder;					2000US-0227182P.
KW	pulmonary disorder; cardiovascular disorder; renal disorder;					2000US-0227009P.
KW	proliferative disorder; inflammation.					2000US-0228924P.
OS	Homo sapiens.					2000US-0229287P.
PN	WO200154474-A2.					2000US-0229343P.
PD	02-AUG-2001.					2000US-0229344P.
XX	17-JAN-2001; 2001WO-US001349.					2000US-0229345P.
XX	31-JAN-2000; 2000US-0179065P.					2000US-0229509P.
PR	04-FEB-2000; 2000US-0180628P.					2000US-0229513P.
PR	24-FEB-2000; 2000US-0184664P.					2000US-0230437P.
PR	02-MAR-2000; 2000US-0186350P.					2000US-0230438P.
PR	16-MAR-2000; 2000US-0189874P.					2000US-0231242P.
						2000US-0231243P.
						2000US-0231244P.
						2000US-0231413P.
						2000US-0231414P.
						2000US-0231968P.
						2000US-0232081P.
						2000US-0232080P.
						2000US-0232397P.
						2000US-0232398P.
						2000US-0232399P.
						2000US-0232400P.
						2000US-0232401P.
						2000US-0233063P.
						2000US-0233064P.
						2000US-0233065P.
						2000US-0234223P.
						2000US-0234274P.
						2000US-0234997P.
						2000US-0234998P.
						2000US-0235484P.
						2000US-0235834P.
						2000US-0235836P.
						2000US-0236327P.
						2000US-0236367P.
						2000US-0236368P.
						2000US-0236369P.
						2000US-0236370P.
						2000US-0236802P.
						2000US-0237037P.
						2000US-0237038P.
						2000US-0237039P.
						2000US-0237040P.
						2000US-0239935P.

PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241825P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 06-DEC-2000; 2000US-0256719P.
PR 08-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI, 2001-476161/51.
XX N-PSDB; ABA06560.
XX
XX Isolated nucleic acid molecule encoding an inflammation-associated
XX peptide is used in preventing, treating or ameliorating a medical
XX condition.
XX
XX Claim 11; SEQ ID NO 646; 859pp + Sequence Listing; English.
XX
XX The present invention provides human cDNAs, proteins and related genomic

CC DNAs. These can be used in the treatment of neural, immune system,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal and proliferative disorders and inflammation. The present sequence
CC is a protein of the invention
XX
XX SQ Sequence 728 AA;

Query Match 75.2%; Score 3799; DB 4; Length 728;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 722; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 239 VKTIELEGGLEDHFETTVKMSYLVAYIVCDHSLSGFTSSGVKVIYASPDKRNOYHY 298
Db 7 VKTIELEGGLEDHFETTVKMSYLVAYIVCDHSLSGFTSSGVKVIYASPDKRNOYHY 66

Qy 299 ALQASLKLLDPYKYFDIYYPLSKLDLIAIPDFAPGAMENWGLITYRETSLLFPKTS 358
Db 67 ALQASLKLLDPYKYFDIYYPLSKLDLIAIPDFAPGAMENWGLITYRETSLLFPKTS 126

Qy 359 SDKLWTRVIAHELAHQWFGNLTMEWWDIWLKEGFAKYMELIAVNATYPQLQDDYFL 418
Db 127 SDKLWTRVIAHELAHQWFGNLTMEWWDIWLKEGFAKYMELIAVNATYPQLQDDYFL 186

Qy 419 NVCFEVITKDSLNSRPI SKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGEKFKQGI 478
Db 187 NVCFEVITKDSLNSRPI SKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGEKFKQGI 246

Qy 479 IQYLKFSYRNAXNDDLLWSSLSNCSLESDFTSQGVCHSDPKMTSNMLAFI GENAEVKEMM 538
Db 247 IQYLKFSYRNAXNDDLLWSSLSNCSLESDFTSQGVCHSDPKMTSNMLAFI GENAEVKEMM 306

Qy 539 TTWTLOKGI PLLVVKQDGC SLRLOQERFLOQVQEDPEWRALQERYLWHIPLTYSTSSN 598
Db 307 TTWTLOKGI PLLVVKQDGC SLRLOQERFLOQVQEDPEWRALQERYLWHIPLTYSTSSN 366

Qy 599 VIHRHLKSKTDTL DLPKTSWVKFNVD SNGYIVHYEGHGWDLITQLNQNH TLLRPKD 658
Db 367 VIHRHLKSKTDTL DLPKTSWVKFNVD SNGYIVHYEGHGWDLITQLNQNH TLLRPKD 426

Qy 659 RVGLIHDVFO LVGAGRLTLDKALDMYTYLOHETSSPALLEGLSYLESFYHMDRRN TSDI 718
Db 427 RVGLIHDVFO LVGAGRLTLDKALDMYTYLOHETSSPALLEGLSYLESFYHMDRRN TSDI 486

Qy 719 SENLKRYLLQVFKPVIDRQSDKGSVWDRMLRSALIKLACDLNHAPCIQKAAELFSQWM 778
Db 487 SENLKRYLLQVFKPVIDRQSDKGSVWDRMLRSALIKLACDLNHAPCIQKAAELFSQWM 546

Qy 779 ESSGKLNIP TDVLKIVYSVGAQT TAGWNYLLEQYELSMSSAEQNKILYALSTSKHQEKLL 838
Db 547 ESSGKLNIP TDVLKIVYSVGAQT TAGWNYLLEQYELSMSSAEQNKILYALSTSKHQEKLL 606

Qy 839 KLIELGMEGVIKTONLAALLHAIAREPKGOOLAWDFVRENWTHLLKFKDLSYDIRMII 898
Db 607 KLIELGMEGVIKTONLAALLHAIAREPKGOOLAWDFVRENWTHLLKFKDLSYDIRMII 666

Qy 899 SGTTAHFSSKDKLQEVKLPFESLEAOGSHLDIFQTVLETTITKNIKWLKKNLPTLRTLMV 958
Db 667 SGTTAHFSSKDKLQEVKLPFESLEAOGSHLDIFQTVLETTITKNIKWLKKNLPTLRTLMV 726

Qy 959 NT 960
Db 727 NT 728

RESULT 6
ABP66925
ID ABP66925 standard; protein; 728 AA.
XX
XX AC ABP66925;
XX
XX DT 09-DEC-2002 (first entry)
XX
XX DE Human polypeptide SEQ ID NO 646.

XX	Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW	immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnery;
KW	antiparkinsonian; antiskilling; antianemic; antiarthritic; cancer;
KW	antichemagic; hepatotropic; cerebroprotective; antiinflammatory;
KW	antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
KW	antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW	neurological disease; infection; nephrotropic; gene therapy; vaccine.
OS	Homo sapiens.
XX	US2002090672-A1.
XX	11-JUL-2002.
XX	17-JAN-2001; 2001US-00764853.
XX	31-JAN-2000; 2000US-0179065P.
PR	04-FEB-2000; 2000US-0180628P.
PR	28-JUN-2000; 2000US-02114886P.
PR	07-JUL-2000; 2000US-0216647P.
PR	07-JUL-2000; 2000US-0216680P.
PR	11-JUL-2000; 2000US-0217487P.
PR	11-JUL-2000; 2000US-0217496P.
PR	14-JUL-2000; 2000US-0218290P.
PR	26-JUL-2000; 2000US-0220963P.
PR	26-JUL-2000; 2000US-0220964P.
PR	14-AUG-2000; 2000US-0224518P.
PR	14-AUG-2000; 2000US-0224519P.
PR	14-AUG-2000; 2000US-0225267P.
PR	14-AUG-2000; 2000US-0225268P.
PR	14-AUG-2000; 2000US-0225270P.
PR	14-AUG-2000; 2000US-0225447P.
PR	14-AUG-2000; 2000US-0225757P.
PR	14-AUG-2000; 2000US-0225758P.
PR	22-AUG-2000; 2000US-0226668P.
PR	30-AUG-2000; 2000US-0228924P.
PR	01-SEP-2000; 2000US-0229287P.
PR	01-SEP-2000; 2000US-0229343P.
PR	01-SEP-2000; 2000US-0229344P.
PR	01-SEP-2000; 2000US-0229345P.
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PR	08-DEC-2000; 2000US-0251869P.
XX	(ROSE/) ROSEN C A.
PA	(RUBE/) RUBEN S M.
PA	(BARA/) BARASH S C.
XX	Rosen CA, Ruben SM, Barash SC;

XX		WP1; 2002-681727/73.
DR		N-PSDB; ABV83897.
XX		
PT		Novel polypeptide useful for diagnosis, prognosis, prevention, and
PT		treatment of immune, hyperproliferative, renal, respiratory,
PT		cardiovascular, reproductive, endocrine, gastrointestinal and
PT		neurological disorders.
XX		
PS		Claim 11; SEQ ID NO 646; 369pp + Sequence Listing; English.
XX		
CC		The invention relates to novel genes (ABV83682-ABV84101) and proteins
CC		(ABP6710-ABP67129) useful for preventing, treating or ameliorating
CC		medical conditions e.g. by protein or gene therapy. The genes are
CC		isolated from a range of human tissues disclosed in the specification.
CC		The nucleic acids, proteins, antibodies and (anti)agonists are useful in
CC		the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC		ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC		breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC		disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC		anaemia, autoimmune rheumatoid arthritis, diabetes mellitus, Crohn's disease,
CC		multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC		cardiovascular disorders such as myocardial ischaemias; (d) wound healing
CC		; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC		infectious diseases such as viral, bacterial, fungal and parasitic
CC		infections. Note: The sequence data for this patent did not form part of
CC		the printed specification, but was obtained in electronic format directly
CC		from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX		
SQ		Sequence 728 AA;
	Query Match	75.2%; Score 3799; DB 5; Length 728;
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Qy	359	SDKLWTTRVIAHELHQFNLVTMEWNWDIWLKEGFPAKMELIAVNATYPELODDYFL 418
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Qy	419	NVCFEVITKDSLNSRRPISKPAETPTQIQMPEVSNYKGACILNMLKDFLGEBSFKQGI 478
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Qy	599	VIIHRHLKSKTDLTLDLPEKTSWYKFNVDSNGYYIVHYEGHWGDLITQLNQNHHTLLRPKD 658
Db	367	VIIHRHLKSKTDLTLDLPEKTSWYKFNVDSNGYYIVHYEGHWGDLITQLNQNHHTLLRPKD 426
Qy	659	RUGLIHDVQLVCAGBLTLDKALDWMTYLLOHETSSPALLEGSLVESFYHMORNRNTSDI 718
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Qy	719	SENLKRYLQYKPVDIDROSWSDKGSWDRMLRSALLKLACDNLNHPACIOKAELFSQWM 778
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Db	607	KLIELGMEGKVIKTONLAALHLAIARRPKGQOLAWDFVRENWTHLLKKFDLGSYDIRMII	666
Qy	899	SGTTAHFSSKDKLOEVKLPFESLEAQSGLDIFQTVLETTITKNIKWLKKNLPLRTWLWV	958
Db	667	SGTTAHFSSKDKLOEVKLPFESLEAQSGLDIFQTVLETTITKNIKWLKKNLPLRTWLWV	726
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AC	AAU22999;		
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DT	18-DEC-2001	(first entry)	
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DE	Novel human enzyme polypeptide #85.		
KW	Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;		
KW	ligase; hyperproliferative disorder; immunodeficiency disorder;		
KW	autoimmune disorder; neurological disorder; metabolic disorder;		
KW	inflammatory disorder; cardiovascular disorder; reproductive disorder;		
KW	blood-related disorder; infectious disorder; cytostatic; anti arthritic;		
XX	nephrotropic; anticoagulant.		
OS	Homo sapiens.		
XX			
PN	WO200155301-A2.		
XX			
PD	02-AUG-2001.		
XX			
PF	17-JAN-2001; 2001WO-US001239.		
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XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI
XX WPI; 2001-476161/51.
DR N-PSDB; ABA06733.
XX
XX Isolated nucleic acid molecule encoding an inflammation-associated
PT polypeptide is used in preventing, treating or ameliorating a medical
PT condition.

XX Claim 11; SEQ ID NO 819; 859pp + Sequence Listing; English.
PS
XX
CC The present invention provides human cDNAs, proteins and related genomic
CC DNAs. These can be used in the treatment of neural, immune system,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal and proliferative disorders and inflammation. The present sequence
CC is a protein of the invention
XX
SQ Sequence 722 AA;

Query Match 74.6%; Score 3770; DB 4; Length 722;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 717; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy 539 TTWTLOKGIPLLVKQDGSRLQOERFLQGVQEDPEWRALQERYLWHIPLTYSTSSN 598
Db 301 TTWTLOKGIPLLVKQDGSRLQOERFLQGVQEDPEWRALQERYLWHIPLTYSTSSN 360

Qy 599 VIHRHILSKTDTLDLPEKTSWVKFNVDNSNGYIYVHGEHGWDLITQLNQNHLLRPKD 658
Db 361 VIHRHILSKTDTLDLPEKTSWVKFNVDNSNGYIYVHGEHGWDLITQLNQNHLLRPKD 420

Qy 659 RVGLIHDVFLQVAGRLTLDKALDMMTYLQHETSSPALLEGISYLESFYHMDRNNISDI 718
Db 421 RVGLIHDVFLQVAGRLTLDKALDMMTYLQHETSSPALLEGISYLESFYHMDRNNISDI 480

Qy 719 SENLRYLLOYPKPIDRQSWDKGSVDRMLRSALLKLACDLNHPACIQKAAELFSQWM 778
Db 481 SENLRYLLOYPKPIDRQSWDKGSVDRMLRSALLKLACDLNHPACIQKAAELFSQWM 540

Qy 779 ESSGKLNTPTDVLKIVYSGAQTAGWNYLLEQYELSSAFONKILYALSTSKHOEKL 838
Db 541 ESSGKLNTPTDVLKIVYSGAQTAGWNYLLEQYELSSAFONKILYALSTSKHOEKL 600

Qy 839 KLIELGMEGKVIKTONLAALLHAIARRPKGQQLAWDFVRENWTHLLKFKDLSYDIRMI 898
Db 601 KLIELGMEGKVIKTONLAALLHAIARRPKGQQLAWDFVRENWTHLLKFKDLSYDIRMI 660

Qy 899 SGTTHAFSSKDLQEVKLPFFESLEAQGSHLDIFQTVLETTITKNIKWLEKNPLTLTLWLV 958
Db 661 SGTTHAFSSKDLQEVKLPFFESLEAQGSHLDIFQTVLETTITKNIKWLEKNPLTLTLWLV 720

Qy 959 NT 960
Db 721 XT 722

RESULT 9
ABP67098
ID ABP67098 standard; protein; 722 AA.
XX
AC ABP67098;

XX
DT 09-DEC-2002 (first entry)
XX
XX Human polypeptide SEQ ID NO 819.
XX
XX Human; neutropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; cancer;
KW antiparkinsonian; antischistosomal; antianemic; antirheumatic; cancer;
KW antihistaminic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
XX US2002090672-A1.
XX
XX 11-JUL-2002.
XX
XX 17-JAN-2001; 2001US-00764853.
XX
XX 31-JAN-2000; 2000US-0179065P.
XX
XX 04-FEB-2000; 2000US-0180628P.
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XX 28-JUN-2000; 2000US-0214886P.
XX
XX 07-JUL-2000; 2000US-0216647P.
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XX 07-JUL-2000; 2000US-0216880P.
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XX 11-JUL-2000; 2000US-0217487P.
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XX 11-JUL-2000; 2000US-0217496P.
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XX 14-JUL-2000; 2000US-0218290P.
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XX 26-JUL-2000; 2000US-0220963P.
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XX 26-JUL-2000; 2000US-0220964P.
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XX 14-AUG-2000; 2000US-0224518P.
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XX 14-AUG-2000; 2000US-0224519P.
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XX 14-AUG-2000; 2000US-0225267P.
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XX 14-AUG-2000; 2000US-0225268P.
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XX 14-AUG-2000; 2000US-0225270P.
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XX 14-AUG-2000; 2000US-0225447P.
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XX 14-AUG-2000; 2000US-0225757P.
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XX 14-AUG-2000; 2000US-0225758P.
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XX 22-AUG-2000; 2000US-0226868P.
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XX 30-AUG-2000; 2000US-0228924P.
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XX 01-SEP-2000; 2000US-0229287P.
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XX 01-SEP-2000; 2000US-0229343P.
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XX 01-SEP-2000; 2000US-0229344P.
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XX 01-SEP-2000; 2000US-0229345P.
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XX 05-SEP-2000; 2000US-0229509P.
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XX 05-SEP-2000; 2000US-0229513P.
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XX 08-SEP-2000; 2000US-0231413P.
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XX 21-SEP-2000; 2000US-0234223P.
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XX 21-SEP-2000; 2000US-0234274P.
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XX 25-SEP-2000; 2000US-0234977P.
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XX 27-SEP-2000; 2000US-0235834P.
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XX 29-SEP-2000; 2000US-0236327P.
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XX 29-SEP-2000; 2000US-0236367P.
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XX 29-SEP-2000; 2000US-0236368P.
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XX 29-SEP-2000; 2000US-0236370P.
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XX 29-SEP-2000; 2000US-0236802P.
XX
XX 02-OCT-2000; 2000US-0237037P.
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XX 02-OCT-2000; 2000US-0237038P.
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XX 02-OCT-2000; 2000US-0237039P.
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XX 13-OCT-2000; 2000US-0237040P.
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XX 13-OCT-2000; 2000US-0239935P.
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XX 20-OCT-2000; 2000US-0240960P.
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XX 20-OCT-2000; 2000US-0241785P.
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XX 20-OCT-2000; 2000US-0241809P.
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XX 01-NOV-2000; 2000US-0244617P.
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XX 17-NOV-2000; 2000US-0249299P.
XX
XX 08-DEC-2000; 2000US-0251856P.
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XX 08-DEC-2000; 2000US-0251868P.
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XX 08-DEC-2000; 2000US-0251869P.
XX
XX (ROSE/) ROSEN C A.

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PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
XX
XX Rosen CA, Ruben SM, Baraah SC;
PI
XX WPI; 2002-681727/73.
DR N-PSDB; ABV84070.
XX
XX Novel polypeptide useful for diagnosis, prognosis, prevention, and
PT treatment of immune, hyperproliferative, renal, respiratory,
PT cardiovascular, reproductive, endocrine, gastrointestinal and
PT neurological disorders.
XX
XX Claim 11; SEQ ID NO 819; 369pp + Sequence Listing; English.
PS
XX The invention relates to novel genes (ABV83682-ABV84101) and proteins
CC (ABP66710-ABP67129) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 722 AA;
SQ
Query Match 74.6%; Score 3770; DB 5; Length 722;
Beat Local Similarity 99.3%; Pred. No. 0;
Matches 717; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 239 VKTTEGLELDEHPETTVKRVSTYLVAIVICDFHSLGFTSSGKVKVIYASPDKRNQTHY 298
DB 1 VKTTEGLELDEHPETTVKRVSTYLVAIVICDFHSLGFTSSGKVKVIYASPDKRNQTHY 60
OY 299 ALQASLKLLDFEYKFDIYYPLSKLDLIAIPDPAPGAMENGLITYRETSLLFPKTS 358
DB 61 ALQASLKLLDFEYKFDIYYPLSKLDLIAIPDPAPGAMENGLITYRETSLLFPKTS 120
OY 359 SDKLWVTRVIAHELAHQWFGNLTVMWWDNIWLKEGFAKYMELIAVNAVATYPDELQDDYFL 418
DB 121 SDKLWVTRVIAHELAHQWFGNLTVMWWDNIWLKEGFAKYMELIAVNAVATYPDELQDDYFL 180
OY 419 NVCEVITKDSINSRPTSKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGEKFKOGI 478
DB 181 NVCEVITKDSINSRPTSKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGEKFKXXGI 240
OY 479 IQYLKKSFRNAKNDLWSSLSNSCLESDFTSGGVCHSDPRTSNMLAFLGENAEVKEMM 538
DB 241 IQYLKKSFRNAKNDLWSSLSNSCLESDFTSGGVCHSDPRTSNMLAFLGENAEVKEMM 300
OY 539 TTWTLOKGIPLLVKQDCSLRLQOERFLQGVQEDPEWRALQERYLWHIPLTYSTSSN 598
DB 301 TTWTLOKGIPLLVKQDCSLRLQOERFLQGVQEDPEWRALQERYLWHIPLTYSTSSN 360
OY 599 VVHRHILKSKTDTLDLPKTSKVNKFNVDNSGYIVHVHVGCHWDOLITQLNQHNTLLRPKD 658
DB 361 VVHRHILKSKTDTLDLPKTSKVNKFNVDNSGYIVHVHVGCHWDOLITQLNQHNTLLRPKD 420
OY 659 RVGLIHDVFLVQAGRLTDLKALDMTYIYLOHETSSPALLGLSYLESFYHMDRNRISDI 718
DB 421 RVGLIHDVFLVQAGRLTDLKALDMTYIYLOHETSSPALLGLSYLESFYHMDRNRISDI 480
OY 719 SENLKRYLLOQVFKPIDRQSDKGSVWDRMLRSALLKLACDLNHAPCIQKAAELFSQWM 778
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Db 481 SENLKRYLLOQVFKPIDRQSDKGSVWDRMLRSALLKLACDLNHAPCIQKAAELFSQWM 540
OY 779 ESSGKLNIPDVLKIVYVGAQTAGWNLYLEQVLSMSAEQNKILYALSTSKHQEKLL 838
|||||
Db 541 ESSGKLNIPDVLKIVYVGAQTAGWNLYLEQVLSMSAEQNKILYALSTSKHQEKLL 600
OY 839 KLIELGMEGVKVIKTONLAALLHAIAARRPKQOQLAWDFVRENWTHLLKKFDLGSYDIRMII 898
|||||
Db 601 KLIELGMEGVKVIKTONLAALLHAIAARRPKQOQLAWDFVRENWTHLLKKFDLGSYDIRMII 660
OY 899 SGTTAHFSSKDKLOEVKLPFESLEAQSHLDIFQTVLETTIKNIKWLKKNLPTLRTWLNV 958
|||||
Db 661 SGTTAHFSSKDKLOEVKLPFESLEAQSHLDIFQTVLETTIKNIKWLKKNLPTLRTWLNV 720
OY 959 NT 960
Db 721 XT 722
RESULT 10
ADR41453
ID ADR41453 standard; protein; 722 AA.
XX ADR41453;
XX
XX 07-OCT-2004 (first entry)
DE Human CD-like molecule HAIDK30, SEQ ID NO:252.
XX
XX Human; CD-like molecule; cluster of differentiation; diagnosis;
XX prevention; immune disorder; immunodeficiency; autoimmune disorder;
XX blood-related disorder; haematological disorder; haemostatic disorder;
XX thrombolytic disorder; hyperproliferative disorder; cancer; tumour;
XX apoptotic disorder; cardiovascular disorder; respiratory disorder;
XX angiogenic disorder; neovascularisation; neurological disorder;
XX endocrine disorder; reproductive system disorder; infectious disease;
XX gastrointestinal disorder; drug screening; tissue regeneration;
XX chemotaxis; gene therapy; antibody therapy; immunophenotyping; cytostatic;
XX chemotaxis; gene therapy; antibody therapy; immunophenotyping; cytostatic;
XX haemostatic; tranquiliser; vulnery; antineoplastic; antitumor;
XX cardiant; antiallergic; anti-HIV; antirheumatic; antiarthritic;
XX antipsoriatic; immunosuppressive; vasotropic; neuroprotective;
XX antithyroid; thyromimetic; gynaecological; virucide; hepatotropic;
XX antibacterial; dermatological; chromosome 16.
XX
XX Homo sapiens.
XX
XX WO200226930-A2.
XX
XX 04-APR-2002.
XX
XX 25-SEP-2001; 2001WO-US029838.
XX
XX 26-SEP-2000; 2000US-0235484P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Birse CE;
XX
XX WPI; 2002-405050/43.
XX N-PSDB; ADR41277.
XX
XX Novel polynucleotides and polypeptides useful for treating, preventing or
XX ameliorating cardiovascular, renal, neurovascular, and autoimmune
XX disorders.
XX
XX Claim 11; SEQ ID NO 252; 1243pp; English.
XX
XX The invention relates to 167 novel human CD (cluster of differentiation)-
XX like molecules (ADR41388-ADR41563) and to cDNAs encoding them (seqid:11)-
XX
XX Sequence 722 AA;
```

Query Match		74.5%;	Score 3763;	DB 5;	Length 722;										
Best Local Similarity		99.3%;	Pred. No. 0;												
Matches 717;		Conservative 0;	Mismatches 5;	Indels 0;	Gaps 0;										
Qy	239	VKTI	EGGLLEDHPETTVKMS	TYLVAVI	VCDPHSLSGFTSSGGVKSVIYASPD	KRNO	THY 298								
Db	1	VKTI	EGGLLEDHPETTVKMS	TYLVAVI	VCDPHSLSGFTSSGGVKSVIYASPD	KRNO	THY 60								
Qy	299	ALQAS	LKLLDFYKYFYDI	YYP	LSKLDLIAIPD	FAPGAMENWGLITYR	ETSL	LLFDPK	TSSA 358						
Db	61	ALQAS	LKLLDFYKYFYDI	YYP	LSKLDLIAIPD	FAPGAMENWGLITYR	ETSL	LLFDPK	TSSA 120						
Qy	359	SDKL	WVTRVIAHEL	HAHQF	GNLVTM	WNNDIWL	KEGFAKYMELIA	VNATY	PELQ	DDYFL 418					
Db	121	SDKL	WVTRVIAHEL	HAHQF	GNLVTM	WNNDIWL	KEGFAKYMELIA	VNATY	PELQ	DDYFL 180					
Qy	419	NVCF	EVITKDS	LSNSR	SPISK	PAETPTQIQ	EMFDEVSYNKGAC	ILNMLK	DFLGE	EKFQGI 478					
Db	181	NVCF	EVITKDS	LSNSR	SPISK	PAETPTQIQ	EMXDEVSYNKGAC	ILNMLK	DFLGE	EKFQGI 240					
Qy	479	IOYL	KKFSYRNA	KNDLW	SSLSN	SCLES	DFTS	GGVCHSDPKMT	SNMLA	FLGENA	EVKEM 538				
Db	241	IOYL	KKFSYRNA	KNDLW	SSLSN	SCLES	DFTS	GGVCHSDPKMT	SNMLA	FLGENA	EVKEM 300				
Qy	539	TTWT	LQKGI	PLLV	KQDGS	RLQO	ERFLOGV	QEDPEWRALQ	ERYL	WHIPL	TYSTSSN 598				
Db	301	TTWT	LQKGI	PLLV	KQDGS	RLQO	ERFLOGV	QEDPEWRALQ	ERYL	WHIPL	TYSTSSN 360				
Qy	599	VIHR	HLKSK	TDTLD	LPEKTS	WVKFN	VDNSNGYI	IVHYEGHGW	DLITQL	NQNHLL	RPKD 658				
Db	361	VIHR	HLKSK	TDTLD	LPEKTS	WVKFN	VDNSNGYI	IVHYEGHGW	DLITQL	NQNHLL	RPKD 420				
Qy	659	RVGL	IHDVFL	VQAGRL	TDLK	ALDMM	TYIQLQ	HETSSPALL	GLSYLES	FYHMDR	NI	718			
Db	421	RVGL	IHDVFL	VQAGRL	TDLK	ALDMM	TYIQLQ	HETSSPALL	GLSYLES	FYHMDR	NI	480			
Qy	719	SEN	KRYLLQ	YKPKVI	DRQSW	SDKGS	VWDRML	RSALLKL	ACDLN	HPACIQ	KAAELF	SQW 778			
Db	481	SEN	KRYLLQ	YKPKVI	DRQSW	SDKGS	VWDRML	RSALLKL	ACDLN	HPACIQ	KAAELF	SQW 540			
Qy	779	ESS	GKLNPT	DVLK	IVYSGA	OTTAG	NVLLEQ	YELSMSSA	EQNKIL	VALSTSR	HOKELL	838			
Db	541	ESS	GKLNPT	DVLK	IVYSGA	OTTAG	NVLLEQ	YELSMSSA	EQNKIL	VALSTSR	HOKELL	600			
Qy	839	KLIE	LGM	EKGK	VIKTQ	NLAAL	HA	IARRP	KGQQL	AWDFV	RENWTH	LLKFDL	GSYDIR	MI 898	
Db	601	KLIE	LGM	EKGK	VIKTQ	NLAAL	HA	IARRP	KGQQL	AWDFV	RENWTH	LLKFDL	GSYDIR	MI 660	
Qy	899	SGTT	AHFSSK	DLQ	EVKLV	FFES	LEAQ	GGHLDI	FQTV	LETTIT	KNIKW	LEKNL	PTLT	WLMV	958
Db	661	SGTT	AHFSSK	DLQ	EVKLV	FFES	LEAQ	GGHLDI	FQTV	LETTIT	KNIKW	LEKNL	PTLT	WLMV	720
Qy	959	NT	960												
Db	721	XT	722												

RESULT 11

ID	AAU07829	standard; protein; 941 AA.
XX	AAU07829;	
XX	04-DEC-2001	(first entry)
XX	Human	ARTS-1 polypeptide.
XX	Human;	aminopeptidase regulator of type I; cytokine signalling; ARTS-1;
XX	KW	tumour necrosis factor receptor ectodomain shedding; interleukin-1;
KW	interleukin-6;	immune disorder; TNF-mediated immune disease;
KW	inflammatory disorder;	anti arthritic; vasotropic; immunomodulator;
XX	immunosuppressive;	antibacterial; gene therapy.

OS	Hom sapiens.	
XX	Key	Location/Qualifiers
FT	Domain	350..361
FT		/label= Zinc_binding domain
FT	Domain	353..376
FT		/label= Zinc_metalloproteinase_catalytic_motif
FT	Domain	372..379
FT		/label= Zinc_binding_catalytic_site
XX	WO200164856-A2.	
XX	07-SEP-2001.	
XX	28-FEB-2001;	2001WO-US006464.
XX	28-FEB-2000;	2000US-0185586P.
XX	(USSH)	US DEPT HEALTH & HUMAN SERVICES.
XX	Levine S;	
XX	WPI;	2001-550175/61.
XX	N-PSDB;	RA03227.
XX	Novel polypeptide useful for the regulation of ectodomain shedding of type I, tumor necrosis factor receptor and other cytokine receptors and for treating disorders and diseases of the immune system.	
XX	Claim 2; Fig 1;	139pp; English.
CC	The present invention relates to the isolation of a novel human polypeptide, defined as aminopeptidase regulator of type I, 55 kDa tumour necrosis factor (TNF) receptor ectodomain shedding (ARTS-1), and the polynucleotide sequence encoding for ARTS-1. The invention describes compositions and methods for the regulation of cytokine signalling through the TNF pathway. The ARTS-1 polypeptide and antibodies that bind ARTS-1 are useful for regulating the shedding of the extracellular domain of a cytokine receptor such as type-1 tumour necrosis factor receptor, type I or II interleukin-1 cytokine receptor and interleukin-6 cytokine receptor alpha-chain gp80, by delivering the molecules to a tissue comprising one or more cells expressing the cytokine receptor or their plasma membrane extracellular surface. The ARTS-1 sequences are useful for treating a subject, preferably human, displaying, suspected of, or at risk of displaying a pathology resulting from abnormal cytokine activity, such as tumour necrosis factor alpha, interleukin-1alpha, lbeta or interleukin-6. A vector comprising the polynucleotide encoding ARTS-1 or interleukin-6. A vector comprising the polynucleotide encoding ARTS-1 is useful in gene therapy. The ARTS-1 sequences are useful in diagnostic and therapeutic regimens in treating immune disorders (e.g. TNF-mediated immune diseases) and inflammatory disorders (e.g. rheumatoid arthritis). The present sequence represents human ARTS-1 polypeptide	
XX	Sequence 941 AA;	

Query Match		49.8%;	Score 2516.5;	DB 4;	Length 941;
Best Local Similarity		51.1%;	Pred. No. 4.4e-218;		
Matches 478;		Conservative 171;	Mismatches 268;	Indels 19;	Gaps 7;
Qy	23	YCLTALPQICICQFSVPSSYHETDPGAPFVATNGRPPWQELRLPSVVIPLHYDLFV	82		
Db	15	FLSSLLALLTV-----STPWCQSTP---ASPCKSDGTPFPWKNIRLPEYVIPHYDILLI	67		
Qy	83	HPNLTSLDFVASEKIEVLVSNATQFIILHKSOLBITNATLQSEDSRMYKPGKELKVL	142		
Db	68	HANLTTLTFWGTTKVEITASOPTSTIILSHHLQISRATLRKGAGERLSE--EPLQVLEH	125		
Qy	143	PAHQIALLVPEKLTPLHLYVAMDFOAKLGDGEGFYKSTYRTILGSTRILATVDPPT	202		
Db	126	PRQIQIALLAPELVLVGLPYTVVHYAGNLSETPHGFYKSTYRTKGBSLRLASTQFPT	185		
Qy	203	QARMAFCFDEPLFKANFSIKIRRESHIALSNMVKVTIEGGLLEDHETTTVMSTY	262		
Db	186	AARMAFCFDEPLFKANFSIKIRRESHIALSNMVKVTIEGGLLEDHETTTVMSTY	245		

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Qy 263 LVAYIVCDFHSLGFTSSGVKSVIYASDPKRNQTHYALQASLKLLDFYKDYFYIYPLSK 322
Dy 246 LVAFIISFVSVKITKSVKSVYAVVDPKINQADYALDAATLLEFVEDYFSPYLPK 305
Qy 323 LDLIAIPDFAGAMENWGLIYRSTSLFDPKTSASDKLWTRVIAHELAHQWFGNLVT 382
Dy 306 QDLAAIPDFQSGAMENWGLIYRSTSLFDPKTSASDKLWTRVIAHELAHQWFGNLVT 365
Qy 383 MEWNDIWLKEGFAKYMELIAVNAVITYPELQDDYFLNVCFEVITKDSINSRPISKAET 442
Dy 366 MEWNDIWLKEGFAKYMELIAVNAVITYPELQDDYFLNVCFEVITKDSINSRPISKAET 425
Qy 443 PTQIOMEDFVSYNKGCACILNMLKDFLGEERFQKGIQYLLKFKSYRNAKNDLWSSLSNS 502
Dy 426 PAQIREMFDDVSVDKGCACILNMLREYLSADAFKSGIYQLKHSYKNTKNEDLWDSMASI 485
Qy 503 CLESDFTS--GVCHSDPKMTNMLAFLEGENAEVKEMMTTWLOKGPLLVVVKQDGSCLR 560
Dy 486 C-PTDGVKMGDFC-SRSQHSSSSHWHQEGVDVKTMTWNTWLOKGPLLITITVGRNVH 543
Qy 561 LQERFLQGVQEDPEWALQERYLWHLPLTYSTSSNVHRIHLKSKTDTLDLPEKTSW 620
Dy 544 MKQEHYMGK-----SDGAPTGYLWHVPLTFITSKSDMVHRFLTKTNDVLLIPEEVEW 597
Qy 621 VKFNVDNSGYIYVHVEGHGWLQITQLNQNHLLRPKDRVGLIHDVFLVAGAGRLTLDKA 680
Dy 598 IKFNVMNGYIYVHVEDDGBSLTGLLKGTHVASSNDRASLINNAQLVSGIKLSIEKA 657
Qy 681 LDMTYLQHETSSPALLBGLSVLSFYHMDRRNISIDENLKYLLQYFKPVIDRQSW 740
Dy 658 LDLSLLKHETEIMPVFQGLNELIPMYKMEKRDWNEVETQKAFRLRLRLDLIDKQWT 717
Qy 741 DKGSVMDWLSALLKLACDLNAPCIQKAEELSQWMESSGKLNIPDVLKVIYVGAQ 800
Dy 718 DEGSVSEMLRSQLLLAACHVNYQCVQASGYFRKWKESNGNLSLPVDVTLAVFAVGAQ 777
Qy 801 TTAGWNYLLEQVELSMSSAEONKILYALSTSKHOKELKLIELGMEGVKVIKTQNLAAHLH 860
Dy 778 STEGWDFLYSKYQFSLSTESKQLEFALCRQNKELQWLDESPKGDKIKTQFPQILT 837
Qy 861 AIARRPKQQLAWDFVRNETHLLKKFDLGSYDIRMISGTHAFHSSKKDLQEVKLFPES 920
Dy 838 LIGRNPVGYLAWOPFLRNWKNLVQKPELGSSIAHVMVGTNQFSTRLEEVKGFSS 897
Qy 921 LEAGSHLDIFQTVLETITTKIKLEKNLPTLRTWL 956
Dy 898 LKENGSQLRCVQQTETIENIGWMDRKNDFKIRVWL 933

RESULT 12
ABB90347
ID ABB90347 standard; protein; 941 AA.
XX
AC ABB90347;
XX
DT 24-MAY-2002 (first entry)
XX
DE Human polypeptide SEQ ID NO 2723.
XX
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
KW vulnery; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiac; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein.
XX
OS Homo sapiens.
XX
PN WO200190304-A2.
XX
PD 29-NOV-2001.
XX
PF 18-MAY-2001; 2001WO-US016450.
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XX 19-MAY-2000; 2000US-020551SP.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
PI Birse CE, Rosen CA;
DR WPI; 2002-122018/16.
DR N-PSDB; ABL90756.
XX
PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
PT prevention of neural, immune system, muscular, reproductive,
PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
PT disorders.
PS Claim 11; SEQ ID NO 2723; 2081pp + Sequence Listing; English.
XX
CC The invention relates to novel genes (ABL9449-ABL90853) and proteins
CC (ABB9040-ABB90444) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, diabetes mellitus, Crohn's disease,
CC anaemia, autoimmune thyroiditis, allergies, autoimmune haemolytic
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at fp.wipo.int/pub/published\_pct\_sequences
XX
SQ Sequence 941 AA;
Query Match 49.8%; Score 2515.5; DB 5; Length 941;
Best Local Similarity 51.0%; Pred. No. 5.5e-218;
Matches 477; Conservative 172; Mismatches 268; Indels 19; Gaps 7;
Qy 23 YCTAILPQICISQSPVSSYHFTDPGAFVATNGERFPWQELRLPSVVIPLHYDLFV 82
Dy 15 FLLSLALLTLTV---STPSWCQSTE---ASPRSDGTFFPMNKIRLPEVIVPHYDILLI 67
Qy 83 HPNLTSLDFVASEKIEVLVSNATQFIILHSKDLLEITNATLQSEEDSRMYKPGKELVLSY 142
Dy 68 HANLTTLTFWGTTKVEITASQPTSTIILSHHQLISRATLURKAGERKLS--EPLQVLEH 125
Qy 143 PAHEQIALLVPEKLTPLHLKYVYVAMDFOAKLGDGFEGFYKSTYRTLGGETRLAVTDPEPT 202
Dy 126 PPOEQIALLAPEPLLVGLPYTVVIHVAGNLSETFHGFYKSTYRTKEGELAILASTQFPT 185
Qy 203 QARMAPCPDEPLFKANFSIKIRRESRHIALSNMPKVTTELGGLEDHFETVTKMSTY 262
Dy 186 AARMAPCPDEPAFKASFSIKIRREPRHLAISNPLVKSVTVAEGLTFHDTVTKMSTY 245
Qy 263 LVAVIYVCDHSLGFTSSGVKSVIYASDPKRNQTHYALQASLKLLDFYKDYFYIYPLSK 322
Dy 246 LVAFIISDFVSVKITKSVKSVYAVVDPKINQADYALDAATLLEFVEDYFSPYLPK 305
Qy 323 LDLIAIPDFAGAMENWGLIYRSTSLFDPKTSASDKLWTRVIAHELAHQWFGNLVT 382
Dy 306 QDLAAIPDFQSGAMENWGLIYRSTSLFDPKTSASDKLWTRVIAHELAHQWFGNLVT 365
Qy 383 MEWNDIWLKEGFAKYMELIAVNAVITYPELQDDYFLNVCFEVITKDSINSRPISKAET 442
Dy 366 MEWNDIWLKEGFAKYMELIAVNAVITYPELQDDYFLNVCFEVITKDSINSRPISKAET 425
Qy 443 PTQIOMEDFVSYNKGCACILNMLKDFLGEERFQKGIQYLLKFKSYRNAKNDLWSSLSNS 502
Dy 426 PAQIREMFDDVSVDKGCACILNMLREYLSADAFKSGIYQLKHSYKNTKNEDLWDSMASI 485
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QY 681 LDMYYLOHETSSPALLGLESLYSEFYHMDRNISDIENLKRVLQYFKPVIDRQWS 740
Db LLSLYLKHETEMPVFOGLNELIPMYKLMKRDWNEVETQKAFILRLDLIDKQWT 717
QY 741 DKGVSWMRLRSALLKLACDLNHPACIOKAALFQWMESSGKLNIPDVLKIVYVGAQ 800
Db DEGSVSERMLRSELLLACVHNYQPCVQRAEGYFRKWKESNGNLSLVDVTLAVFAVGAQ 777
QY 801 TTAGWNYLLEQVELSMSSAEONKILYALSTSKHQBKLLKLIELGMGKVIKTONLAALLH 860
Db STEGWDPLYSKYQFSLSTESQIBFALCQNKELQWLDESFPKDKIKTQEPQILT 837
QY 861 AIARPKGOQLAWDFVRENWTHLLAKFDLGSYDIRMIISGTTAHFSSKDKLQEVKLPFES 920
Db LIGRNPVGYPLAWQFLRKNNKLVQKFLGSSIAHMYGTTNQFSTRLEEVKGFPS 897
QY 921 LEAQSHLDIFQTVLETITKNIKWLKKNLPTLRWL 956
Db LKENGSQLRCVQQTETIENIGWMDKKNFDIRVWL 933
RESULT 15
ABR00040
ID ABR00040 standard; protein; 941 AA.
XX ABR00040;
AC ABR00040;
XX
DT 03-APR-2003 (first entry)
XX
DE Human gene 30 encoded secreted protein HDPBA28, SEQ ID NO:329.
XX
KW Human; secreted protein; digestive disorder; gastrointestinal disorder;
KW mouth; oesophagus; stomach; small intestine; large intestine; liver;
KW biliary tract; pancreas; cancer; tumour; hyperproliferative disorder;
KW immune disorder; inflammation; infection; wound healing; drug screening;
KW chromosome identification; chromosome mapping; cytostatic; gene therapy;
KW antiinflammatory; immunosuppressive; vulnerary; chromosome 5q14.3.
XX
OS Homo sapiens.
XX
PN WO200276488-A1.
XX
PD 03-OCT-2002.
XX
PF 19-MAR-2002; 2002WO-US008276.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
FA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2003-029900/02.
DR N-PSDB; ABZ71219.
XX
PT New human secreted proteins and nucleic acids, useful for detecting,
PT preventing, diagnosing, prognosticating, treating and/or ameliorating
PT e.g. gastrointestinal diseases and disorders, or cancers.
XX
PS Claim 13; Page 953-955; 1216pp; English.
XX
CC ABZ71190-ABZ71478 represent cDNAs corresponding to 178 human secreted
CC protein genes, and ABP00011-ABP00299 represent the proteins they encode.
CC ABZ71479-ABZ71540 represent human secreted protein genomic fragments. The
CC invention also encompasses antibodies specific for the secreted proteins,
CC the use of the secreted proteins in drug screening, and recombinant
CC vectors and host cells comprising a nucleic acid of the invention. The
CC secreted proteins, nucleic acids encoding them, antibodies or antibody
CC fragments specific for the secreted proteins, and modulators of protein
CC activity are useful for diagnosing, treating, ameliorating or preventing
CC digestive disorders. Such conditions include disorders of the mouth,

CC oesophagus, stomach, small intestine, large intestine, liver, biliary
CC tract and pancreas, and include cancers of these organs and tissues. The
CC secreted proteins and their nucleic acids may also be used in the
CC treatment of immune disorders, inflammation, infection,
CC hyperproliferative disorders, and to promote wound healing. Nucleic acids
CC of the invention may be used for chromosome identification, chromosome
CC mapping, in gene therapy, for identifying individuals from minute
CC biological samples, as hybridisation probes, and as molecular weight
CC markers. The present sequence represents a human secreted protein of the
CC invention
XX
SQ Sequence 941 AA;

Query Match 49.8%; Score 2515.5; DB 6; Length 941;
Best Local Similarity 51.0%; Pred. No. 5.5e-218;
Matches 477; Conservative 172; Mismatches 268; Indels 19; Gaps 7;

QY 23 YCLTAIILPQICICQSFVSPSSYHFTEDPGAPVATNGERRPPQELRLPSVVIPLHYDLFV 82
Db FLSSLLALLTV-----STPSWCQSTE---ASPKSDGTPFPWNKIRLPEYVIPVHYDILLI 67
QY 83 HPNLTSLDFVASEKIEVLVSNATQFIILHSKDLBITNATLQSEBDSRYMKPKELKVLVS 142
Db HANLTTLTFWGTTKVEITASQPTSTIILHSHHLQISRATLAKGAGERLSE--EPLQVLEH 125
QY 143 PAHQIALLVPEKLTPLHLKYVAMDFOAKLGDGEGFYKSTYRTLGGSTRILAVTDPEPT 202
Db PPQEQIALLAPEPLLVGLPYTVVIHYAGNLSETHFGFYKSTYRTKEGELRLASTQFEPT 185
QY 203 QARNAFCDEPLKANKFSIKIRRESRHIALSNMPKVKTIIEGGLLEDHDEPTTVKMSTY 262
Db AARNAFCDEPAPKASFSIKIRPREHLAISNPLVKSIVVAEGLIEDHEDFVTVKMSTY 245
QY 263 LVAYIVCDFHSLSGFTSSGVKSVIYASPKENQTHYALQASLKLLDFEYKFDIYIPLSK 322
Db LVAFIISDFESVSKITKSGVKSVYAVDPKNQADYALDAAVTLLEFYEDYFISYPLPK 305
QY 323 LDLIAIPDFAPGAMENGLITYRETSLLFPDKTSASDKLVWTRVIAHELAHQFNGNLVT 382
Db QDLAAIPDFQSGAMENGLITYRESALLFDAEKSASSKLGITMTVAHELAHQFNGNLVT 365
QY 383 MEWMDNLWKEGFAKYMELTAVNATYPELODFVFNVCREVITKDSINSSRPSTKPAET 442
Db MEWMDNLWKEGFAKFMFVSVSVTHPELKVGDYFFGKCFDAMEVDALNSHPSTPVEN 425
QY 443 PTOIEMFDEVSNKGACILNMLKDFLGEKFKQGIQYKKFSYRNAKNDLMSLSNS 502
Db PAQIREMFDDVSYDKGACILNMLREYLSADAFKSGIVQLQKHSYKNTKNEDLNDSMASI 485
QY 503 CLESDFTS--GVCHSDPKMTSNMLAFGENAEVKEMMTTWTLOKIPLLVVKQDGCCLR 560
Db C-PTDGVKMGDGC--SRSQHSSSSSHWHQEGVDVKTWMTWTLOKGFPLITITVRGNVH 543
QY 561 LOQERFLQGVQEDPEWRALQERYLWHIPLTYSTSSSNVHRHILKSTDTLDLPEKTSW 620
Db MKQEHYKMG-----SDGAPDTGYLWVPLTFTITSKSDMVHRFLTKTDLVLLPEEVEM 597
QY 621 VKFNVDNGYIYVHVEGHGMDQLITQLNQNHLLRPKDRVGLIHDVFOLVAGARLTLDKA 680
Db IKFNVGNGYIYVHVEDDGDWDSLTLGLKGTHTAVSSNDRASLINNAQVLSIGKLSIEKA 657
QY 681 LDMYYILOHETSSPALLGLESLYSEFYHMDRRNISDIENLKRVLQYFKPVIDRQWS 740
Db LLSLYLKHETEMPVFOGLNELIPMYKLMKRDWNEVETQKAFILRLDLIDKQWT 717
QY 741 DKGVSWMRLRSALLKLACDLNHPACIOKAALFQWMESSGKLNIPDVLKIVYVGAQ 800
Db DEGSVSERMLRSELLLACVHNYQPCVQRAEGYFRKWKESNGNLSLVDVTLAVFAVGAQ 777
QY 801 TTAGWNYLLEQVELSMSSAEONKILYALSTSKHQBKLLKLIELGMGKVIKTONLAALLH 860
Db STEGWDPLYSKYQFSLSTESQIBFALCQNKELQWLDESFPKDKIKTQEPQILT 837

Qy	861	AIARRPKGQQLAWDFVRENWTHLLKKFDLGSYDIRMIISGTTAHFSSKDKLQEVKLEFES	920
Db	838	LIGRNPVGYPLAQFLRKNWKLQKFEFGSSIAHVMGTTNQFSTRTRLEEVKGFSS	897
Qy	921	LEAGSHLDIFQTVLETITKNIKWLEKNLPTLRTWL	956
Db	898	LKENGSQLRCVQQTETIETIENIGWMDKNFDKIRVWL	933

Search completed: September 26, 2005, 06:07:26
Job time : 177 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 26, 2005, 06:03:26 ; Search time 48 Seconds
(without alignments)
1924.335 Million cell updates/sec

Title: US-10-039-073-1
Perfect score: 5052
Sequence: 1 MFHSSAMVNSHRKWFNTHR.....NIKMLEKNLPTLRWLMVNT 960

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: piri:*
2: piri:*
3: piri:*
4: piri:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	%			DB	ID	Description
	Score	Match	Length			
1	1999	39.6	1006	2	A59384	oxytocinase/insuli
2	1999	39.6	1025	2	A59383	oxytocinase/insuli
3	1771	35.1	916	2	I55441	vp165 - rat
4	1440	28.5	957	2	A47531	glutamyl aminopept
5	1390.5	27.5	945	2	S30398	aminopeptidase N h
6	1327	26.3	1025	2	I59331	thyrotropin-releas
7	1312	26.0	965	2	A32852	membrane alanyl am
8	1269	25.1	963	2	A53984	membrane alanyl am
9	1264.5	25.0	967	2	A30325	membrane alanyl am
10	1214	24.0	920	2	T10052	aminopeptidase (EC
11	1176	23.3	805	2	S07099	membrane alanyl am
12	1151	22.8	884	2	T29637	hypothetical prote
13	1116	22.1	844	2	S37794	aminopeptidase ysc
14	1067	21.1	856	2	S46750	aminopeptidase f
15	1047.5	20.7	882	2	T3789	hypothetical prote
16	1039	20.6	988	2	T24668	laeverin - human
17	1031	20.4	990	2	JC8058	glutamyl aminopept
18	899.5	17.8	873	2	T05189	lysyl aminopeptida
19	895.5	17.7	849	2	JC7959	aminopeptidase y
20	893.5	17.7	849	2	JU0191	aminopeptidase Y (
21	888.5	17.6	785	2	S73098	aminopeptidase (EC
22	875	17.3	844	2	S47274	membrane alanyl am
23	873	17.3	846	2	A86663	tricorn proteinase
24	871.5	17.3	784	2	B90442	membrane alanyl am
25	870	17.2	843	2	S38364	membrane alanyl am
26	868	17.2	844	2	JC4054	membrane alanyl am
27	865	17.1	848	2	B97960	membrane alanyl am
28	864	17.1	848	2	E95092	aminopeptidase N [
29	856	16.9	846	2	JN0324	lysine aminopeptid

RESULT 1

A59384

oxytocinase/insulin-responsive aminopeptidase, variant 2 [imported] - human

C:Species: Homo sapiens (man)

C:Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 20-Apr-2001

C:Accession: A59384

R:Rasmussen, T.E.; Pedraza-Diaz, S.; Hardre, R.; Lausteen, P.G.; Carrion, A.G.; Kristens

Eur. J. Biochem. 267, 2297-2306, 2000

A:Title: Structure of the human oxytocinase/insulin-regulated aminopeptidase gene and 1c

A:Reference number: A59384; MUID:20223264; PMID:10759854

A:Accession: A59384

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1006 <STO>

A:Cross-references: GB:CA894753; NID:G8574036; PIDN:CA894753.1

C:Superfamily: membrane alanyl aminopeptidase

Query Match	39.6%;	Score 1999;	DB 2;	Length 1006;
Best Local Similarity	44.2%;	Pred. No. 3.8e-118;	Indels 36;	Gaps 6;
Matches	400;	Conservative 160;	Mismatches 310;	
Qy	54	PVATNGERFPWQELRLPSVWIPLHYDLFVHPNLTSLDFVASEKLEVLVSNATQFIILHSK	113	
Db	134	PFATNGKLPFWAQLRLPTAVVPLRYELSLHPNLTSMTPRGSVTISVQALQVTWNILLST	193	
Qy	114	DLEITNATLQSEEDSRYMKGKELKVLISYPAGEQIALVPEKLTPLHLYKYVAMDFQAKLG	173	
Db	194	GHNISRVTFMSAVSQ-----EKQAEILEYAHGQIAIYVAPALLAGHNYITKIKIESANIS	249	
Qy	174	DGFEFGYKSTYRTILGGETRIILAVTDPEPTQARMAPPCDEPLFKANFSIKIRRESRHIAL	233	
Db	250	SSYGYGFYSYTDSENEKKYPAATQFEPLAARSAPPCDEPAFAKATFIKIIRDQYALT	309	
Qy	234	SNMKYKTIIEGGLLEHDHFTTKMSTLYVAYVCDPHSLSGFTSSGVKSYIYASPKR	293	
Db	310	SNMKPKSVWLDDGLVQDFESVKMSYLVAFIVGEMKNLSQ-DVNGTLVSIYAVPENI	368	
Qy	294	NOTHYALQASLKLDFYKDYDIYVPLSKLDLIAIPDPAPGAMENWGLITVRETSLLFDP	353	
Db	369	QGVHYALETTVKLLEFFQNYFEIQYPLKLLDLVAIPDFEAGAMENWGLITVRETSLLFDP	428	
Qy	354	KTSSASDKLWTRVIAHELAHQWFGNVLVTMWNNDIWLKEGFAKYMELIANNATYPEIQF	413	
Db	429	NTSSMAADKLVTKIIAHELAHQWFGNVLVTMWNNDIWLKEGFAKYMELIANNATYPEIQF	488	
Qy	414	DDYFLNVCFEVITKDSINSSRPISKPAETPQIQEMFDEVSYNKGCATLNMKPLGEEK	473	
Db	489	YEDFLDARFTMKKDSINSSHPISSSVQSSQISEMFDLSYFKGSSLLMLKTYLSDDV	548	
Qy	474	FOKGIIOYLLKFKFSYRNKAKNDLWSLSNCSLESDFTSGGVCHSDPKMTSNMLAFGENAE	533	
Db	549	FQHAVVLYLHNHVASIQSDLLWDSFN-----EVTNQTL-----D	583	


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Db 213 GNISSVTMSAVSQ-----EKQVEILEYYPYHEQIAVAPESLLTGHNYTLKIEYSANIS 268
Qy 174 DGFEGFYKSTYRTLGGETRIILAVTDFEPTQARMAPCPDEPLFKANFSIKIRRESRHIAL 233
Db 269 NSYGYFYGYITDKSNEKKVFAATQEPLEAARSAPCFDEPAFAKATFIKIRDRHHTAL 328
Qy 234 SNMPKVKTIELBGGLELDEHFETVTKMSYLVAYIVCDPHSLSGFTSSGVKYSIYASPKR 293
Db 329 SNMPKKSVPTEBGLIQDEFSSVSKMSYLVAFIVGEMRNLSQ-DVNGTLVSVYAPKEI 387
Qy 294 NOTHYALQASLKLDFYKVDYIYVPLSKLDLIAIPDFAPGAMENWGLITVRETSLLDPP 353
Db 388 DQVYHALDQTVKLLSFYQNYPEIQIPLKLDLVAIPDFEAGAMENWGLITFREETSLLYDN 447
Qy 354 KTSASDKLWVTRVTAHSLAHQWFGNLVTMEWNDIWLKKEGFAKYMELIYVAVNATYPELQF 413
Db 448 ATSSVADRLKVTKIITAHSLAHQWFGNLVTMQWMDLWLNQEGFATPMWFYSVEKIPKELNS 507
Qy 414 DDYFLNVCFEVTIKDLSNRRSPISKAPETPTQIQEMFDEVSNKACILNMLKDFLGEEK 473
Db 508 YEDFLDARFKMRKDSLNSHPISSSVQSSEQIEEMFDSLSYFKGASLLMLKSYLSDEV 567
Qy 474 FQKGIQYLYKFSYRNKNDLWSSLNSCLESDFTSQGVCHSDPKMTSNMLAFIENAE 533
Db 568 FOHALILYLNHNSYAAIQSDDLWDSFNE-----VTGKTLTD 602
Qy 534 VKEMMTWTLOKGIPLLVVKGDCSLRLQQRFLQGVQEPDEWRALQERYLWHIPLTYS 593
Db 603 VKQMKWTWLOKGFPLVTVQKGTTELLQQRFFPSM--QPEIQDSDTSLHWHIPISYV 659
Qy 594 TSSSNVHRRH---ILKSTDTLDLPEKTSVWKNFVDSNGYIVHYEGHGWOLITQLNQ 650
Db 660 TDGRNYSYRSVSLDKSDVINLQEQVQVKNVTNMTGYIVHYAHGWAALINQLKRN 719
Qy 651 HTLLRPKRVGLIHDVQVGLVAGRLTLDKALDMTYLLOHETSSPALLSGLSVLESFYHM 710
Db 720 PYVLSKDRANLINNIFELAGLGKVPLOQWAFPLIDYLRNETHAPTALFQTDIYNLL 779
Qy 711 DRRNISDISENLKRYLLQVFKPVIDRQWSKGSVMDRLRSALIKLACDLNHAPCIQA 770
Db 780 EKLGHMDLSRLVTRVHKLLNQIQOQTWDEGTFSMRELSALLFEACASLENCTTWA 839
Qy 771 AELFSQWMESSKUMIPTDLVKIVYSGAQTAGNYYLLEQYELSMSSAEQNKILYALST 830
Db 840 TKLFDGWMASNGTSLPTDVMVTTFKVGARTEKGMFLFMSYSSMGSAEKDKILEALAS 899
Qy 831 SKHQEKL 837
Db 900 SADAHKL 906

RESULT 4
A47531
Glutamyl aminopeptidase (EC 3.4.11.7) - human
N:Alternate names: aminopeptidase A; differentiation antigen gp160
C:Species: Homo sapiens (man)
C:Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 09-Jul-2004
C:Accession: A47531; A48287
R:Li, L.; Wang, J.; Cooper, M.D.
Genomics 17, 657-684, 1993
A:Title: cDNA cloning and expression of human glutamyl aminopeptidase (aminopeptidase A)
A:Reference number: A47531; MUID:94063909; PMID:8244382
A:Accession: A47531
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-957 <Lia>
R:Nanus, D.M.; Engelstein, D.; Gastl, G.A.; Gluck, L.; Vidal, M.J.; Morrison, M.; Finsta
Proc. Natl. Acad. Sci. U.S.A. 90, 7069-7073, 1993
A:Title: Molecular cloning of the human kidney differentiation antigen gp160: human amin
A:Reference number: A48287; MUID:93348214; PMID:8346219
A:Accession: A48287
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A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-217, 'A', 219-957 <NAN>
A:Cross-references: GB:L14721; NID:g291853; PIDN:AAA35522.1; PID:g291854
C:Genetics:
A:Gene: GDB:ENPEP
A:Cross-references: GDB:L38283; OMIM:L38297
A:Map position: 17pter-17p12
C:Superfamily: membrane alanyl aminopeptidase
C:Keywords: aminopeptidase; glycoprotein; transmembrane protein

Query Match 28.5%; Score 1440; DB 2; Length 957;
Best Local Similarity 34.1%; Pred. No. 7.3e-83;
Matches 322; Conservative 178; Mismatches 362; Indels 82; Gaps 19;

Qy 40 VPSSYHFTEDPGAPFV-----ATNGERFPWQELRVPVPIPLHYDLFVHPNLTSLDFV 92
Db 60 LPSS---TASPSGPPAQDQDICPASEDSGQMKNFRLPDFVNPVHYDLHVRPLLEEDTYT 116
Qy 93 ASEKIVLVSNATQFIILHSKDLBITNATLOSEDSRYMKP-GKELKV---LSYPAHQEI 148
Db 117 GTVSGISINLSAPTRYLMHLRETRITRL-----PELKRPESGQVQVRCFCFYKQBYV 169
Qy 149 ALLVPEKLTPLH---KYVAMDFOAKLGDGPEGFVKSTYRTLGGETRIILAVTDREPTOAR 205
Db 170 VVEAEELTPSSGGLYLLTMEFAGLNGSLVGFRITTY-TENGRVKSIIVATDHEPTDAR 228
Qy 206 MAFFCFDEPLPKANFSIKIRRESRHIALSNMPKVKTIIELEGGLLEDHFETVTKMSYLV 265
Db 229 KSFFCFDEPNKATYITSIHPKEYGALSNMPKAKEESVDDKWTRTTTEKSVPMNLTSLVC 288
Qy 266 YIVCDFHSLSGFTSSGVKYSIYASPKRNOHYALQASLKLDDFYKFDYIYPLSKLDL 325
Db 289 FAVHQFDSVKRISNSGKPLTIYVQPEQKHTAEYAANITKSVDFYFEEYFAMNYSPLKDK 348
Qy 326 IAIIDPAPGAMENWGLITVRETSLLFPKTSASDKLWTVTVIAHSLAHQWFGNLVHMEW 385
Db 349 IAIIDFGTGAMENWGLITVRETNLLYDPKESASSNQQRVATVVAHELHQVFGNIVTMDM 408
Qy 386 WNDIWLKGEFAKYMELIYVAVNATYPELAF-DDYFLNVCFEVTIKDLSNRRSPISKAETPT 444
Db 409 WEDLMLNEGFAFPFELGVNHAETDQWRDQMLLEDVLVPEQEDDSLMSSHPIIVTTPD 468
Qy 445 QIQEMFDEVSNKACILNMLKDFLGEEKFQKGIQYLYKFSYRNKNDLWSSLNSGL 504
Db 469 EITSVFDGISYSGSSILRMLDEWIKPENFOKGCQVLEKYQFKNAKTSDFWAALAEA-- 526
Qy 505 ESDFTSGGVCHSDPKMTSNMLAFIENAEVKEMMTWTLOKGIPLLVVKGDCSLRLOQE 564
Db 527 -----SRLPVKEVMDTWTQMGYPVLNV--NGVK-NITQK 558
Qy 565 RFLQGVFQEDPEWRALQF---RYLWHIPLTY-----STSSSNVVIHRHILKSTDTLDLPEK 617
Db 559 RFLD-----DPRANPSQPPSDGLYTWIIPVKWTDENITSSVLFPNRSKEGITLSSNPSG 613
Qy 618 TSWKFNVDNGYIVHYEGHGWOLITQLNQNTLLRPKDRVGLIHDVQVGLVAGRLTL 677
Db 614 NAFKLINPDHIGFVRVNVVATWDSIATLSLNKHTFSSADRSALIDDAFALARAQLLDY 673
Qy 678 DKALDMTYLLOHETSS---PALLSGLSVLESFYHMDRRNISDISENLKRYLLQVFKPVI 734
Db 674 KVALNLTLYLKRNEFLFPQWRVISAVTYIISMF-----EDDKELYPMIEEYFQGVKRIA 728
Qy 735 DRQWSKGSVMDRLRSALIKLACDLNHAPCIQKAAELFSQWMESSKUMIPTDLVKIV 794
Db 729 DSLGWNDAQDHVTKLRLSSVLGFPACKMGDREALNASSLFEQWL--NGTVSLPVLNRLLV 786
Qy 795 YSVGAQTTA---GWNYYLLEQYELSMSSAEQNKILYALSTSKHQEKLKLIBEGHEGKVIK 851
Db 787 YRYQMONGNEISNNYTLQYQKTSLAQEKELLYGLASVKNVTLRLSYRLDLLKDTNLIK 846
Qy 852 TQNLALLHAIRAPKQQLAWDPVRENWTHLLKFKFDLGSYDIRMILSGTTAHSFSSKDKL 911
Db 911
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Db 847 TQDVFTVIRYISYNGKNMANNIQLNWDVLYNRYTINNRNLGRIVT-IAEPNTELOL 905

Qy 912 QEVKLFRESLEAQSGLDIFQTVLETTITKNIKMLEKNLPTLRW 955

Db 906 WQMESFFAKYPQAGAGKPREQVLETVKNINIEWLKQHRNTIREW 949

RESULT 5

S30398

aminopeptidase N homolog BP-1/6C3 - mouse

N/Alternate names: surface antigen BP-1/6C3

C/Species: Mus musculus (house mouse)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

R/Wu, Q.; Lahti, J.M.; Air, G.M.; Burrows, P.D.; Cooper, M.D.

Proc. Natl. Acad. Sci. U.S.A. 87, 993-997, 1990

A/Title: Molecular cloning of the murine BP-1/6C3 antigen: a member of the zinc-dependent

A/Reference number: S30398; MUID:90139003; PMID:1689065

A/Accession: S30398

A/Molecule type: mRNA

A/Residues: 1-945 <WUQ>

A/Cross-references: UNIPROT:P16406; EMBL:M29961; NID:g191947; PIDN:AAB47732.1; PID:g3091

C/Superfamily: membrane alanyl aminopeptidase

C/Keywords: disulfide bond; glycoprotein; homodimer; membrane protein; phosphoprotein; s

Query Match 27.5%; Score 1390.5; DB 2; Length 945;

Best Local Similarity 34.0%; Pred. No. 9.6e-80;

Matches 322; Conservative 168; Mismatches 373; Indels 85; Gaps 20;

Qy 26 TAILPQICICQSFVSPSYHFTDPGAPPVATNGERFPWQELRPSVVIPLHYDLFVHPN 85

Db 60 TALPQ-----DQNVCPDS-----ESGE-----WKNFLRDPFINPVHYDLEVKAL 101

Qy 86 LTSLDVFASEKIEVLVSNATQFIILHSDKLEITNATLQSEDSRYMKPGKE-----LKVL 141

Db 102 MEEDRYTGIVTISVNLKPTKTRDLWHIRETKITKL-----PELRPSPGEQVPIRCFE 154

Qy 142 YPAHEQIALLVPEKL-----TPHLKYVAVMDFOAKLGDGEGFYKTYRTLGETRILAVTD 198

Db 155 YKQEVYVIOAEDLAATSGDSVRLTMEFKGLWLSLGVFYKTYME-DQIRSIATD 213

Qy 199 FEPTQARMAPCFDEPIFLKANSIKIRRESRIALSNMVKVTIELEGGLLEDFETTVK 258

Db 214 HEPTDARKSPFCDEPNKSTYSIIHPKEYSALSNNPEKSBWDDNKKTTFVKSP 273

Qy 259 MSTYLVAIVCDFHSLSGFTSSGVKVSIIYASPKRQNTQHYALQASLKLLDFEYKYPDIY 318

Db 274 MSTYLVCFAVHRFTAIRKRSRGKPLKYVQPNQKETAAYAANITQAVFYDFYFAMEY 333

Qy 319 PLSKLDLIAIPDFAPGAMENGLITYRETSLLFPDKTSSASDKLWTVRIAHELHQWFG 378

Db 334 ALPKLDKIAIPDFGTGAMENGLITYRETNLLYDPLLSASNNQORVASVAHELHVQWFG 393

Qy 379 NLVTMEWNMDLWKEGFAKYMELIAVNATYPELO- FDDYFLNVCFEYVITKDSLNSSRPIS 437

Db 394 NTVTMDWDDLWLNQEGFASPEFLGVNHAERQWMLSQVLLEDVFPPQEDDSLMSSHPV 453

Qy 438 KPAETPTQIQEMFDEVSYNKGCATILNMLKDFLGEKFKQGIIOYLKFKFSYRNKNDLWS 497

Db 454 VTVSTPAEITSVDFGISYSGKASILRLQDWITPEKTKQKQIYLYKKFPQANAKTSDPFD 513

Qy 498 SLSNSCLESDFTSGGVCHSDPKMTSNMLAFUGENAEVKEMTTWTLOKGIPLLVV--KQD 555

Db 514 SLQEA-----SNLPVKEVMDWTWSQMGYPVTVTSGRQN 546

Qy 556 GCSLRLOQERFLQGVQEDPEWRALQERYLWHIPLTYSTSSN--VIHRHLKSKTDTLD 613

Db 547 -----ITQKRLD--SKADPSQPPSELGYTNIPVRWADNDNSRITVYNRLDKGGITLNA 600

Qy 614 LPEKTSWKNVDSNGYIVHVEGHWDOLITQLNQHTLLRPKDRVGLHIDVQLVAG 673

Db 601 NLSGDAFLKINPDHIGFYRVNYEGGTMDWIAEALSSNHSNTRFSAADRSSFIDDAFALAAQ 660

Qy 674 RLTLDKALDMTYLYQHETSS---PALLEGSLYSLEFHYHMMDRRNISDISENLKRYLLQYF 730

Db 661 LLNYKIALNLTWYLKSEEDFLPWERTVSSVYIISMPE--DDRELYPMIET--YFQGV 715

Qy 731 KPVIDRQSWSDKGSVMDRLMRSALLKLACDLNHPACTQKAAELFSQMSSESGKLNIPDV 790

Db 716 KPVADLLGMQDTGSHITKLLRASITGLFPACKGMDREALGNASQLFDSWLK--GSASIPVNL 773

Qy 791 LKIVYSUGAQT---AGWNYLLBOYELSMSSAQNKILYALSTSKHQEKLKLTLELWEG 847

Db 774 RLIVRYGMQNSGNEAAWNTLBOYQKTSLAQEKLLYGLASVKDKLLARYLEMLKDP 833

Qy 848 KVIKTQNLAAALLHAIARRPKGQQLAWDFVRENTHLLKKPDLGSDYDIRMIISGTTAHFSS 907

Db 834 NIKTQDVFTVIRYISYNSYSGKTMANNIQLNWDVLYSRETINDRYLGRIVT-IAEPNT 892

Qy 908 KDKLQEVKLPFESLEAQSGLDIFQTVLETTITKNIKMLEKNLPTLRW 955

Db 893 ELQLWQMSFPFAKYPNAGAGKPREQVLETVKNINIEVLNVRQSIREW 940

RESULT 6

I59331

thyrotropin-releasing hormone degrading enzyme (EC 3.4.11.-) - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C/Accession: I59331

R/Schneider, B.; Schomburg, L.; Kohrle, J.; Bauer, K.

Proc. Natl. Acad. Sci. U.S.A. 91, 9534-9538, 1994

A/Title: Cloning of a cDNA encoding an ectoenzyme that degrades thyrotropin-releasing ho-

A/Reference number: I59331; MUID:95023946; PMID:7937801

A/Accession: I59331

A/Status: preliminary; translated from GB/EMBL/DBDJ

A/Molecule type: mRNA

A/Residues: 1-1025 <RES>

A/Cross-references: UNIPROT:Q10836; EMBL:X80535; NID:g558636; PIDN:CAA56675.1; PID:g558636

A/Note: in Genbank entry RRTHRD, release 113.0, the source is designated as Rattus rattus

C/Superfamily: membrane alanyl aminopeptidase

C/Keywords: aminopeptidase

Query Match 26.3%; Score 1327; DB 2; Length 1025;

Best Local Similarity 32.3%; Pred. No. 1.1e-75;

Matches 302; Conservative 171; Mismatches 399; Indels 62; Gaps 16;

Qy 50 PGAPPVATNGER--FPWQELRPSVVIPLHYDLFVHPNLTSLDFVASEKIEVLVSNATOF 107

Db 121 PSAHPSEEBEQWQWPTQLRSLGHLKPLHYNLMTAFMENPTFSGEVNVVIAIQNAIRY 180

Qy 108 IILHSDKLEITNATLQSEDSRYMKFKELKVLISYPAHEQIALLVPEKLTPLHLYKYVAMD 167

Db 181 VVLHARVAVEK--VQVAED-RAFQAVPVAGFFLYPQTQVLVVVNLNRTLDAQRHYNLKII 237

Qy 168 FOAKLGDGFGFYKTYRTLGGETRILAVTDFTQARMAPCFDEPLFKANSIKIRRE 227

Db 238 YNALIENELLGPFSSY-VIHGERRFLGVTFQSPTHARKAPCFDEPIYKATFKISIKHQ 296

Qy 228 SRHIALSNMVKVTIELEGGLLEDFETTVKMTSYLVAVIYVCDPHSLSGFTSSGVKYSIY 287

Db 297 ATYLSNMPVETSVFEEDGWTDFHSQTFPLMSTIYLAWAICNFTYRETTKSGVVVRLY 356

Qy 288 ASPD--KRNTHYALQASLKLLDFEYKYPDIYPLSKLDLIAIPDFAPGAMENGLITYR 345

Db 357 ARPDAIRRGSDYALHITKELIEFYEDYFKVPYSLPKLDDLAVPKHPYAAENMGLSIFV 416

Qy 346 ETSLLFPDKTSSASDKLWTVRIAHELHQWFGNLVTMEWNMDLWKEGFAKYMELIAVN 405

Db 417 EQRIILLDPSSVSSYLLDVTMVIWHEICHQWFGDLVTPVWMDVWLKEGFAHYEFVGTD 476

Qy 406 ATYP--ELQDQDDYFLNVCFEYVITKDSLNSSRPISKPAETPTQIQEMFDEVSYNKGCATILN 463

Db 477 YLPSWNMEKQRFELTVLHEVMDLGLASSHPVSQEVLRATDIDKVPDWTAYKGAALIR 536

Qy 464 MLKDFLGEKFKQGIIOYLKFSYRNKNDLWLSLNSCLESDFTSGGVCHSDPKWTSN 523

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Db 537 MLANFMGHSVFORGIQDYLTIHKYGNARNDLWNTLSALKRN----- 579
Qy 524 MLAFIENAEVEMMTTTLQKGIPLLVVQDGCs---LRQOERFLOQVQEDPEWRAL 580
Db 580 ----GKYVQIEQVMDVQTLQMGYPVITILGNMTAENRILITQOHFIYDIGAUKTALQ 634
Qy 581 QERYLWHIPLTYSTSS-SNVIRHIL-----KSKTDTLDLPEKTSVWKNVDSNGYIVHY 635
Db 635 NSSYLWQIPLTIVVGNRSHVSEALIIWVSNKSEHRIITYLDKGSWILGNINQTYGFRVNY 694
Qy 636 EGHGWDQLITOLNQNHITLLRPKDRVGLIHDVQLVAGAGRLTLDKALDMTYYLQHETS-- 693
Db 695 DLNRWRLIDQIRNHEVLSVNSRAGLDDAFSLARAGTLPONIPLEIRYLSBEKOFPLP 754
Qy 694 -PALLEGISYLESFYHMDRRNISDISENLRYLLQYFKPVIDROSWS------RGS 744
Db 755 WHAASRALYPLDKLDRMENYNI-----FNEYILKQVATTYSKLGPKNNGSVVQAS 808
Qy 745 VDRMLRALLKACLNLHAPICIAELFSQWMESSKLNIPITDVLKIVSVGAGTQTAG 804
Db 809 YQHELRREVIMLACSGFKHCHQOASTLISDWI--SSNRNRIPLNVRDVIYCTGVSLDE 867
Qy 805 --WNYLLQYELSMSSAQNKILYALSTSKQEKLLKILGMECKVIKTONLAALHAI 862
Db 868 DWVEFIWKFHSTTAVSEKKILLEALTCSDRNLSRLNLSNSEVVDQDAIDVITHV 927
Qy 863 ARRPQGOALWDVRENTHLLKPKDLGASDIYRMIISGTTAFHSSKDKLOEVKLPFESLE 922
Db 928 ARNPHGRDLAWKFFRDKWKILNTRYGEALFWNSKLISGTFEFLNTEGELKELKNFMKSYD 987
Qy 923 AQGSHLDIFQTVLEITITKNIKWLEKNLPLTRLTWL 956
Db 988 GVAS--ASFSAVETVEANVRWKRLYQDELFWL 1019

RESULT 7
A32852
membrane alanyl aminopeptidase (EC 3.4.11.2) - rat
N:Alternate names: aminopeptidase N; microsomal aminopeptidase
C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Nov-1989 #sequence revision 22-Nov-1989 #text_change 09-Jul-2004
C:Accession: A32852; A32448; A61250
R:Watt, V.M.; Yip, C.C.
J. Biol. Chem. 264, 5480-5487, 1989
A:Title: Amino acid sequence deduced from a rat kidney cDNA suggests it encodes the Zn-P
A:Reference number: A32852; MUID:89174587; PMID:2564389
A:Accession: A32852
A:Molecule type: mRNA
A:Residues: 1-965 <WAT>
A:Cross-references: UNIPROT:P15684; GB:M25073; NID:g205108; PIDN:AAA41502.1; PID:g205109
R:Malfoy, B.; Kado-Fong, H.; Gros, C.; Giros, B.; Schwartz, J.C.; Hellmiss, R.
Biochem. Biophys. Res. Commun. 161, 236-241, 1989
A:Title: Molecular cloning and amino acid sequence of rat kidney aminopeptidase M: a mem
A:Reference number: A32448; MUID:89273642; PMID:2567164
A:Accession: A32448
A:Molecule type: mRNA
A:Residues: 1-801,'SC',805-806,'A',808-812,'ATVPER',819-830,'VGR',834-965 <MAL>
A:Cross-references: GB:M26710; NID:g601864; PIDN:AAA57129.1; PID:g601865
R:Punkhouser, J.D.; Tangada, S.D.; Jones, M.; O, S.J.; Peterson, R.D.A.
Am. J. Physiol. 260, L274-L279, 1991
A:Title: p146 type II alveolar epithelial cell antigen is identical to aminopeptidase N.
A:Reference number: A61250; MUID:91206591; PMID:1673322
A:Accession: A61250
A:Molecule type: protein
A:Residues: 2-19;68-84;206-212,'X',214-215;286-289,291-299;364-371 <PUN>
C:Superfamily: membrane alanyl aminopeptidase
C:Keywords: aminopeptidase; glycoprotein; membrane protein
F:114,128,234,242,264,555,606,624,780/Binding site: carbohydrate (Asn) (covalent) #statu

Query Match 26.0%; Score 1312; DB 2; Length 965;
Best Local Similarity 32.6%; Pred. No. 96-75; Indels 96; Gaps 26;
Matches 326; Conservative 165; Mismatches 413;
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RESULT 8

A53984

membrane alanyl aminopeptidase (EC 3.4.11.2) - pig

```
Qy 20 RGFY-----CLTALPQICICISQFSVPSSVSHFTED-----PGAPPVATN--- 58
Db 3 KGFYISKTLGILGLGVAACCTIIAALSVVVYAOEKRNAENSAIAPTLPGSTATTSTTN 62
Qy 59 ---GERPWOELRPSVVIPLHYDLFVHPNLTSLD-----FVASEKIEVLVSNATQETIL 110
Db 63 PAIDESKPMQRYRUKTILIPDSYQVTLRPYUTPNEQGLYIFKGSSTVFTCNETTNNVLI 122
Qy 111 HSKDLEITN-----ATLQSEDSRYMKPGKELKVLSPAH-EQIALLVPEKLTPHLKYVV 164
Db 123 HSKKLVNTKGNHRVALRGDGT---PAPNIDITTELVERTEYLVVHLQGLSVKGHQVEM 178
Qy 165 AMDPQAKLGDGFEGFYKSTYRTLTGETRILAVTDFPTQARMAPCFDEPIFKANFSKI 224
Db 179 DSEFQGLADLAGFYRSEYME-QGNKKVWATTQMAADARKSPPCFDEPAMKASFNITL 237
Qy 225 RRESRHIALSNM-PK-VKTILEGGLLEDHPETTVTKMSTYLVAIVTCDHFSLSGPTSSGV 282
Db 238 IHPNNLIALSNMLPKDRTIQEDPSWNVTEFHTPKMSTYLLAYIVSEFKYVEAVSPNRV 297
Qy 283 KVSIVASPKRKNQTH--YALQASLKLLDFEYKFDIYYPLSKLDLIAIPDFAPGAMENWG 340
Db 298 QIRIWARPSAIDEGGDYALQVTGPILNFFPAQHYNTAYPLEKSDQIALPDFNAGAMENWG 357
Qy 341 LITVRETSLPLDPKTSASDKLWTRVIAHELAWHGFNGLVTMEWWDNIWLKEGFAKME 400
Db 358 LVTYRESALVPDQSSSISNKRVTVTIAHELAWHGFNGLVTVDWMNDLWNEGFASVYE 417
Qy 401 LIAVNATYPELQFDYF-LNVCPVITKDSINSRPIKSPA--ETPTQIOEMFDEVSYN 456
Db 418 FLGADYABPTWNLDLVLNDVYRMAVDALASSHPLESSPANEVNTPAQISELFDSTIYS 477
Qy 457 KGACILNMLDFLGEERFKGIIQYLKKFSYRNAKNDLWSSLSNCSLESFTSGGVCHS 516
Db 478 KGASVLRMLSFLLTEDLFKKGLSSYLHTFQYSNTIYLDLWEHLQAV----- 524
Qy 517 DPKWTSNMLAPLGNAEVKEMTTWTQKGIPLLVVQDGCsLRLQGRFLOQVQEDP- 575
Db 525 -DSQTAIKLP-----ASVSTIMDRWILQMGFPVITVNTS--TGEIYQSHFLL-----DPT 571
Qy 576 --EWRALQERYLWHIPLTYSTSSSNVIRHILKSKTDTLDLPEKTS-VWKNVDSNGYVI 632
Db 572 SKTPRPSDFNYLWIVPIPY-LJNKGEDHYWLETENQSAEFQTSNNEWLLNINVTGYIQ 630
Qy 633 VHYEGHGWQDLITQLNQNHITLLRPKDRVGLIHDVQLVAGAGRLTLDKALDMTYYLQHETS 692
Db 631 VNYDENWKRKIQNLQTDLSVIPINRAQIIHDSFNLASACKLSITLPLSNTLFLASETE 690
Qy 693 SPALLEGLSYLESFYHMDRRNISDISENLRY-----LLQYFKPVIDROSWSDK-GS 744
Db 691 YMPWEAALSSLYNYPKLMFDR---SEVYGPWKRYLKKQVTPLPFAYFK--IKTNMILDRPPT 745
Qy 745 VMDRLRSALLKACLNLHAPICIAELFSQWMESSKLNIPITDVLKIVY--SVGAQTT 802
Db 746 LMEQYNEINAISTACSGLEBCDRDLVVGLYSQMMNNSDNNPIHPNLRSTVYCNIAFQGE 805
Qy 803 AGWNYLLEQVELSNESSAEQNKILYALSTSKQEKLLKILGMECKVIKTONLAALHAI 862
Db 806 EEWNFANEQPKATLVNNEADKLRSLACSNVWILNRYLSYTLNPDYIRKQDATSTIVSI 865
Qy 863 ARRPKGOALWDVRENTHLLKPKDLGASDIYRMIISGTTAFHSSKDKLOEVKLPFESLE 922
Db 866 ANNVVGQTLVWDFVRSNNWKKLFEDYGGGFSFANLIQGVTRRFSSEFELOEQEKEDNS 925
Qy 923 AQ--GSHLDIFQTVLEITITKNIKWLEKNLPLTRLTWLVNT 960
Db 926 ATGFGSGTRALEQALEKTKANIKWKENKDVVLKWFTEENS 965
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N;Alternate names: aminopeptidase N; microsomal aminopeptidase N; surface glycoprotein C
 C;Species: Sus scrofa domestica (domestic pig)
 C;Date: 09-Oct-1994 #sequence revision 15-Oct-1994 #text_change 09-Jul-2004
 C;Accession: A53984; S24020; S05040; S13177
 R;Delmas, B.; Gelfi, J.; Kut, E.; Sjoestroem, H.; Noren, O.; Laude, H.
 J. Virol. 68, 5216-5224, 1994
 A;Title: Determinants essential for the transmissible gastroenteritis virus-receptor interaction
 A;Reference number: A53984; MUID:94309188; PMID:7913510
 A;Accession: A53984
 A;Molecule type: mRNA
 A;Residues: 1-963
 A;Cross-references: UNIPROT:P15145; GB:Z39522; NID:G525286; PIDN:CAA82641.1; PID:G525287
 R;Delmas, B.; Gelfi, J.; L'Haridon, R.; Vogel, L.K.; Sjoestroem, H.; Noren, O.; Laude, H.
 Nature 357, 417-420, 1992
 A;Title: Aminopeptidase N is a major receptor for the entero-pathogenic coronavirus TGEV
 A;Reference number: S24020; MUID:92278435; PMID:1330661
 A;Accession: S24020
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 2-31 <DE2>
 R;Olse, J.; Sjoestroem, H.; Noren, O.
 FEBS Lett. 251, 275-281, 1989
 A;Title: Cloning of the pig aminopeptidase N gene. Identification of possible regulatory
 A;Reference number: S05040; MUID:89325681; PMID:2568950
 A;Accession: S05040
 A;Molecule type: DNA
 A;Residues: 1-294 <OLS>
 A;Cross-references: EMBL:X16088
 R;See, H.; Reithmeier, R.A.F.
 Biochem. J. 271, 147-155, 1990
 A;Title: Identification and characterization of the major stilbene- diethylphosphate- and co
 A;Reference number: S13177; MUID:91024918; PMID:1977382
 A;Accession: S13177
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 2-40 <SEE>
 C;Genetics:
 A;Introns: 200/2; 248/1
 A;Note: the list of introns may be incomplete
 C;Superfamily: membrane alanyl aminopeptidase
 C;Keywords: aminopeptidase; glycoprotein; transmembrane protein
 F;1-8/Domain: intracellular #status predicted <INT>
 F;9-32/Domain: transmembrane #status predicted <TM>
 F;33-963/Domain: extracellular #status predicted <EXT>

Query Match 25.1%; Score 1269; DB 2; Length 963;
 Best Local Similarity 31.9%; Pred. No. 4.7e-72;
 Matches 323; Conservative 174; Mismatches 386; Indels 130; Gaps 28;
 Qy 20 RGFY-----CLTALPQICICQSFSSVHFTEPCGAPFVATNG----- 59
 Db 3 KGFYISKALGILGLGVAATIALSVYAQENKNAEHPQAPSPITTTAATLD 62
 Qy 60 ERFPQBELRPSVVIPLHYDLVHPNIT-SLD-----FVASEKIEVLVSNATQFIILHSD 114
 Db 63 QSKPWRNRYLPTLLPDSYFVTLRPLYPILTNADGLYIFKGSIVRLLCQEPDVIHHSKK 122
 Qy 115 LEITN----ATLQSEDSRYMKPKG-ELKVLVSYPAHQIALLVPEKLTPLHKYVVMDFQ 169
 Db 123 LNYTQGHMVVLRGVGDSQVPEIDRTTELVELT-----EYLVVHLKGSLOPHGMVMESEFQ 178
 Qy 170 AKLGDGEGFYKSYRTLGGSTRILAVTDFEPTQARMAFPFCDFPLPKAFSIKIRRES 229
 Db 179 GELADDLAGFYRSEYME-GNVKVLATQMQSTDARKSFCCDFEPAMKATFNITLIHPNN 237
 Qy 230 HIALSNPKVKTIIELEGG---LLBED-----HFPTVMSTYLVAIVCDPFHSLSGFTSS 280
 Db 238 LTALSNMPP-----KGSSTPLAEDPNWSVTEFETPTVMSTYLVAIVSFQSVNETAQN 291
 Qy 281 GVKYSIVASPKRQNTQTH--VALQASLKLDDVEKYFDIYVPLSKLDLIAIPDFRAPGAWEN 338
 Db 292 GVLIRIWARPNIAEGHGMALNTGPIILNFNFANHTSYPLPKSDQIALPDPFNAGAWEN 351

RESULT 9

A30325

membrane alanyl aminopeptidase (EC 3.4.11.2) precursor - human

N;Alternate names: aminopeptidase N; cell surface glycoprotein CD13

C;Species: Homo sapiens (man)

C;Date: 02-Feb-1990 #sequence revision 02-Feb-1990 #text_change 09-Jul-2004

C;Accession: A30325; S01658; I39442; S35688; S56098; S56099

R;Look, A.T.; Ashmun, R.A.; Shapiro, L.H.; Peiper, S.C.

J. Clin. Invest. 83, 1299-1307, 1989

A;Title: Human myeloid plasma membrane glycoprotein CD13 (gp150) is identical to aminope

A;Reference number: A30325; MUID:89198086; PMID:2564851

A;Accession: A30325

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-967 <LOO>

A;Cross-references: UNIPROT:P15144; UNIPROT:Q9UCE0; GB:M22324; NID:g178535; PIDN:AA51517

R;Olse, J.; Cowell, G.M.; Konigshofer, E.; Danielson, E.M.; Moller, J.; Laustsen, L.; H

FEBS Lett. 239, 307-314, 1988

A;Title: Complete amino acid sequence of human intestinal aminopeptidase N as deduced fr

A;Reference number: S01658; MUID:89005706; PMID:2901990

A;Accession: S01658

A;Molecule type: mRNA

A;Residues: 1-85,'R',87-535,'E',537-602,'M',604-886,'P',888-967 <OLS>

R;Shapiro, L.H.; Ashmun, R.A.; Roberts, W.M.; Look, A.T.

J. Biol. Chem. 266, 11999-12007, 1991

A;Title: Separate promoters control transcription of the human aminopeptidase N gene in

A;Reference number: I39442; MUID:91268079; PMID:1675638

A:Accession: I39442
A:Molecule type: DNA
A:Residues: 1-15 <RES>
A:Cross-references: GB:M55522; NID:g178532; PIDN:AAA83399.1; PID:g178533
R:Nunez, L.; Amigo, L.; Rigotti, A.; Pugliese, L.; Mignone, G.; Greco, A.V.; Nervi, F.
EBBS Lett. 329, 84-88, 1993
A:Title: Cholesterol crystallization-promoting activity of aminopeptidase-N isolated from
A:Reference number: S35688; MUID:93359071; PMID:8102610
A:Accession: S35688
A:Molecule type: protein
A:Residues: 2-18 <NUN>
R:Watanabe, Y.; Iwaki-Egawa, S.; Mizukoshi, H.; Fujimoto, Y.
Biol. Chem. Hoppe-Seyler 376, 397-400, 1995
A:Title: Identification of an alanine aminopeptidase in human maternal serum as a membra
A:Reference number: S56098; MUID:96066273; PMID:7576235
A:Accession: S56098
A:Molecule type: protein
A:Residues: 2-20 <WAT>
A:Accession: S56099
A:Status: preliminary
A:Molecule type: protein
A:Residues: 70-77, 'X', 79-81 <WA2>
C:Genetics:
A:Gene: GDB:ANBP; CD13; PEPN
A:Cross-references: GDB:118728; OMIM:151530
A:Map position: 15q25-15q26
C:Superfamily: membrane alanyl aminopeptidase
C:Keywords: aminopeptidase; glycoprotein; transmembrane protein

Query Match 25.0%; Score 1264.5; DB 2; Length 967;
Best Local Similarity 31.4%; Pred. No. 9.1e-72;
Matches 325; Conservative 158; Mismatches 386; Indels 167; Gaps 26;

QY 20 RGFYCLTAI-----LPOICICQSFSPSSVYHTEDPGAPPA----- 56
DB 3 KGFYISKSLGILGVAACVITIALSVYSQEKKNKANSFVASTTPSASATNPASA 62
QY 57 -TNGERFPQELRPSVPIPLHYDLFVHPNLTSLD-----FVASKIEVLVSNATQFIIL 110
DB 63 TTLDSQKAWNRVRLNTLKPDSYQVTLRPYLTPNDRLGVKFGSSVTRFTCKEATDVIII 122
QY 111 HSKOLEITNATLQSEDSRYMKGELKVLVSY-----PAHEQIALVLP-EKLTPLK----- 161
DB 123 HSKKLYNT-----LSQGRHVRVLRGVGSGQPPDIDKTELVEPTLYLVHVLKGL 170
QY 162 -----YYVAMDFOAKLGDGFEGFYKSTYRTLGGETRILAVTDPEPTQARMAPPCEDEPLF 216
DB 171 VKDSQYENDSEFEGELADDLAGFYSEYWE-GNVRKVATVQMQAADARKSFPCEDEPAM 229
QY 217 KANFSIKIRRESRHIALSNM-PVKRTIIEGGLED-----HFETTYMSTYLVAYIVC 269
DB 230 KAENFNTLIHPKDLTALSMLPKGPSSTLP-----EDPNMNVTEPHTTPKMSTYLLAFIVS 285
QY 270 DPHLSLGSFTSSGVKSVIYASPKRQNTQ-----YALQASLKLLDPYKDYFYVPLSKLDLIA 327
DB 286 EFDYVEKQASNGILIRIWARPSAIAAGHDYALNVTGPIILNPFAGHYDTPYPLPKSDQIG 345
QY 328 IPDPAPGAMENGLITYRETSLLPDKTSSASDKLVTRVIAHELAHQFNGLVMTMWN 387
DB 346 LPDFNAGAMENGLITYRENSLLPDLSSSSNKERVTVIAHELAHQFNGLVMTMWN 405
QY 388 DIWLKEGFAKYMELIAVNATYPELODDYF-LNVCFEVIKDSLNSSRPISKPA-----ETP 443
DB 406 DLWLNEGFAVYVEYLGDYAEPTWNLKDLVLNDVYRVAVDALASSHPLSTPASEINTP 465
QY 444 TOIQEMFDEVSNKACILNMLKDFLGEKFKGIIQYLYKFSYNKAKNDLWSSL----- 499
DB 466 AQISELFAISYKSGASVLRMLSSLSEDPVFKGLASYLHTPAYQNTIYLNLDHQLQAV 525
QY 500 SNCSLESDDPTSGGVCHSDPKMTSNMLAFIGENAEVKEWMTTWTLQKGIPLLVKDGCSL 559
DB 526 NNRSIQLPPTT-----VRDINRWTLQMGFPVITV---DTSTG 559

QY 560 RLQERFLQGVFQSDPE---WRALQERYLWHIPUT-----YST 594
DB 560 TLSQEHFLL-----DPDSNVTRPSEFNVTVPITSIRDSGRQQQDYMLIDVRAQNLDLEST 614
QY 595 SSSNVIRHILKSKTDTLDLPEKTSWKFNVDNGYIVHYEGHGWDLITQLNQNHTLL 654
DB 615 SGN-----EWLLNLNVGYRVYNDENWRKIQQLQQRDHSAI 653
QY 655 RPKDRVGLIHDVQLVGAGRLTLKALDMTYLLOHETSSPALLGLESLYSEFYHMMDRRN 714
DB 654 PVINRAQIINDAFNLASAHKVPVTLALNNTLFLTEERQYMPWEAALSLSYFKLMFDR-- 711
QY 715 ISDISENLKRYLLOQYFKPVI-----DRQSWSD-KGSVWDRMLRSALLKLACDLNHPACIQ 768
DB 712 -SEYVGMKNYKQVTPFLTHFRNNTNNMREIPENLMDQYSEVNAISTAGSNGVPECEE 770
QY 769 KAELFSOMESSCKLNIPTDVLKIVY--SVGAQTTAGWNYLLEQYELSMSSAEONKILY 826
DB 771 MVSGLFQOMENPNNNPIHPNLRSTVYCNALTAQGEEDWDFAWQFRNATLVNEADKLRA 830
QY 827 ALSTSKHQEKLLKLIELGMEGKVIKTONLAALLHAIARRPKGQQLAWDFVRENTHLLKK 886
DB 831 ALACSKELWILNRYLSYTLNPDILRKQDATSTIISITNNVIGQGLVMDVQSNWKKLPND 890
QY 887 PDLGSYDIRMIISGTTAHSKOKLQEVKLPFESLEAQ--GSHLDIFQTVLETITKNIKW 944
DB 891 YGGSGFSFNLIQAVTRFRFSTEYELQQLQEQPKONEETGFGSGTRALEQALEKTKANIKW 950
QY 945 LEKNLPTLRTWLMVNT 960
DB 951 VKENKEVVLQMTENS 966

RESULT 10
TI0052
aminopeptidase (EC 3.4.11.-) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: TI0052
R:Constam, D.B.; Tobler, A.R.; Rensing-Ehl, A.; Kemler, I.; Hersh, L.B.; Fontana, A.
J. Biol. Chem. 270, 26931-26939, 1995
A:Title: Puromycin-sensitive aminopeptidase sequence analysis, expression, and functiona
A:Reference number: Z16922; MUID:96070789; PMID:7592939
A:Accession: TI0052
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-920 <CON>
A:Cross-references: UNIPROT:Q11011; EMBL:U35646; NID:g1184160; PIDN:AAC52409.1; PID:g118
A:Note: puromycin-sensitive
C:Superfamily: membrane alanyl aminopeptidase
C:Keywords: aminopeptidase; metalloprotein; zinc

Query Match 24.0%; Score 1214; DB 2; Length 920;
Best Local Similarity 32.2%; Pred. No. 1.3e-68;
Matches 305; Conservative 167; Mismatches 353; Indels 122; Gaps 26;

QY 55 VATNGERFPQELRPSVPIPLHYDLFVHPNLTSLDFVASEKIEVL--VSNATQFIILHS 112
DB 43 LAAMPEKRPPE--RLPAEVSPIYSLCKPDL--LDPTFEKLEAAAQVROATNQIVMNC 98
QY 113 KDLBITNATLQSEDSRYMKEG-----KELKVLVSYPAHEQIALLVPEKLTPLHLYYVAM 166
DB 99 ADIDIITASVAPEDEDEIHATGFNYQNEDEKVTLSFPSTLQTG-----TGTLLK---- 147
QY 167 DFOAKLGDGEGFYKSTYRTLGGETRILAVTDPEPTQARMAPPCEDEPLFKFANFSIKIRR 226
DB 148 DFGELNDKMGKGYRSTYTPAGEVRYAAVTFEATDPRRAPPCWDEPAIKATFDISLVV 207
QY 227 ESRIIALSNMPKV--KTIELEGGLLEDHFETTYMSTYLVAYIVCDFHLSLGSFTSSGVK 284
DB 208 PKDRVALSNMNVDRKPYPDENLVKFKFARTPMVSTYLVAFVVGVEYDFVETRSKDGCV 267
QY 285 SIYASPKRKNQTHVALQASLKLLDFYKDYFYVPLSKLDLIAIPDFAPGAMENWGLITY 344

Db 268 RVYTPVKGAEQCKFALEVAAKTLTFYKDYFNVYPLPKIDILAIADFAAGAMENWGLVY 327
Qy 345 RETSLLDPKPTSSASDKLWTRVIAHDLAHQWFGNLTVMHWNDIWLKEGPAKYNELIAV 404
Db 328 RETALLDPKNSCSSRQWALVVGHELAHQWFGNLTVMHWNTLWLNIEGSPASIEYLCV 387
Qy 405 NATYPELQFDYFLNVCPEVITK-DSLNSSRPISKPAETPTQIQEMFDEVSYNKAGACILN 463
Db 388 DHCFPEVDIWTQFVSADYTRAQELDALDNSHIPIEVSVGHFSEVDEIFDAISYSGASVIR 447
Qy 464 MLKDFLGEKFKQGIIOYLKFKFSYRNAKNDDLWSSLSNCSLESDFTSGGVCHSDPKMTSN 523
Db 448 MLHDYIGDKPKKGWNYLTKFQCKNAATEDLWESLESA----- 486
Qy 524 MIAFLGENAEVKEKMTWTTLQKGIPLLVVK-----ODGCSRLQOERF-LQGVF--QEDPE 576
Db 487 -----SGKPIAAVNTWTQMGFPFLIYVEAEQVEDDRVLKLSQKFCASGPYGEDCPQ 540
Qy 577 WRALQERYLWHIPLTYSTSS-NVTHRHILKSKTD---TLDLPKTSWVKFNVDSNGYII 632
Db 541 WM-----VPITISSEDPNOAKLILMDKPEMSVVLXNVKPDQWVKNLIGTVGFYR 591
Qy 633 VHYEGHGDQIITQLNQNHLLRPKRVGLIHDVFLVAGRLTLDKALDWTYYLQHETS 692
Db 592 TOYSSAMLESLLPGIRD--LSLPPVDRGLQNDLFLSLARAGII----- 632
Qy 693 SPALLEGLSYLESFYHMDRRNIDIS-----ENLKYLLQYFKPVDR 736
Db 633 --STVEVLKVNFAFNEPNYTWSDLSNGLISTLASHDTDFYBEIQEFKDVESPTGER 690
Qy 737 QSWSDK--GSVDRMLRSALLKLACDLNHAPCIQKAAELFSOMESSGKLNIPDVLKI 793
Db 691 LGWDPKGEGLH-DALLRGLVLKLGKAGHKATLEARRRKEVE--GKQLISADLRSP 747
Qy 794 VYVGAQTTAG--WNYLLEQVELSSSAEQNKILYALSTSKHQKLLKLIELGMEGVKIK 851
Db 748 VYLVKHXGDGATLIDIMLKLHQADMQEENRIERVLGATLSPELIQKVLTFALSEVR-R 806
Qy 852 TONLAALLHATARP-KQOLAWDFVRENWTHLLKDKDLSYDIRMIISGTTAHHFSSKDK 910
Db 807 PQDVTYVGGVAGSGKGRKAAWFKIDNMBELHRYQ-GGFLSRILKLSVGEFAVDKM 865
Qy 911 LQEVKLFESLEAQSHLDIPQTVLETTITKNIKWLEKNLPLRLTWLM 957
Db 866 AGEVKAFESHAPSAERTI-QCCENILLNAWLKRDADSIHQYLL 911
RESULT 11
S07099
membrane alanine aminopeptidase (EC 3.4.11.2) - rabbit (fragments)
N:Alternate names: leukemia antigen CD13; microsomal aminopeptidase N
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 30-Sep-1991 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C:Accession: S07099; B25985
R:Noren, O.; Dabelsteen, E.; Hoyer, P.E.; Olsen, J.; Sjoestrom, H.; Hansen, G.H.
FEBS Lett. 259, 107-112, 1989
A:Title: Onset of transcription of the aminopeptidase N (leukemia antigen CD 13) gene at
A:Reference number: S07099; MUID:90092508; PMID:2574692
A:Accession: S07099
A:Molecule type: mRNA
A:Residues: 15-805 <NOR>
A:Cross-references: UNIPROT:P15541; EMBL:X51508; NID:g1447; PIDN:CRAA35873.1; PID:g1448
R:Faracci, H.; Maroux, S.; Bonicel, J.; Desnuelle, P.
Biochim. Biophys. Acta 684, 133-136, 1982
A:Title: The amino acid sequence of the hydrophobic anchor of rabbit intestinal brush bo
A:Reference number: A90640; MUID:82113673; PMID:6120002
A:Accession: B25985
A:Molecule type: protein
A:Residues: 1-14 <FE>
A>Note: this sequence represents the detergent-released form; a proteinase-released form
C:Superfamily: membrane alanine aminopeptidase
C:Keywords: aminopeptidase; glycoprotein; membrane protein; surface antigen; zinc

F;70,98,391,409,463,487,573,656/Binding site: carboxyhydrate (Aen) (covalent) #status pred
F;223,224,227/Binding site: zinc (His, Glu, His) #status predicted
Query Match 23.3%; Score 1176; DB 2; Length 805;
Best Local Similarity 33.6%; Pred. No. 2.7e-66;
Matches 279; Conservative 147; Mismatches 326; Indels 78; Gaps 22;
Qy 168 FOAKLGDGPGFVKYSTVTLGGETRIILAVT--DFEPTQARMAPPCDEPLFKANFSKIR 225
Db 16 FOELADDLAGFTRSEYME-GNVRKVAVTTQMOMQAADARKSPCPDEPASKATFNITLI 74
Qy 226 RESRHIALSNM-PKVKTIETIELEGGLED-----HFETTVMSTYLVAYIVCDHSLSGFT 278
Db 75 HPRDYTALSNNLRSST-----ALPEDPNWTVTEFTTPKMYSTYLLAYIVSEFTNIEAQS 129
Qy 279 SSGVKSYIYASPKRKNQTH--YALQASLKLLDPYKFDIYIPLSKLDLIAIDPFARCAM 336
Db 130 PNVQIRIWARPSAISSEGHQYALNVTGPILNFANHYNTPYPLEKSDQIGLDFNAGAM 189
Qy 337 ENMGLITYRETSLLPKPTSSASDKLWTRVIAHDLAHQWFGNLTVMHWNDIWLKEGPA 396
Db 190 ENMGLITYRESALLFDPLVSSISNKERVTVVAHDLAHQWFGNLTVDWNDIWLKEGPA 249
Qy 397 KYMELIAVNATYPELOFDYF-LNVCFEVTIKDSLNSRPIKPAE---TPTQIQEMFDE 452
Db 250 SYVEYLGA DYAEPTWNLKDLIIVLNELHSMVAVDALASSHPLSSPADEVNTPAQISELFS 309
Qy 453 VSYNKGACILNMLKDFLGEKFKQGIIOYLKFKFSYRNAKNDDLWSSLSNCSLESDFTS 512
Db 310 ITYSKGA SVLRMLSSFLTEDLPKEGLASYLHTFAYQNTIYLDLWEHLQAAV----- 360
Qy 513 VCHSDPKMTSNMLAFELGENAEVKEKMTWTTLQKGIPLLVVK-ODGCSRLQOERFLOGVF 571
Db 361 -----NSQATQLPASVRDIDMRWILQMGFPVTVNTNGI---ISQHHFL--- 404
Qy 572 QEDPE--WRALQERYLWHIPLTYSTSSNVIIHR-----ILKSKTDTLDLPKTSWVK 622
Db 405 --DPTSNVTRPSDFNYLWIPV---SSMRNGVQQQBFWLEGVETQNSLPRVEGDNNWIL 459
Qy 623 FNVDSNGYIIVHYEGHGDQIITQLNQNHLLRPKRVGLIHDVFLVAGRLTLDKALD 682
Db 460 ANLNVTYGVQVNVDEGNWKKLQLOTFNPSVIPINRAQIIHDFAFNLASQAPVPTLALD 519
Qy 683 MTYLQHEHTSSPALLEGLSYLESFYHMDRRNIDISENKLRYLLQVFKPEVIDR-----Q 737
Db 520 NTLFLRETEYMPQAAALSLNYFKLMFDR--SEVYGPKNYLSKQVRPLFEHFKNITN 576
Qy 738 SWSDK-GSVDRMLRSALLKLACDLNHAPCIQKAAELFSOMESSGKLNIPDVLKIVY- 795
Db 577 DWTRRPDTLMDQYNEINAISTACSGNGIQECETLVSDLFKQWMDPSPNNPIHPNLTVTYC 636
Qy 796 ---SVGAQTTAGNYLLEQVELSSSAEQNKILYALSTSKHQKLLKLIELGMEGVKIK 852
Db 637 NATALGGERE--WDFAWEQFRNATLVNEADKRSALACSNEVWILNRYSLTNLPDVI 694
Qy 853 QNLAAALLHATARP-KGQOLAWDFVRENWTHLLKDKDLSYDIRMIISGTTAHHFSSKDK 912
Db 695 QDATSTINSIASNVIGTLVWDFVQSNWKKLPEDFGGSGFSFANLIRAVTRRSTSEYELQ 754
Qy 913 EVKLF-FESLEAO-GSHLDIFQVLETTITKNIKWLEKNLPTLRLTWLMVNT 960
Db 755 QLEQFRLNLDITFGSGTQRALEQALQETRANIKWQENKEAVLWFTANS 804
RESULT 12
T29637
hypothetical protein F49B8.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T29637
R:Murray, J.; Wohlmann, P.
submitted to the EMBL Data Library, June 1996
A:Description: The sequence of C. elegans cosmid F49B8.


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Qy      877 RENWTHLLKKF-DLGSYDYMIIISGTAHFSSKKDLQEVKLP-----ESLDAQSHLD 929
Db      794 CEHIKFLDKYGANSLFQRCCLKFAGESFGNEKRAVEFQDFPCNCNVLSDDTDROTLLARP 853
Qy      930 IFOTVLETTIKIKWLEKN 948
Db      854 IGQTV-EAIRLNARLLESN 871

RESULT 13
S37794
aminopeptidase yecII (EC 3.4.11.-) - yeast (Saccharomyces cerevisiae)
N/Alternate names: protein YKL157w; protein YKL611
C/Species: Saccharomyces cerevisiae
C/Date: 03-May-1994 #sequence revision 03-May-1994 #text_change 09-Jul-2004
C/Accession: S37794; S37987; S44571; S19642
R/Vandenbol, M.; Bolle, P.; Dion, C.; Portetelle, D.; Hilger, F.
submitted to the EMBL data Library, September 1993
A/Description: DNA sequencing of a 36.2 kb fragment located between the FAS1 and LAP4
A/Reference number: S37786
A/Accession: S37794
A/Molecule type: DNA
A/Residues: 1-844 <VAN>
A/Cross-references: UNIPROT:P32454; EMBL:Z26877; NID:g407482; PIDN:CAA81497.1;
A/Experimental source: strain S288C
R/Vandenbol, M.; Bolle, P.A.; Dion, C.; Portetelle, D.; Hilger, F.
submitted to the Protein Sequence Database, March 1994
A/Reference number: S37976
A/Accession: S37987
A/Molecule type: DNA
A/Residues: 1-844 <VAB2>
A/Cross-references: EMBL:Z28157; NID:g486272; PIDN:CAA81999.1; PID:g486273; MIP:
A/Experimental source: strain S288C
R/Vandenbol, M.; Bolle, P.A.; Dion, C.; Portetelle, D.; Hilger, F.
Yeast 10, 35-40, 1994
A/Title: DNA sequencing of a 36.2 kb fragment located between the FAS1 and LAP4
A/Reference number: S44563
A/Accession: S44571
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-844 <VAB3>
A/Cross-references: EMBL:Z26877; NID:g407482; PIDN:CAA81497.1; PID:g407491
A/Experimental source: strain S288C
A/Note: The nucleotide sequence was submitted to the EMBL Data Library, Septemb
R/Garcia-Alvarez, N.; Cueva, R.; Suarez-Rendueles, P.
Eur. J. Biochem. 202, 993-1002, 1991
A/Title: Molecular cloning of soluble aminopeptidases from Saccharomyces cerevi
A/Reference number: S19642; MUID:92111552; PMID:1765107
A/Accession: S19642
A/Molecule type: DNA
A/Residues: 1-163, 'V', 165-441, 'E', 443-843, 'VNRDRDVVNYKLENGYV' <GAR>
A/Cross-references: EMBL:XG3398; NID:g3367; PIDN:CAA45403.1; PID:g3368
C/Genetics:
A/Gene: SGD:APB2; LAP1
A/Cross-references: SGD:S0001640; MIPS:YKL157w
A/Map position: 11L
C/Superfamily: membrane alanyl aminopeptidase
C/Keywords: aminopeptidase; glycoprotein; metalloprotein; zinc
F/290,622/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/305,309/Binding site: zinc (His) #status predicted
F/306/Active site: Glu #status predicted

Query Match 22.1%; Score 1116; DB 2; Length 844;
Best Local Similarity 31.4%; Pred. No. 1.8e-62;
Matches 281; Conservative 171; Mismatches 372; Indels 72; Gaps 24;

Qy      63 PMQELRLSPVVIPLHYDLFVHPNLTSLDFVASKIEVLVSN-ATQFIILHSKOLEITNAT 121
Db      6 PNREI-LPNNVPLHYDLTVPEDFKFKEGSVKIELKINNPDAITVLTNTVTDIHSAK 64
Qy      122 LQSEDSRYMKPKELKVLGYSPAHEQIALVLPKLTPLHLYKYVMD--FOAKLGDGFEGF 179
Db      65 IGDVTSG-----EIISEEBQQVTTFAFPKGTWSSFKGNAPLDIKFTGIINDNMGF 115

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Db      781  LQSPSPVLGGVLTGLTNFTSFEALEKISAPSRKVTKGFDQTIAQ-ALDTIRSKAQWVS 839
Qy      947  KNLPFLRLTWL 956
       ::      :  ||
Db      840  RDREIVATYL 849

RESULT 15
T39789
aminopeptidase - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T39789
R:Seeger, K.; Harris, D.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1999
A:Reference number: Z21816
A:Accession: T39789
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-882 <SEE>
A:Cross-references: UNIPROT:Q9USX1; EMBL:AL122033; PIDN:CAB58971.1; GSPDB:GN000067; SPDB:
A:Experimental source: strain 972h; cosmid c1921
C:Genetics:
A:Gene: SPDB:SPBC1921.05
A:Map position: 2
C:Superfamily: membrane [alanyl] aminopeptidase

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Search completed: September 26, 2005, 06:04:26
Job time : 52 secs

Db	578	DRAGLIADVASLSRAGYGVKSVSTLIDLITKWDENFVVFVFAEMLARNGIKSTL-RFESSD	636
Qy	718	ISENLKRYLLQYFPVIDROSWSKGSYWD----RMLRSALLKLACDLNHAPCIOKAABL	773
Db	637	IIAAMKKLVLEVSATKAHSLGWEPKAN--DDHIIIRQKFTVYVAGLFQDDRVVVDALSK	694
Qy	774	FSQWMESSGKLNIPTDVLKIVYV-----GAQTTAGWNLYLEQVLSNSSAEONKILVAL	828
Db	695	FDAY-ASGNKSAINDNRSVAFNIAIRYGGAKS--WDQLLEIYTKTNDPPYRNSCLRAF	750
Qy	829	STSKHQEKLKLILBLGMEGVKIKTONLAALHAIAARRPKGOOLAWDFVRENTWTHLLKKPD	888
Db	751	GVTEDEKYIQKTLDTLD-PIVKEQDIYLLVTLSTHKGVLAMWKFATSNWDKLLSRLP	809
Qy	889	LG-----SVDIRMIISGTTAHFESSKDKLOE-----VKLFPESLEAQQSHLDFQTVLETI	938
Db	810	VAGTMRGVVRFVTSGGFT-HASADIKIEFFADKDKTKUYERAL-----QQSLDTI	858
Qy	939	TKNIKWLKKNLPTLRTWLMVN	959
Db	859	SANSFFDKSLDDITRWLKEN	879

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C/Gene: SPDB:SPBC1921.05
A:Map position: 2
C:Superfamily: membrane alanyl aminopeptidase

Query Match          20.7%; Score 1047.5; DB 2; Length 882;
Best Local Similarity 30.1%; Pred. No. 4.1e-58;
Matches 277; Conserved 162; Mismatches 391; Indels 91; Gaps 24

QY 69 LPSWVPLHYDLFVPHNLTSLDFVASEKIEVLVSNATQFIILHSKDLLEITNATLQSEEDS 128
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 20 LPKVNPRIHYDLSLPDLSTFFYGGKVVTVLVLEDSNITLHGINRILTALEWGSQT 79
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 129 RYMKPGKELKVLSPAHQIALLVPEKLTPLHKYTVAMDFOAKLGDGFEFYKSTYRTLG 188
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 80 WVASE-----VSY-GDERIVLQFSTVPANSVAVLTLPTTARLSSGMEGFYSSVDSD 132
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 189 GETRIILAVTDFFETQARMAFFCFDPLPKANFSTKIRRESHIALSNMPKVTIELEGG 248
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 133 GNTKYLATTOMSEPTARRAPPCWDSPALKATFTIDITAKENYITLSNNAVBE-TVK 191
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 249 LEDHPETTYVMSTYLVAIVTCDHSLSGFTSS-----GVKSVIYASPKRQTHYALQAS 304
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 192 KTAIFAETCRMSTYLLAWIVALEVYVFTPKCHCPRLVRVYVTPGFSQGFAAELGA 251
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 305 KLLADFYEKYFDIYVPLSKDLLTAIPDEAPGAMENGLTYRETSLLPDPKTSSASDKLW 364
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 252 KTLDFSGVGGPYPUPKCDMWAI PPFAGAMENGLVYTKLAILVS-SDSAATVIERV 310
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 365 TRYIAHELHQFNGNLVTMEMWNDIWLKEGFAKTMELIANNATYPELQ-FDDYFLNVCPE 423
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 311 AEVVQHLELHQFNGNLVTMQFDWGLWLNEGFATWMSWFCNHFFPEKWVWESYTDNLQS 370
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 424 VITKDSLSRPTSKPAETPTQIQEMFDEVSNYKAGACILNMLKDFLGEEXFKQGIIOYK 483
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 371 ALSLDALRSHPPIEVPIMHDEYINGIFDAISYKSGSCVIRWVSKYVGEDTFIKGIQK 430
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 484 KFSYRNAKNDLWSSLSNSCLESDFTSKGVCHSDPKMTSNMLAFLGENAIEKEMMTITWL 543
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 431 KHRYGNTVTEDLWAALSAS-----SGDISSTMEHNWTK 463
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 544 QKGIPLLVKQ--DGCSLRLQERFLQGVQEDPEWRALQERYLWHIPLTVYSTSSN--- 598
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 464 KTGYPVLVSUETNDG-ELLIEQHRFL-STGDVKPE-----EDTVIWAPLKLTWKDGKAV 517
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 599 VIHRHILKSKTDTLDL-PEKTSWVKFNVDNSGYIVHYHGEHGWDLQTLQNLQHTLLRPK 657
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 518 VDEKAVLSDRSKKIKVDEKALESYKLNSEQSGIYRVNYSDHLKKLSQIAVEKPDYLSVE 577
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 658 DRYGLIHDVQLVGAGRLTKDALDWTYYLQHETSSPALLEGSLYBESFYHMDRRNISD 717
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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GenCore version 5.1.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 26, 2005, 06:10:40 ; Search time 103.689 Seconds
(without alignments)
6246.842 Million cell updates/sec

Title: US-10-039-073-2
Perfect score: 5912
Sequence: 1 ccccgctccggcatgattt.....aaaaaaaaaaaaaaaaaaaaa 3366

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+n2p.model -DEV=xlp
-O=/cgn2.1/USPTO.spool_p/US10039073/runat_26092005_070410_21316/app_query.fasta_1.6606
-DB=PIR -OPWT=fastan -SUFFIX=rdr -MINMATCH=0.1 -LOOPECL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10039073 @CNC 1 1 317 @runat_26092005_070410_21316 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR 79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1999	33.8	1006	2	A59384 oxytocinase/insuli
2	1999	33.8	1025	2	A59383 oxytocinase/insuli
3	1771	30.0	916	2	I55441 vpl65 - rat
4	1440	24.4	957	2	A47531 glutamyl aminopept
5	1390.5	23.5	945	2	S30398 aminopeptidase N h
6	1327	22.4	1025	2	I59331 thyrotropin-releas
7	1312	22.2	965	2	A32852 membrane alanyl am
8	1269	21.5	963	2	A53984 membrane alanyl am
9	1264.5	21.4	967	2	A30325 membrane alanyl am
10	1214	20.5	920	2	T10052 aminopeptidase (BC
11	1176	19.9	805	2	S07099 membrane alanyl am
12	1151	19.5	884	2	T29637 hypothetical prote
13	1116	18.9	844	2	S37794 aminopeptidase ysc
14	1067	18.0	856	2	S46750 aminopeptidase AAP

15	1047.5	17.7	882	2	T39789 aminopeptidase - f
16	1039	17.6	988	2	T24668 hypothetical prote
17	1031	17.4	990	2	JC8058 laeverin - human
18	899.5	15.2	873	2	T05189 glutamyl aminopept
19	895.5	15.1	849	2	JC7959 lysyl aminopeptida
20	893.5	15.1	849	2	JU0191 aminopeptidase Y (
21	888.5	15.0	785	2	S73098 aminopeptidase (BC
22	875	14.8	844	2	S47274 membrane alanyl am
23	873	14.8	846	2	A86663 aminopeptidase N (
24	871.5	14.7	784	2	B90442 tricorn proteinase
25	870	14.7	843	2	S38364 membrane alanyl am
26	868	14.7	844	2	JC4054 membrane alanyl am
27	865	14.6	848	2	B9760 membrane alanyl am
28	864	14.6	848	2	E35092 aminopeptidase N (
29	856	14.5	846	2	JN0324 lysine aminopeptid
30	856	14.5	846	2	S23157 membrane alanyl am
31	837.5	14.2	1016	2	T30942 aminopeptidase (BC
32	832.5	14.1	1016	2	T30943 aminopeptidase (BC
33	820.5	13.9	1009	2	T18533 CryIAC toxin-bindi
34	810.5	13.7	783	2	T37457 Tricorn proteinase
35	774.5	13.1	780	2	T37456 Tricorn proteinase
36	705	11.9	747	2	T23882 hypothetical prote
37	702	11.9	786	2	T23883 hypothetical prote
38	692	11.7	899	2	H88572 protein T16G12.1 (
39	683	11.6	885	2	S42841 T16G12.1 protein -
40	630	10.7	1071	2	T18597 hypothetical prote
41	626	10.6	919	2	S42842 T16G12.2 protein -
42	498	8.4	946	2	S48397 hypothetical prote
43	450	7.6	862	2	G87094 probable aminopept
44	425	7.2	861	2	B70866 probable aminopept
45	404	6.8	613	4	C40201 artifact-warning s

ALIGNMENTS

RESULT 1

A59384 oxytocinase/insulin-responsive aminopeptidase, variant 2 [imported] - human
C:Species: Homo sapiens (man)
C>Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 20-Apr-2001
C:Accession: A59384
R:Rasmussen, T.E.; Pedraza-diaz, S.; Hardre, R.; Laustsen, P.G.; Carrion, A.G.; Kristens
Eur. J. Biochem. 267, 2297-2306, 2000
A>Title: Structure of the human oxytocinase/insulin-regulated aminopeptidase gene and l
A:Reference: GB:CA894753; NID:98574036; PIDN:CA894753.1
A:Accession: A59384
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1006 <STO>
A:Cross-references: GB:CA894753; NID:98574036; PIDN:CA894753.1
C:Superfamily: membrane alanyl aminopeptidase

Alignment Scores:
Pred. No.: 6,84e-128 Length: 1006
Score: 1999.00 Matches: 400
Percent Similarity: 61.81% Conservative: 160
Best Local Similarity: 44.15% Mismatches: 310
Query Match: 33.81% Indels: 36
DB: 2 Gaps: 6

US-10-039-073-2 (1-3366) x A59384 (1-1006)

QY	305	CCAGTAGCCACTAATGGGAAACGATTTCTTTGGAGGAGCTAAGGCTCCCGAGTGTGTC	364
DB	134	ProphealaThraAenGlyLysLeuPheProTrpAlaGlnIleArgLeuProThraAlaVal	153
QY	365	ATTCTCTCCATTATGACCTCTTTGTCCACCCCAATCTCACCTCTCTGGACTTTGTTGCA	424
DB	154	ValProLeuAArgTyGluLeuSerLeuHisProLeuLeuThrSerMetThrPheArgGly	173
QY	425	TCTGAGAGATCGAAGTCTTGGTCAGCAATCTACCCAGTTTATCATCTTTCACACACAAA	484
DB	174	SerValThrIleSerValGlnAlaLeuGlnValThrTrpAenIleIleLeuHisSerThr	193


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Db      881 SerGluAspValArgLysLeuTyrTrpLeuMetLysSerSerLeuAsnGlyAspAsnPhe 900
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      2696 AAGACACAGAACTTGGCAGCTCTCTTCATGCGATGGCAGCTCCAAAGGGCGAGCAA 2755
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db      901 ArgThrGlnLysLeuSerPheIleIleArgThrValGlyArgHisPheProGlyHisLeu 920
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      2756 CTAGCATGGGATTTGTAAGAGAAAATTTGGACCCATCTCTCGAAAATTTGACTTGGGC 2815
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      921 LeuAlaTrpAspPheValLysGluAsnTrpAsnLysLeuValGlnLysPheProLeuGly 940
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      2816 TCATATGACATAAGATGATCATCTCTGGCACACAGCTCACTTTCTTCCAAAGGATAAG 2875
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      941 SerTyrThrIleGlnAsnIleValIleArgSerThrTyrLeuPheSerThrLysThrHis 960
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      2876 TTGCAAGAGGTGAACATACTTTTGAATCTCTTGAGGCTCAAGGATCATCTCGATATT 2935
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      961 LeuSerGluValGlnAlaPhePheGluAsnGlnSerGluAlaThrPheArgLeuArgCys 980
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      2936 TTTCAAACTGTTCTGGAACGATACCCAAAATATAAATGCTCGAGAGAAATCTTCG 2995
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      981 ValGlnGluAlaLeuGluValIleGlnLeuAsnIleGlnTrpMetGluLysAsnLeuLys 1000
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      2996 ACTCTGAGGACTTGGCTA 3013
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1001 SerLeuThrTrpTrpLeu 1006
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 2
A59383
oxytocinase/insulin-responsive aminopeptidase, variant 1 [imported] - human
C:Species: Homo sapiens (man)
C:Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 09-Jul-2004
C:Accession: A59383
R:Rasmussen, T.B.; Pedraza-Diaz, S.; Hardre, R.; Laustsen, P.G.; Carrion, A.G.; Kristsen,
Eur. J. Biochem. 267, 2297-2306, 2000
A:Title: Structure of the human oxytocinase/insulin-regulated aminopeptidase gene and lo
A:Reference number: A59383; MUID:20223264; PMID:10759854
A:Accession: A59383
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1025 <STO>
A:Cross-references: UNIPROT:O9UIQ6; GB:CAB61646; NID:66468766; PIDN:CAB61646.1
C:Superfamily: membrane alanyl aminopeptidase

Alignment Scores:
Pred. No.: 6.87e-128 Length: 1025
Score: 1999.00 Matches: 400
Percent Similarity: 61.81% Conservative: 160
Best Local Similarity: 44.13% Mismatches: 310
Query Match: 33.81% Indels: 36
DB: 2 Gaps: 6

US-10-039-073-2 (1-13366) x A59383 (1-1025)
Qy      305 CAGTAGCCACTAATGGGAAACGATTTCTTGGCAGGAGCTAAGGCTCCCGAGTGTGTC 364
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      153 ProPheAlaThrAsnGlyLysLeuPheProTrpAlaGlnIleArgLeuProThrAlaVal 172
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      365 ATTCTCTCCATATGACTCTTTGTCACCCCAATCTCACCTCTCGACTTGTGCA 424
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      173 ValProLeuArgTyrGluLeuSerLeuHisProAsnLeuThrSerMetThrPheArgGly 192
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      425 TCTGAGAAGATCGAAGTCTGTGTCAGCAATGTCTACCCAGTTTATCATCTTGCACAGCAA 484
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      193 SerValThrIleSerValGlnAlaLeuGlnValThrTrpAsnIleIleLeuHisSerThr 212
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      485 GATCTTGAATCAGNATGCCACCTTCAGTCAGAGGAGATTCAGATACATGAACCA 544
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      213 GlyHisAsnIleSerArgValThrPheMetSerAlaValSerSerGln----- 228
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      545 GCAAAAGAACTCAAGTTTGTAGTTTACCTGCTCATGAACAAATTTGCACTGCTGTTCCA 604
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      229 GluLysGlnAlaGluLeuGluTyrAlaTyrHisGlyGlnIleAlaIleValAlaPro 248
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Qy      605 GAGAACTTACGCTCACCTGAAATACTATGTGCTATGAGACTTCCAAAGCCCAAGTTAGT 664
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      249 GluAlaLeuLeuAlaGlyHisAsnTyrThrLeuLysIleGluTyrSerAlaAsnIleSer 268
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      665 GATGCTTTGAAGGCTTTTATAAAGCACATACAGAACTCTTGGTGGTGAACAAGAATT 724
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      269 SerSerTyrTyrGlyPheTyrGlyPheSerTyrThrAspGluSerAsnGluLysLysTyr 288
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      725 CTTCAGTAAACAGATTTTGAAGCCAAACCCAGCAGCATGGCTTTCCCTTGTCTTGATGAA 784
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      289 PheAlaAlaThrGlnPheGluProLeuAlaAlaArgSerAlaPheProCysPheAspGlu 308
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      785 CCGTTGTTCAAGCAACTTTTCAATCAAGATACGAGAGAGAGAGAGAGCATATTGCACTA 844
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      309 ProAlaPheLysAlaThrPheIleIleLysIleLeuArgAspGluGlnTyrThrAlaLeu 328
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      845 TCCAACATGCCAAAGGTTAAGACAATGAACTGAAGGAGGCTTTTGGAAAGATCACATTT 904
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      329 SerAsnMetProLysLysSerSerValValLeuAspAspGlyLeuValGlnAspGluPhe 348
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      905 GAAACTACTGTAAAATAGAGTACATACCTTGTAGCTACATAGTTTGTGATTTCCACTCT 964
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      349 SerGluSerValLysMetSerThrTyrLeuValAlaPheIleValGlyGluMetLysAsn 368
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      965 CTGAGTGGCTTCACTTCAATCAGGGGTCAAGGTGTCATCTATGATCCCAAGACAAACGG 1024
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      369 LeuSerGln---AspValAsnGlyThrLeuValSerIleTyrAlaValProGluAsnIle 387
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1025 AATCAAAACACATTTATGCTTTCAGCGCATCACTGAAGCTTACTTGTATTTTATGAAAAGTAC 1084
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      388 GlyGlnValHisTyrAlaLeuGluThrThrValLysLeuLeuGluPhePheGlnAsnTyr 407
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1085 TTTGATATCTACTATCCACTCTCCAAACTGGATTAATTTGCTATTTCTGACTTTGCACCT 1144
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      408 PheGluIleGlnTyrProLeuLysLysLeuAspLeuValAlaIleProAspPheGluAla 427
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1145 GGAGCCATGGAATAATTTGGGGCTCATACATATAGGAGAGCTCACTGCTTTTGCACCCC 1204
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      428 GlyAlaMetGluAsnTrpGlyLeuLeuThrPheArgGluGluThrLeuLeuTyrAspSer 447
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1205 AAGACCTTCTCTGCTTCGATAAACTGGGTGCTCACCAGAGTCATAGCCCATGAACCTGGG 1264
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      448 AsnThrSerSerMetAlaAspArgLysLeuValThrLysIleIleAlaHisGluLeuAla 467
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1265 CACCAGTGGTTTGGCAACCTGGTCACAAATGGAATGGTGAATATGATTTGGCTTAAGAG 1324
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      468 HisGlnTrpPheGlyAsnLeuValThrMetLysTrpTrpAsnAspLeuTripleAsnGlu 487
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1325 GGTTTTGCAAAATACATGGAACTTATCGCTGTTAATGCTACATATCCAGAGCTGCAATTT 1384
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      488 GlyPheAlaThrPheMetGluTyrPheSerLeuGluLysIlePheLysGluLeuSerSer 507
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1385 GATCACTATTTTGAATGTGTGTTTGAAGTAATAACAAAGATTCATTGAATTCATCC 1444
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      508 TyrGluAspPheLeuAspAlaArgPheLysThrMetLysLysAspSerLeuAsnSerSer 527
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1445 CGCCTATCTCCAAACCCAGCGAAACCCCGACTCAAAATACAGGAAATGTTTGTATGAAGTT 1504
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      528 HisProIleSerSerSerValGlnSerSerGluGlnIleGluGluMetPheAspSerLeu 547
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1505 TCCTATTAACAGGAGCTTGTATTTTGAATATGCTCAAGGATTTTCTGGGTGAGAGAAA 1564
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      548 SerTyrPheLysGlySerSerLeuLeuMetLeuLysThrTyrLeuSerGluAspVal 567
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1565 TTCCAGAAAGAAATAATTTCAGTACTTAAAGAAAGTTTCAGTATAGAAATGCTAAGATCAT 1624
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      568 PheGlnHisAlaValLeuTyrLeuHisAsnHisSerTyrAlaSerIleGlnSerAsp 587
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1625 GACTTGTGGAGCAGCTCTGCTCAATAGTTGTTTGTAGAAAGTGTATTTTACATCTGGTGGAGTT 1684
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      588 AspLeuTrpAspSerPheAsn----- 594
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Qy 1685 TGTCATTCCGATCCCAAGATCAACAAGTAACATGCTCGCCTTCTCTGGGGGAAAAATGCAGAG 1744
Db      :::::::::::GluValThrAsnGlnThrLeu-----Asp 602
Qy 1745 GTCAAAAGAGATGACTACATGAGCTCTCCAGAAAAGAAATCCCTCGTGGTGGTTAAA 1804
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 603 VallysArgMetMetLysThrTrpThrLeuGlnLysGlyPheProLeuValThrValGln 622
Db      :::::::::::GluValThrAsnGlnThrLeu-----Asp 602
Qy 1805 CAAGACGGGTGTTCACTCCGACTCAACAGAGAGCGCTTCTCCAGAGGGGGTTTTCCAGAA 1864
Db      :::::::::::GluValThrAsnGlnThrLeu-----Asp 602
Qy 623 LysLysGlyLysGluLeuPheIleGlnGluArgPhePheLeuAsnMet----- 639
Db      :::::::::::GluValThrAsnGlnThrLeu-----Asp 602
Qy 1865 GACCTCGAATCGAGGGCCCTCAGAGAGAGTACCTGTGGCATATCCCATTCACCTACTCC 1924
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 640 LysProGluIleGlnProSerAspThrSerTyrlLeuTrpHisIleProLeuSerTyrlVal 659
Db      :::::::::::GluValThrAsnGlnThrLeu-----Asp 602
Qy 1925 ACGAGTCTCTTAATGTGATCCACAGACAC-----ATTCTAAATCAAGACAGAT 1975
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 660 ThrGluGlyArgAsnTyrlSerLysTyrlGlnSerValSerLeuLeuAspLysLysSerGly 679
Db      :::::::::::GluValThrAsnGlnThrLeu-----Asp 602
Qy 1976 ACTCTGGATCTACCTGAAAGACCACTGGGTGAAATTTAATGTGGACTCAATGGTTAC 2035
Db      :::::::::::GluValThrAsnGlnThrLeu-----Asp 602
Qy 680 VallieAsnLeuThrGluGluValLeuTrpValLysValAsnIleAsnMetAsnGlyTrp 699
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2036 TACATCGTTCACTATGAGGGTCATGGATGGGACCAACTCATTACACAGCTGAATCAGAAC 2095
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 700 TyrlleValHisTyrlAlaAspAspTrpGluAlaLeuIleHisGlnLeuLysIleAsn 719
Db      :::::::::::GluValThrAsnGlnThrLeu-----Asp 602
Qy 2096 CACACACTTCAGACCTAAGCAGAGTAGGTCTGATTCATGATGTGTTTCAGCTAGTT 2155
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 720 ProTyrlValLeuSerAspLysAspArgAlaAsnLeuIleAsnAsnIlePheGluLeuAla 739
Db      :::::::::::GluValThrAsnGlnThrLeu-----Asp 602
Qy 2156 GGTCCAGGAGACTGACCCCTAGACAAAGCTCTTCACATGACTTACTACCTCCCAACGAA 2215
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 740 GlyLeuGlyLysValProLeuLysArgAlaPheAspLeuIleAsnTyrlLeuGlyAsnGlu 759
Db      :::::::::::GluValThrAsnGlnThrLeu-----Asp 602
Qy 2216 ACAAGCAGCCCGCACCTCTCGAAGGTCTGAGTTACTTGAATCGTTTACCACATGATG 2275
Db      :::::::::::GluValThrAsnGlnThrLeu-----Asp 602
Qy 760 AsnHisThrAlaProIleThrGluAlaLeuPheGlnThrAspLeuIleTyrlAsnLeuLeu 779
Db      :::::::::::GluValThrAsnGlnThrLeu-----Asp 602
Qy 2276 GACAGAGGAATATTTTCAGATATCTCTGAAACCTCAAGCGTTACCTTCTTCAGATTTT 2335
Db      :::::::::::GluValThrAsnGlnThrLeu-----Asp 602
Qy 780 GluLysLeuGlyTyrlMetAspLeuAlaSerArgLeuValThrArgValPheLysLeuLeu 799
Db      :::::::::::GluValThrAsnGlnThrLeu-----Asp 602
Qy 2336 AAGCCAGTGTTCACAGCAAGCTGGAGTCAAGGGCTCAGTCTGGGACAGATGCTC 2395
Db      :::::::::::GluValThrAsnGlnThrLeu-----Asp 602
Qy 800 GlnAsnGlnIleGlnGlnGlnThrTrpThrAspGluGlyThrProSerMetArgGluLeu 819
Db      :::::::::::GluValThrAsnGlnThrLeu-----Asp 602
Qy 2396 CGCTCGGCTCTCTTGAAGCTCGCTGTGACCTGAACCATGCTCTCTGATCCAGAAAGCT 2455
Db      :::::::::::GluValThrAsnGlnThrLeu-----Asp 602
Qy 820 ArgSerAlaLeuLeuGluPheAlaCysThrHisAsnLeuGlyAsnCysSerThrAla 839
Db      :::::::::::GluValThrAsnGlnThrLeu-----Asp 602
Qy 2456 GCTGAATCTTCTCCCGATGGAATCCAGTGGAAATTAATATATACCAAGATGTT 2515
Db      :::::::::::GluValThrAsnGlnThrLeu-----Asp 602
Qy 840 MetLysLeuPheAspAspTrpMetAlaSerAsnGlyThrGlnSerLeuProThrAspVal 859
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Qy 2516 TTAAGATGTCGATCTCTGCGGTGCTCAGACACAGCAGATGGAATACCTTTTAGAG 2575
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Qy 860 MetThrThrValPheLysValGlyAlaLysThrAspLysGlyTrpSerPheLeuLeuGly 879
Db      :::::::::::GluValThrAsnGlnThrLeu-----Asp 602
Qy 2576 CAATATGAATCTCAATGCTCAAGTCTGAAACAAACAAATTTCTGTATGCTTTCTCAACG 2635
Db      :::::::::::GluValThrAsnGlnThrLeu-----Asp 602
Qy 880 LysTyrlleSerIleGlySerGluAlaGluLysAsnLysIleLeuGluAlaLeuAlaSer 899
Db      :::::::::::GluValThrAsnGlnThrLeu-----Asp 602
Qy 2636 AGCAAGCATCAGGAAAGTTACTGAAGTAAATGAATCAGGAATGGAAGAAAGGTTATC 2695
Db      :::::::::::GluValThrAsnGlnThrLeu-----Asp 602
Qy 900 SerGluAspValArgLysLeuTyrlTrpLeuMetLysSerSerLeuAsnGlyAspAsnPhe 919
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Qy 2696 AAGCACAGACTTGGCAGCTCTCTTCATCGGATGCCAGACCTCCAAAGGGCGACCAA 2755
Db      :::::::::::GluValThrAsnGlnThrLeu-----Asp 602
Qy 920 ArgThrGlnLysLeuSerPheIleArgThrValGlyArgHisPheProGlyHisLeu 939
Db      :::::::::::GluValThrAsnGlnThrLeu-----Asp 602
Qy 2756 CTAGCATGGGATTTGTAAAGAAATTTGGACCCATCTCTCTGAAAAAATTTGACTTGGC 2815
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Db 940 LeuAlaTrpAspPheValLysGluAsnTrpAsnLysLeuValGlnLysPheProLeuGly 959
Qy 2816 TCATATGACATAAGGATGATCATCTCTGGCACAACAGCTCCTTTCTTCCAGGATAAG 2875
Db 960 SerTyrlThrIleGlnAsnIleValAlaGlySerTyrlLeuPheSerThrLysThrHis 979
Qy 2876 TTCACAAGAGGTGAACATATTTTGAATCTCTTGGAGCTCAAGGATCAGATCTGGATATT 2935
Db 980 LeuSerGluValGlnAlaPhePheGluAsnGlnSerGluAlaThrPheArgLeuArgCys 999
Qy 2936 TTTCAAACTGTTCTCGAAACGATAACCAAAAAATATAAAATGGCTGGAGAGAATCTTCG 2995
Db 1000 ValGlnGluAlaLeuGluValIleGlnLeuAsnIleGlnTrpMetGluLysAsnLeuLys 1019
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Db 1020 SerLeuThrTrpTrpLeu 1025
RESULT 3
I55441
vp165 - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: I55441
R/Keller, S.R.; Scott, H.M.; Mastick, C.C.; Aebersold, R.; Lienhard, G.E.
J. Biol. Chem. 270, 23612-23618, 1995
A/Title: Cloning and characterization of a novel insulin-regulated membrane aminopeptidase
A/Reference number: I55441; MUID:96007507; PMID:7559527
A/Accession: I55441
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residues: 1-916 <RES>
A/Cross-references: UNIPROT:P97629; EMBL:U32990; NID:gl041726; PIDN:AAB38021.1; PID:gl041726
C/Superfamily: Membrane alanyl aminopeptidase
Alignment Scores:
Pred. No.: 2,09e-112 Length: 916
Score: 1771.00 Matches: 352
Percent Similarity: 61.88% Conservative: 135
Best Local Similarity: 44.73% Mismatches: 264
Query Match: 29.96% Indels: 36
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Qy 365 ATTCTCTCCATATGACCTCTTTGTCCACCCCAATCTCACCTCTCTGGACTTTGTTGCA 424
Db 173 IleProGlnArgTyrlGluLeuSerLeuHisProAsnLeuThrSerMetThrPheArgGly 192
Qy 425 TCTGAGAAGATCGAAGTCTTGGTCCAGCAATGCTACCCAGTTTATCATCTTTCACAGCAAA 484
Db 193 SerValThrIleSerLeuGlnAlaLeuGlnAspThrArgAspIleIleLeuHisSerThr 212
Qy 485 GATCTTGAATACAGATGCCACCTTCAGTCAGAGAGAGATCAAGATACATACAGAACCA 544
Db 213 GlyHisAsnIleSerValThrPheMetSerAlaValSerSerGln----- 228
Qy 545 GGAAGAAGACTGAAGTTTGTAGTTACCTGCTCATGAACAAATATGCACCTGCTGGTTCCA 604
Db 229 GluLysGlnValGlnIleLeuGluTyrlProTyrlHisGlnIleAlaValAlaPro 248
Qy 605 GAGAAACTTACGGCTCACCTGAAATATCTATGTGGCTATGGACTTCCAAAGCCAAATAGGT 664
Db 249 GluSerLeuLeuThrGlyHisAsnTyrlThrLeuLysIleGluTyrlSerAlaAsnIleSer 268
Qy 665 GATGGCTTTGAGGGTTTATATAAAGCACATACAGAACTCTTGGTGGTGAACAGAAATT 724
Db 269 AsnSerTyrlTyrlGlyPheTyrlGlyIleThrTyrlThrAspLysSerAsnGluLysLysAsn 288
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Qy	860	GTTAAGACAATGAACCTTGAAGGAGGTCTTTTGGAAAGATCACTTTTGAAAACACTACTGTAAAA	919
Db	254	GlulysSerGluMetValAspAsnTrpIlysThrPheValLysSerValPro	273
Qy	920	ATGAGTACATACCCTTGTAGCCTACATAGTTGTGATTTCACICTCTCGAGTGGCTTCAC	979
Db	274	MetSerThrIyrLeuValCysPheAlaValHisArgPheThrAlaIleGluArgLysSer	293
Qy	980	TCATCAGGGGTCAAGGTGTCATCATCTATGCATCCCGACAGAACCGAAATCAAACACATTTAT	1039
Db	294	ArgSerGlyLysProLeuLysValIyrValGlnProAsnGlnLysGluThrAlaGluTyr	313
Qy	1040	GCTTTGAGGAGCATCCTGAAGCTACTTGATTTTTATGAAAGTACTTTTGATTACTACTACT	1099
Db	314	AlaAlaAsnIleThrGlnAlaValPheAspIyrPheGluAspIyrPheAlaMetGluTyr	333
Qy	1100	CCACTCTCCAAACHTGGATTTAATTTGCTATTCTCTGACTTTCACCTGGAGGCCATGGAAAT	1159
Db	334	AlaLeuProLysLeuAspLysIleAlaIleProAspPheGlyThrGlyAlaMetGluAsn	353
Qy	1160	TGGGGCTCTAATACATATAGGAGAGCTCACTGCTTTTTCACCCCAAGACCTCTCTGCT	1219
Db	354	TrpGlyLeuValThrTyArgGluThrAsnLeuLeuTyrAspProLeuLeuSerAlaSer	373
Qy	1220	TCCGATAAATCTGGGTCCACAGAGTCATAGCCCCCATGAACTGGGGCACCACTGGTTGGC	1279
Db	374	SerAsnGlnArgValAlaSerValAlaHisGluLeuValHisGlnTrpPheGly	393
Qy	1280	AACCTGTGTCAATGGAAATGGTGAATGATATTGGCTTAAAGGAGGCTTTTGCAAAATAC	1339
Db	394	AsnThrValThrMetAspTrpTrpAspLeuIyrPheAsnGluGlyPheAlaSerPhe	413
Qy	1340	ATGGAACCTTATCGCTGTTAATGTCTACATATCCAGAGCTGCAA---TTTGATGACTATTTT	1396
Db	414	PheGluPheLeuGlyValAsnHisAlaGluLysAspTrpGlnMetLeuSerGlnValLeu	433
Qy	1397	TTGAATGTGTGTTTTGAAGTAATTTACAAAGATTCATTGAATTCATCCCCTCATCTCC	1456
Db	434	LeuGluAspValPheProValGlnGluAspSerLeuMetSerSerHisProValVal	453
Qy	1457	AAACCAGCGGAAACCCGACTCAATACAGGAATGTTTCATGAAGTTCCTTCTATAACAAG	1516
Db	454	ValThrValSerThrProAlaGluIleThrSerValPheAspGlyIleSerTyrSerLys	473
Qy	1517	GGAGCTGTGATTTTGAATATGCTCAAGATTTTCTGGGTGAGGAGAATTCACAGAAGGA	1576
Db	474	GlyAlaSerIleLeuArgMetLeuGlnAspTrpIleThrProGluLysPheGlnLysGly	493
Qy	1577	ATAATTCAGTACTTAAAGAGTTTCAGCTATAGAAATCTAAGAATGATGACTTGTGGAGC	1636
Db	494	CysGlnIleTyrLeuLysLysPheGlnPheAlaAsnAlaLysThrSerAspPheTrpAsp	513
Qy	1637	AGTCTGTCAAAATAGTTGTTTAGAAAGTAGTTTACATCTGCTGGAGTTCCTTCATTCGGAT	1696
Db	514	SerLeuGlnGluAla-----	518
Qy	1697	CCCAAGATGACAACTAATACATCTCGCTTCTTCTGGGGGAAAATCGAGAGTCCAAGAGATG	1756
Db	519	-----SerAsnLeuProValLysGluVal	526
Qy	1757	ATGACTACATGGACTCTCCAGAAAGGAATCCCCTGCTGCTGTT-----AAACAGAC	1810
Db	527	MetAspThrTrpThrSerGlnMetGlyTyrProValValThrValSerGlyArgGlnAsn	546
Qy	1811	GGGTGTTCACTCCGACTGCACAGGAGCGTTCCTCCAGGGGGTTTTTCCAGGAGAGCCCT	1870
Db	547	-----IleThrGlnLysArgPheLeuLeuAsp---SerLysAlaAspPro	560
Qy	1871	GAATGGAGGGCCCTGCAGGAGAGGTACTGTGGCATATCCATTCAGCTACTCCACGAGT	1930
Db	561	SerGlnProSerGluLeuGlyTyrThrTrpAsnIleProValArgTrpAlaAspAsn	580

QY	1931	TC	TCTCTAAT-----GTGATCCACAGACACATTTCTAAATCAAAGACAGATATCTCTGGAT	1986																			
DB	581	ASP	ASN	SER	ARG	ILE	THR	VAL	TYR	ASN	ARG	LEU	ASP	GLY	GLY	ILE	THR	LEU	ASN	ALA	600		
QY	1985	CT	ACT	CAAA	AAAG	ACC	AGC	TGG	TGG	GAATTTAA	TGTGG	AGCTCAAA	TGTTACT	ACTACAT	CGTT	2044							
DB	601	ASN	LEU	SER	GLY	ASP	ALA	PH	LEU	LYS	ILE	ASN	PROM	ASP	HIS	ILE	GLY	PH	TYR	ARG	VAL	620	
QY	2045	CAC	TAT	GAG	GGT	CAT	GAT	GGG	ACCA	CACTCAT	TAC	CAC	AGT	GAAT	CAGAA	CCAC	CAC	ACT	2104				
DB	621	ASN	TYR	GLU	GLY	THR	TRP	ASP	TRP	ILE	ALA	GLU	ALA	LEU	SER	ASN	HIS	THR	ARG	640			
QY	2105	CT	CAG	ACCT	TAAG	CAC	AGAG	TAG	TCT	CATT	CAT	GAT	GTCT	TTT	CGC	TAG	TTG	TGTC	GAG	GGG	2164		
DB	641	PH	SER	ALA	ALA	ASP	ARG	SER	SER	PH	ILE	ASP	ASP	ALA	PH	ALA	LEU	ALA	ARG	ALA	GLN	660	
QY	2165	AG	ACT	GAC	CCCT	TAG	CAAA	AGCT	TCT	TG	ACAT	GAC	TACT	TACT	CTCA	CAAC	ATG	GAAC	CAAG	CAGC	2224		
DB	661	LEU	LEU	ASN	TYR	LYS	ILE	ALA	LEU	ASN	LEU	THR	WET	TYR	LEU	LYS	SER	GLU	ASP	PHE	680		
QY	2225	-----	CCG	CAC	TTTCT	CGA	AGG	TCT	CAG	TTTACT	TGG	AAATCG	TTT	TACC	ACAT	GTATG	2275						
DB	681	LEU	PRO	TRP	GLU	ARG	VAL	ILE	SER	SER	VAL	SER	TYR	ILE	SER	MET	PHE	GLU	-----	698			
QY	2276	GAC	AGA	AAAG	GAATAT	TTT	CAG	ATA	TCT	CTG	AAAC	CTCT	CAAG	CGT	TACT	CTTCT	CAG	TAT	TTT	2335			
DB	699	ASP	ASP	ARG	GLU	LEU	TYR	PRO	MET	ILE	GLU	THR-----	TYR	PHE	GLN	GLY	GLN	VAL	715				
QY	2336	AAG	CCAG	TG	TAT	GAC	AGG	CAAA	AGCT	GG	AGT	GA	GTG	CA	AGG	GGT	CAC	TCT	CTGG	CAC	AGAT	GTCT	2395
DB	716	LYS	PRO	VAL	ALA	ASP	LEU	LEU	GLY	TRP	GLN	ASN	THR	GLY	SER	HIS	ILE	THR	LYS	LEU	LEU	735	
QY	2396	CGC	T	CGG	CTCT	TTG	AAG	CTGG	CGCT	GTG	ACT	CAAC	CACT	CTCT	CTT	GCAT	C	CAG	AAAG	CT	2455		
DB	736	ARG	ALA	SER	ILE	LEU	GLY	PHE	ALA	CYS	LYS	MET	GLY	ASP	ARG	GLU	ALA	LEU	GLY	ASN	ALA	755	
QY	2456	GCT	GA	ACT	TTCT	CCC	AGT	GGAT	GGAA	TCCAG	TGG	AAATTA	ATAAT	TAC	CAAC	CAG	ATG	TT	2515				
DB	756	SER	GLN	LEU	PHE	ASP	SER	TRP	LEU	LYS-----	GLY	SER	ALA	SER	ILE	PRO	VAL	ASN	LEU	773			
QY	2516	TTA	AAG	ATT	GTGT	ATCT	GTG	GGT	GTCT	CAC	ACA	CA-----	CC	AGAT	CGA	ATTAC	2566						
DB	774	ARG	LEU	LEU	VAL	TYR	ARG	TYR	GLY	MET	GLN	ASN	SER	GLY	ASN	GLU	ALA	ALA	TRP	ASN	TYR	793	
QY	2567	CT	TTT	TAG	CAAT	AT	GA	ACT	GTCT	CAAT	GTCT	CAAG	TGCT	CAAC	AAAC	CAAA	ATTC	TGT	ATG	CT	2626		
DB	794	THR	LEU	GLU	GLN	TYR	GLN	LYS	THR	SER	LEU	ALA	GLN	GLY	LYS	LEU	LEU	TYR	GLY	813			
QY	2627	TTG	TCA	ACG	AGC	AGC	AT	CAG	GAAT	TACT	GAA	GTG	TAAT	TGCA	ACT	TAG	GAAT	TGG	AAAG	2686			
DB	814	LEU	ALA	SER	VAL	LYS	ASP	VAL	LYS	LEU	LEU	ALA	ARG	TYR	LEU	GLU	MET	LEU	TYS	ASP	PRO	833	
QY	2687	AAG	GT	TAT	CAAG	CAC	ACA	ACT	TTGG	CAG	CTCT	CTCT	TAT	CGAT	GTCT	CCG	ACAG	CTCC	CAA	AG	2746		
DB	834	ASN	ILE	LEU	LYS	THR	GLN	ASP	VAL	PHE	THR	VAL	ILE	ARG									

Db 933 AsnArgGlnSerIleArgGluTrp 940
RESULT 6
159331
thyrotropin-releasing hormone degrading enzyme (EC 3.4.11.-) - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I59331
R:Schneider, B.; Schomburg, L.; Kohrle, J.; Bauer, K.
Proc. Natl. Acad. Sci. U.S.A. 91, 9534-9538, 1994
A:Title: Cloning of a cDNA encoding an ectoenzyme that degrades thyrotropin-releasing hormone
A:Reference number: I59331; MUID:95023946; PMID:7937801
A:Accession: I59331
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
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A>Note: in Genbank entry RRTHRD, release 113.0, the source is designated as Rattus rattus
C:Superfamily: membrane alanyl aminopeptidase
C:Keywords: aminopeptidase
Alignment Scores:
Pred. No.: 3 18e-82 Length: 1025
Score: 1327.00 Matches: 302
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Best Local Similarity: 32.33% Mismatches: 399
Query Match: 22.45% Indels: 62
DB: 2 Gaps: 16
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Db 121 ProSerAlaHisProSerGluGluGluGlnGlnTrpGlnProTrpThrGlnLeu 140
QY 347 AGGCTCCCGAGTGGTCTTCTCCATATGACCTCTTGTGTCACCCCAATCTCACC 406
Db 141 ArgLeuSerGlyHisLeuLysProLeuHisTrpAsnLeuMetLeuAlaPheMetGlu 160
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Db 161 AsnPheThrPheSerGlyGluValAsnValGluIleAlaCysGlnAsnAlaThrArgTyr 180
QY 467 ATCATCTTGCACCAAGATCTTGAAATACGAATGCCACCTTCAGTCTCAGAGGAAGT 526
Db 181 ValValLeuHisAlaSerArgValAlaValGluLys-----ValGlnValAlaGluAsp 198
QY 527 TCAAGATACATGAACACCGAAGAAAGTCTGAGTACCTGCTCCTGCTCATGACAA 586
Db 199 ---ArgAlaPheGlyAlaValProValAlaGlyPhePheLeuTyrProGlnThrGlnVal 217
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Db 218 LeuValValLeuLeuAsnArgThrLeuAspAlaGlnArgHisTrpAsnLeuLysIle 237
QY 647 TTCCAGGCCAAGTTAGTGGCTTTTGAAGGGTTTATAAAGGCACATACAGAACTCTT 706
Db 238 TyrAsnAlaLeuIleGluAsnGluLeuGlyPhePheArgSerSerTyr---ValIle 256
QY 707 GGTGTGAACAAGATCTTCCAGTAAACAGTTTGTAGCCNACCCAGGACGCTGCT 766
Db 257 HisGlyGluArgPheLeuGlyValThrGlnPheSerProThrHisAlaArgLysAla 276
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QY 827 AGCAGGCATATTGCATCTCCAAATGCCAAAGGTTAAAGACTTGAAGGAGGT 886
Db 297 AlaThrTyrLeuSerLeuSerAsnMetProValGluThrSerValPheGluGluAspGly 316
QY 887 CTTTGGGAAGATCACTTTGAAACTACTGTAAATATGAGTACATACCTTGTAGCCCTACATA 946

Db 317 TrpValThrAspHisPheSerGlnThrProLeuMetSerThrTyrTyrLeuAlaTrpAla 336
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Db 337 IleCysAsnPheThrTyrArgGluThrThrThrLysSerGlyValValValArgLeuTyr 356
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Db 397 LeuAlaValProLysHisProTyrAlaAlaMetGluAsnTrpGlyLeuSerIlePheVal 416
QY 1181 GAGAGCTCAGTCTTTTGGACCCCAAGACCTCTCTGCTTCGGATTAACACTGTGGGTACC 1240
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QY 1415 GTAATTACAAAGATTCATTAATTCATCCCGCCTATCTCCAAACACGAGCGGAACCCCG 1474
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Db 537 MetLeuAlaAsnPheMetGlyHisSerValPheGlnArgGlyLeuGlnAspTyrLeuThr 556
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Db 577 LysArgAsn----- 579
QY 1715 ATGCTCGCTTCTGCGGGAATAATGCAGAGGTCAAGAGATGATGACTACATGAGCTCTC 1774
Db 580 -----GlyLysTyrValAsnIleGlnGluValMetAspGlnTrpThrLeu 594
QY 1775 CAGAAAGAAATCCCGCTGCTGGTGGTTAAACAACAGCGGTGTTC-----CTCGA 1825
Db 595 GlnMetGlyTyrProValIleThrIleLeuGlyAsnMetThrAlaGluAsnArgIleLeu 614
QY 1826 CTGCAACAGGAGCGCTTCTCCAGGGGTTTTCAGGAAGACCCCTGAAATGAGGGCCCTG 1885
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Qy 1991 GAAAGACCGACTGGGTGAAATTTAAATGTCGACTCAAAATGTTACTACATCGTTCACTAT 2050

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Qy 2051 GAGGGTCATGGATGGGACCAACTCATTACACAGCTGAATCAGAACCAACACACTTCTCAGA 2110

Db 695 AspLeuArgAsnTrpArgLeuLeuIleAspGlnLeuIleArgAsnHisGluValLeuSer 714

Qy 2111 CCTAAGACACAGTAGCTGATTCATGATCTGTTTTCAGTAGTGTGTGAGGAGACTG 2170

Db 715 ValSerAsnArgAlaGlyLeuIleAspAlaPheSerLeuAlaArgGlyTyLeu 734

Qy 2171 ACCCTAGACAAAGCTCTTGACATGACTTACTACCTCAACATGAAACAAGCAGC----- 2224

Db 735 ProGlnAsnIleProLeuGluIlelleArgTyLeuSerGluGluLysAspPheLeuPro 754

Qy 2225 ---CCCAGACTTCTCGAAGGTCGTGAGTTACTTGGAAATCGTTTACCACATGATGGACAGA 2281

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Qy 2282 AGGAATATTTTCAGATATCTCTGAAACCTCAAGCGTTTACCTTCTTCAGTATTTTAAGCCA 2341

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Qy 2342 GTGATTGACAGGCAAAAGCTGGAGTGAC-----AAGGGGTCA 2377

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Qy 2732 GCCAGACGTCCAAAGGGCGCAACACTAGCATGGGATTTGTAAGAGAAATTTGGACCCAT 2791

Db 928 AlaArgAsnProHisGlyArgAspLeuAlaTrpLysPhePheArgAspLysTrpLysIle 947

Qy 2792 CTTCTGAAAAAATTTGACTTGGGCTCATATGACATAGGATGATCATCTCTGSCACAACA 2851

Db 948 LeuAsnThrArgTyRgLyGluAlaLeuPheMetAsnSerLysLeuIleSerGlyValThr 967

Qy 2852 GCTCACTTTTCTTCCAGGATAAGTGTGCAAGAGGTGAAACTATTATTTTGAATCTCTTGAG 2911

Db 968 GluPheLeuAsnThrGluGlyGluLeuLysGluLeuLysAsnPheMetLysSerTyRAsp 987

Qy 2912 GCTCAAGATCATCTGGATATTTTCAACTGTTCTGGAAACGATPAAACAAATATATA 2971

Db 988 GlyValAlaSer-----AlaSerPheSerArgAlaValGluThrValGluAlaAsnVal 1005

Qy 2972 AAATGGCTGGAGAGAATCTTCCGACTCTGAGGACTGGCTA 3013

Db 1006 ArgTrpLysArgLeuTyRglnAspGluLeuPheGlnTrpLeu 1019

RESULT 7

A32852
membrane alanyl aminopeptidase (EC 3.4.11.2) - rat
N;Alternate names: aminopeptidase N; microsomal aminopeptidase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1989 #sequence revision 22-Nov-1989 #text_change 09-Jul-2004
C;Accession: A32852; A32448; A61250
R;Watt, V.M.; Yip, C.C.
J. Biol. Chem. 264, 5480-5487, 1989
A;Title: Amino acid sequence deduced from a rat kidney cDNA suggests it encodes the Zn-peptidase aminopeptidase N.
A;Reference number: A32852; MUID:89174587; PMID:2564389
A;Accession: A32852
A;Molecule type: mRNA
A;Residues: 1-965 <WAT>
A;Cross-references: UNIPROT:P15684; GB:M25073; NID:G205108; PIDN:AAA41502.1; PID:G205109
R;Malfroy, B.; Kado-Fong, H.; Gros, C.; Giros, B.; Schwartz, J.C.; Hellmies, R.
Biochem. Biophys. Res. Commun. 161, 236-241, 1989
A;Title: Molecular cloning and amino acid sequence of rat kidney aminopeptidase M: a member of the S1 family of metalloproteases.
A;Reference number: A32448; MUID:89273642; PMID:2567164
A;Accession: A32448
A;Molecule type: mRNA
A;Residues: 1-801, 'SC', 805-806, 'A', 808-812, 'ATVPER', 819-830, 'VGR', 834-965 <MAL>
A;Cross-references: GB:M26710; NID:G601864; PIDN:AAA57129.1; PID:G601865
R;Funkhouser, J.D.; Tangada, S.D.; Jones, M.; O, S.J.; Peterson, R.D.A.
Am. J. Physiol. 260, L274-L279, 1991
A;Title: p146 type II alveolar epithelial cell antigen is identical to aminopeptidase N.
A;Reference number: A61250; MUID:91206591; PMID:1673322
A;Accession: A61250
A;Molecule type: protein
A;Residues: 2-19;168-84;206-212, 'X', 214-215;286-289, 291-299;364-371 <FUN>
C;Superfamily: membrane alanyl aminopeptidase
C;Keywords: aminopeptidase; glycoprotein; membrane protein
F;114,128,234,242,264,555,606,624,780/Binding site: carbohydrate (Asn) (covalent) #status: predicted

Alignment Scores:
Pred. No.: 3,28e-81 Length: 965
Score: 1312.00 Matches: 326
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Best Local Similarity: 32.60% Mismatches: 413
Query Match: 22.19% Indels: 96
DB: 26 Gaps: 26

US-10-039-073-2 (1-3366) x A32852 (1-965)

Qy 203 AGAGGATTTTAC-----TGCTTAACAGCCATCTTGCCCAATATGC 244

Db 3 LysGlyPheTyRlleSerLysThrLeuGlyIleLeuGlyIleLeuGlyValAlaA 22

Qy 245 ATTTGTTCTCAGTCTCAGTGCATCTAGTTATCATTCTCAGTGAGAT----- 292

Db 23 ValCysThrIlelleAlaLeuSerValValTyRAlaGlnGluLysAsnArgAsnAlaGlu 42

Qy 293 -----CTGGGGCTTCCAGTAGCCACTAAT----- 319

Db 43 AsnSerAlaIleAlaProThrLeuProGlySerThrSerAlaThrThrSerThrAsn 62

Qy 320 -----GGGAACGATTTCTTCGCGAGGACCTAAGCTCCCGAGTGTGGTCACTTCT 370

Db 63 ProAlaIleAspGluSerLysProTrpAsnGlnTyRArgLeuProLysThrLeuIlePro 82

Qy 371 CTCCATTATGACCTCTTGTGCCACCCCAATCTCACCTCTCTGAC----- 415

Db 83 AspSerTyRglnValThrLeuArgProTyRLeuThrProAsnGluGlnGlyLeuTyRile 102

Qy 416 TTGTGTCATCTCAGAAAGATCGAAGTCTTGGTCAGCAATGCTACCCAGTTTATCATCTTG 475

Db 103 PheLysGlySerSerThrValArgPheThrCysAsnGluThrThrAsnValIleIleIle 122

Qy 476 CACAGCAAAAGATCTTCAAAATCAGAAAT-----GCCACCTTTCAGTCAGAG 520

Db 123 HisSerLysLeuAsnTyRThrAsnLysGlyAsnHisArgValAlaLeuArgAlaLeu 142

Db 826 LysLeuArgSerAlaLeuAlaCysSerAsnGluValTrpIleLeuAsnArgTyrLeuSer 845
Qy 2672 CTAGGATGGAGGAGTTATCAAGACACAGAACTTGGCAGCTCTCTTCATGCGATT 2731
Db 846 TyrThrLeuAsnProAspTyrIleArgLysGlnAspAlaThrSerThrIleValSerIle 865
Qy 2732 GCCAGAGCTCCAAAGGGCAGCAACTAGCATGGGATTTTGTAAAGAGAAATTTGCCACCAT 2791
Db 866 AlaAsnAsnValValGlyGlnThrLeuValTrpAspPheValArgSerAsnTrpLysLys 885
Qy 2792 CTTCTGAAAAAATTTGACTGGGTCTATACATATAGGATGATCATCTCTGGCACAAACA 2851
Db 886 LeuPheGluAspTyrGlyGlySerPheSerPheAlaAsnLeuIleGlnGlyValThr 905
Qy 2852 GCTCAGCTTTCTTCCAGGATAAGTTGCAAGAGGTGAAACTATTATTTTGAATCTCTTGGAG 2911
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Db 926 AlaThrGlyPheGlySerGlyThrArgAlaLeuGluGlnAlaLeuGluLysThrLysAla 945
Qy 2966 AATATAAATCGCTGGAGAGAAATCTCCGACTCTGAGGACTTGGCTAATGGTTAATACT 3025
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RESULT 8
A:53984
membrane alanyl aminopeptidase (EC 3.4.11.2) - pig
N:Alternate names: aminopeptidase N; microsomal aminopeptidase N; surface glycoprotein C
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 09-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 09-Jul-2004
C:Accession: A53984; S24020; S05040; S13177
R:Delmas, B.; Gelfi, J.; Kut, E.; Sjoestrom, H.; Noren, O.; Laude, H.
J. Virol. 68, 5216-5224, 1994
A:Title: Determinants essential for the transmissible gastroenteritis virus-receptor interaction
A:Reference number: A53984; PMID:94309188; PMID:7913510
A:Accession: A53984
A:Molecule type: mRNA
A:Residues: 1-963
A:Cross-references: UNIPROT:P15145; GB:Z29522; NID:G525286; PIDN:CAA82641.1; PID:G525287
R:Delmas, B.; Gelfi, J.; L'Hardon, R.; Vogel, L.K.; Sjoestrom, H.; Noren, O.; Laude, H.
Nature 357, 417-420, 1992
A:Title: Aminopeptidase N is a major receptor for the entero-pathogenic coronavirus TGEV
A:Reference number: S24020; PMID:92278435; PMID:1350661
A:Accession: S24020
A>Status: preliminary
A:Molecule type: protein
A:Residues: 2-31 <DE2>
R:Olson, J.; Sjoestrom, H.; Noren, O.
FEBS Lett. 251, 275-281, 1989
A:Title: Cloning of the pig aminopeptidase N gene. Identification of possible regulatory
A:Reference number: S05040; PMID:89325681; PMID:2568950
A:Accession: S05040
A:Molecule type: DNA
A:Residues: 1-294 <OLS>
A:Cross-references: EMBL:X16088
R:See, H.; Reithmeier, R.A.F.
Biochem. J. 271, 147-155, 1990
A:Title: Identification and characterization of the major stilbene- disulphonate- and co
A:Reference number: S13177; PMID:91024918; PMID:1977382
A:Accession: S13177
A>Status: preliminary
A:Molecule type: protein
A:Residues: 2-40 <SES>
C:Genetics:
A:Introns: 200/2; 248/1
A:Note: the list of introns may be incomplete
C:Superfamily: membrane alanyl aminopeptidase
C:Keywords: aminopeptidase; glycoprotein; transmembrane protein
F:1-8/Domain: intracellular #status predicted <INT>
F:9-32/Domain: transmembrane #status predicted <TM>
F:33-963/Domain: extracellular #status predicted <EXT>

Alignment Scores:
Pred. No.: 2,74e-78 Length: 963
Score: 1269.00 Matches: 323
Percent Similarity: 49.06% Conservative: 174
Best Local Similarity: 31.89% Mismatches: 386
Query Match: 21.46% Indels: 130
DB: 2 Gaps: 28
US-10-039-073-2 (1-3366) x A53984 (1-963)
Qy 203 AGAGGATTTTAC-----TGC 217
Db 3 LysGlyPheTyrIleSerLysAlaLeuGlyIleLeuGlyIleLeuGlyValAlaAala 22
Qy 218 TTAACAGCCATCTTGGCCCCAAATATGCAATTTGTTCTTCAGTTCTCAGTGCCATCTAGTTAT 277
Db 23 ValAlaThrIleIleAlaLeuSerValValTyrAlaGlnGluLysAsnLysAsnAlaGlu 42
Qy 278 CACTTCAGTGGAGTCTGGGGCTTCCAGTAGCCACTAATGGG----- 322
Db 43 HisValProGlnAlaProThrSerProThrIleThrThrAlaAlaIleThrLeuAsp 62
Qy 323 GAACGATTTCTTGGCAGGAGCTAAAGCTCCCGCTGCTGCTCTCTCCATTATGAC 382
Db 63 GlnSerLysProTrpAsnArgTyrArgLeuProThrThrLeuLeuProAspSerTyrPhe 82
Qy 383 CTCTTTGTCCACCCCAATCTCACCC---TCTCTGGAC-----TTTGTTCATCT 427
Db 83 ValThrLeuArgProTyrLeuThrProAsnAlaAspGlyLeuTyrIlePheLysGlyLys 102
Qy 428 GAGAAGATCGAAGTCTTGGTCAGCAATGTCTACCCAGCTTTTATCATCTTGCACAGCAAGAT 487
Db 103 SerIleValArgLeuLeuCysGlnGluProThrAspValIleIleIleHisSerLysLys 122
Qy 488 CTTGAAATCACGAAT-----GCCACCTTCAGTCAGAGGAAGATTCAGATAC 535
Db 123 LeuAsnTyrThrThrGlnGlyHisMetValValLeuArgGlyValGlyAspSerGlnVal 142
Qy 536 ATGAACACAGGAAAA---GAACCTGAAAGTTTTCAGTTTACCCTCTCATGAACAAATGCA 592
Db 143 ProGluIleAspArgThrGluLeuValGluLeuThr-----GluTyrLeuVal 158
Qy 593 CTGCTGTTCCAGAGAACTTACGCTCACCTACCTGAAATACTATGTGCTGCTGATGGATTTCCAA 652
Db 159 ValHisLeuLysGlySerLeuGlnProGlyHisMetTyrGluMetGluSerGluPheGln 178
Qy 653 GCCAAGTTAGTGATCGCTTTGAGGGTTTTTATAAAGCACATACAGAACTCTTGGTGGT 712
Db 179 GlyLeuAlaAspAspLeuAlaGlyPheTyrArgSerGluTyrMetGlu---GlyAsn 197
Qy 713 GAAACAGGAATCTTCAGTAACAGATTTTGAGCCCAACCCAGGACGCTGCTTCCCT 772
Db 198 ValLysValValAlaThrThrGlnMetGlnSerThrAspAlaArgLysSerPhePro 217
Qy 773 TGCTTTGATGACCGTGTGTTTCAAGCCAACTTTTCAATCAAGATACGAGAGAGAGCAGG 832
Db 218 CysPheAspGluProAlaMetLysAlaThrPheAsnIleThrLeuIleHisProAsnAsn 237
Qy 833 CATATTGCACTATCCAACTGCGCAAGGTTTAAAGCAATTTGAACATTTGAAGGAGGT----- 886
Db 238 LeuThrAlaLeuSerAsnMetProPro-----LysGlySerSerThr 251
Qy 887 ---CTTTTGAAGAT-----CACTTTGAAACTACTGTAAAAAATGAGT 925
Db 252 ProLeuAlaGluAspProAsnTrpSerValThrGluPheGluThrThrProValMetSer 271
Qy 926 ACATACCTGTAGCCCTACATAGTTTGTGATTTTCCACTCTCTGAGTGCGCTTCACTTCATCA 985
Db 272 ThrTyrLeuLeuAlaTyrIleValSerGluPheGlnSerValAsnGluThrAlaGlnAsn 291
Qy 986 GGGGTCAAGGTGTCCATCTATGATCCCTCCAGACAACGGAATCAACACAT-----TAT 1039
Db 986 GGGGTCAAGGTGTCCATCTATGATCCCTCCAGACAACGGAATCAACACAT-----TAT 1039

Db 292 GlyValLeuIleArgIleTrpAlaArgProAsnAlaIleAlaGluGlyHisGlyMetTyr 311
Qy 1040 GCTTTGCGGACATCACTGAAGCTACTTGATTTTATGAAAGTACTTTGATATCTACTAT 1099
Db 312 AlaLeuAenValThrGlyProIleLeuAenPhePheAlaAenHisTyrAsnThrSerTyr 331
Qy 1100 CCACCTCTCAAACTGGATTAATTCCTATTCTGACTTTGACCTGGAGGCCATGGAATAAT 1159
Db 332 ProLeuProLysSerAspGlnIleAlaLeuProAspPheAsnAlaGlyAlaMetGluAen 351
Qy 1160 TGGGCGCTCATTTACATATAGGAGAGCTGCTGCTGCTTTTGGCCCAAGACCTCTTCGCT 1219
Db 352 TrpGlyLeuValThrTyrArgGluAenAlaLeuPheAspProGlnSerSerSerIle 371
Qy 1220 TCCGATAAATCTGTGGGTCAACAGCTCATAGCCCACTGAACCTGGCGCACCAGTGGTTGGC 1279
Db 372 SerAenLysGluArgValThrValIleAlaHisGluLeuAlaHisGlnTrpPheGly 391
Qy 1280 AACCTGGTCAACATGGAATGGTGAATGATATTTGGCTTAAGGAGGGTTTGCMAAATAC 1339
Db 392 AenLeuValThrLeuAlaTrpTrpAsnAspLeuTrpLeuAenGluGlyPheAlaSerTyr 411
Qy 1340 ATGGAACTTATCGCTGTTAATGCTACATATCCAGAGCTGCAATTTGTGATGACTATTTTGT 1399
Db 412 ValGluTyrLeuGlyAlaAspHisAlaGluProThrTrpAenLeuLysAspLeuVal 431
Qy 1400 ---AATGTGTGTTTGAAGTAAATACAAAAGATTCAATTGAATTCATCCGCCCTATCTCC 1456
Db 432 ProGlyAspValTyrArgValMetAlaValAlaLeuAlaSerSerHisProLeuThr 451
Qy 1457 AAACAGCGGAA-----ACCCGACTCAATATACAGGAAATGTTTGTGAAGTTTCC 1507
Db 452 ThrProAlaGluGluValAsnThrProAlaGlnIleSerGluMetPheAspSerIleSer 471
Qy 1508 TATAACAGGGAGCTGTATTTTGAATATGCTCAAGGATTTCTGGGTGAGGAGAAATTC 1567
Db 472 TyrSerLysGlyAlaSerValIleArgMetLeuSerAenPheLeuThrGluAspLeuPhe 491
Qy 1568 CAGAAGAAATTAATTCAGTACTTAAGAAAGTTTCAGCTATAGAAATGCTAAGAAATGATGAC 1627
Db 492 LysGluGlyLeuAlaSerTyrLeuHisAlaPheAlaTyrGlnAenThrThrTyrLeuAsp 511
Qy 1628 TTGTGGAGAGCTCTCAAAATAGTTGTTTAGAAAGTGAATTTACATCTGGTGGAGTTGT 1687
Db 512 LeuTrpGluHisLeuGlnLysAlaVal----- 520
Qy 1688 CATTCGGATCCCAAGATGACAGTAAACATGCTCGCTTCTCGGGGAAAATGCAGAGTCT 1747
Db 521 -----AspAlaGlnThrSerIleArgLeuPro-----AspThrVal 532
Qy 1748 AAAGAGATGATGACTACATGGAATCTCCAGAAAGGAATCCCGCTGCTGGTGTAAACAA 1807
Db 533 ArgAlaIleMetAspArgTrpThrLeuGlnMetGlyPheProValIleThrVal----- 550
Qy 1808 GACGGGTGTTTACTCCGATCGAACAGGAGCGCTTCTCCAGGGGGTTTTCCAGGAAGAC 1867
Db 551 AspThrLysThrGlyAsnIleSerGlnLysHisPheLeu-----LeuAspSerGluSer 568
Qy 1868 CTTGAATGGGGCCCTCGCAGAGAGGTACTGTCGATATCCCATTTGACCTACTCCAGC 1927
Db 569 AenValThrArgSerSerAlaPheAspTyrLeuTrpIleValProIle-----SerSer 586
Qy 1928 AGTTCTTCTAATGTGATCCACAGACAC----- 1954
Db 587 IleLysAenGlyValMetGlnAspHisTyrTrpLeuArgAspValSerGlnAlaGlnAen 606
Qy 1955 ----ATTCTAAATCAAGACAGATCTCTGGATCTACTGGAAGACAGTGGGTGAAA 2011
Db 607 AspLeuPheLysThrAlaSerAsp-----AspTrpValLeu 618
Qy 2012 TTTAATGTGACTCAATGGTTTACTACATCGTTTCACTATGAGGTCATGGATGGGACCAA 2071
Db 619 LeuAenValAsnValThrGlyTyrPheGlnValAenTyrAspGluAspAsnTrpArgMet 638

RESULT 9

A30325

membrane alanyl aminopeptidase (EC 3.4.11.2) precursor - human

N;Alternate names: aminopeptidase N; cell surface glycoprotein CD13

Qy 2072 CTCATTACACAGCTGAATACGAACCAACACACTTCTCAGACCTTAAGGACAGAGTAGGTCGT 2131
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Qy 2132 ATTCAATGATGTTTACGCTAGTTGGTGCGAGGAGACTGACCCCTAGACAAAGCTCTTCAC 2191
Db 659 IleTyrAspSerPheAenLeuAlaThrAlaHisMetValProValThrLeuAlaLeuAsp 678
Qy 2192 ATGACTTACTACCTCCCAACATGAACAGCAGCGCCCGCAGCTTCTCGAAGGCTCTGAGTTAC 2251
Db 679 AsnThrLeuPheLeuAenGlyGluLysGluTyrMetProTrpGlnAlaAlaLeuSerSer 698
Qy 2252 TTGGAATCGTTTACCACATGATCGACAGAGGAATATTTTCAGATATCTCTGAACACCTC 2311
Db 699 LeuSerTyrPheSerLeuMetPheAspArg-----SerGluValTyrGlyProMet 715
Qy 2312 AAGCGTTTACCTTCTCAGTATTTTAAGCCAGTGTGACAGG-----CAA 2356
Db 716 LysLysTyrLeuArgLysGlnValGluProLeuPheGlnHisPheGluThrLeuThrLys 735
Qy 2357 AGCTGGAGTGCACAAG---GGCTCAGTCTGGGACAGGATGCTCCGCTCGGCTCTCTTGAAG 2413
Db 736 AsnTrpThrGluArgProGluAenLeuMetAspGlnTyrSerGluIleAenAlaIleSer 755
Qy 2414 CTGCGCTGTGACCTGAAACCATGCTCTTGGCATCCAGAAAGCTGTGAACTCTTCTCCAG 2473
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Db 776 TrpMetSerAspProGluAenAsnProIleHisProAenLeuArgSerThrIleTyrCys 795
Qy 2531 -----TCTGGGCTGCTCAGACAAACAGCAGGATGGAATTAACCTTTTAGAGCAATAT 2581
Db 796 AsnAlaIleAlaGlnGlyGlyGlnAspGln-----TrpAspPheAlaTrpGlyGlnLeu 813
Qy 2582 GAACGTCAATGTCAAGTGTGAAACAAACAAATTCGTATGCTTTGTCAACGAGCAAG 2641
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Qy 2978 CTGGAGAGAAATCTTCGACTCTGAGGACTTGGCTAATG 3016
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C;Species: Homo sapiens (man)
C;Date: 02-Feb-1990 #sequence, revision 02-Feb-1990 #text change 09-Jul-2004
C;Accession: A30325, S36158, I39442; S35688; S56098; S56099
R;Look, A.T.; Ashmun, R.A.; Shapiro, L.H.; Peiper, S.C.
J. Clin. Invest. 83, 1299-1307, 1989
A;Title: Human myeloid plasma membrane glycoprotein CD13 (gp150) is identical to aminopeptidase N
A;Reference number: A30325; MUID:89198086; PMID:2564851
A;Accession: A30325
A>Status: preliminary
A:Molecule type: mRNA
A:Molecule type: mRNA
A;Residues: 1-967 <LOO>
A;Cross-references: UNIPROT:P15144; UNIPROT_Q9UCE0; GB:M22324; NID:g178535; PIDN:AAA5171
R;Olson, J.; Cowell, G.M.; Konigshofer, E.; Danielsen, E.M.; Moller, J.; Lauetsen, L.; H.
FEBS Lett. 238, 307-314, 1988
A;Title: Complete amino acid sequence of human intestinal aminopeptidase N as deduced from cDNA
A;Reference number: S01658; MUID:89005706; PMID:2901990
A;Accession: S01658
A:Molecule type: mRNA
A;Residues: 1-85, 'R', 87-535, 'E', 537-602, 'M', 604-886, 'P', 888-967 <OLUS>
A;Cross-references: EMBL:X13276
R;Shapiro, L.H.; Ashmun, R.A.; Roberts, W.M.; Look, A.T.
J. Biol. Chem. 266, 11999-12007, 1991
A;Title: Separate promoters control transcription of the human aminopeptidase N gene in liver and kidney
A;Reference number: I39442; MUID:91288079; PMID:1675638
A;Accession: I39442
A:Molecule type: DNA
A;Residues: 1-15 <RES>
A;Cross-references: GB:M55522; NID:g178532; PIDN:AAA83399, 1; PID:g178533
R;Nunez, L.; Amigo, L.; Rigotti, A.; Puglielli, L.; Mingrone, G.; Greco, A.V.; Nervi, F.
FEBS Lett. 329, 84-88, 1993
A;Title: Cholesterol crystallization-promoting activity of aminopeptidase-N isolated from sheep erythrocytes
A;Reference number: S35688; MUID:93359071; PMID:8102610
A;Accession: S35688
A:Molecule type: protein
A;Residues: 2-18 <NUM>
R;Watanabe, Y.; Iwaki-Egawa, S.; Mizukoshi, H.; Fujimoto, Y.
Biochim. Biophys. Acta 1187, 397-400, 1995
A;Title: Identification of an alanine aminopeptidase in human maternal serum as a membrane protein
A;Reference number: S56098; MUID:96066273; PMID:7576235
A;Accession: S56098
A:Molecule type: protein
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A;Gene: GDB:ANPEP; CD13; PEPN
A;Cross-references: GDB:I18728; OMIM:151530
A;Map position: 15q25-15q26
C;Superfamily: membrane ananyl aminopeptidase
C;Keywords: aminopeptidase; glycoprotein; transmembrane protein

Alignment Scores:
Pred. No.: 5,55e-78 Length: 967
Score: 1264.50 Matches: 325
Percent Similarity: 46.62% Conservative: 158
Best Local Similarity: 31.37% Mismatches: 386
Query Match: 167
DB: 2 Gaps: 26

US-10-039-073-2 (1-3366) x A30325 (1-967)

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:::|||||
Qy 239 ATATGCAATTGGTTCAGTTCTCAGTCCCATCTAGTTATCACCTCAGTAGGATCCTGGG 298
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Db 23 ValCysThrIlelleAlaLeuSerValValtyrSerGlnGluLysAsnLysAsnAlaAsn 42
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Qy 299 GTTTTCCCAGTAGGCC----- 313
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Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 406 AspLeuTrpLeuAsnGluGlyPheAlaSerTyrValGluTyrLeuGlyAlaAspTyrAla 425
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 1367 TATCCAGAGCTCAATTTGATGACTATTTT---TTGAATGTGTGTTTGAAGTAATTACA 1423
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QY 426 GluProThrTrpAsnLeuLysAspLeuMetValLeuAsnAspValTyrArgValMetAla 445
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 1424 AAAGATTTCATTGAATTCATCCCGCCCTATCTCCAAACCAGCG------GAAACCCCG 1474
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 446 ValAspAlaLeuAlaSerSerHisProLeuSerThrProAlaSerGluLeuAsnThrPro 465
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 1475 ACTCAATACAGAAATGTTGATGAAGTTTCTTATACAGGGAGCTGTGATTTTGAAT 1534
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 466 AlaGlnIleSerGluLeuPheAspAlaIleSerTyrSerLysGlyAlaSerValLeuArg 485
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 1535 ATGCTCAAGGATTTTCTGGTCGAGAGAAATTCACAGAAAGGAATAATTCAGTACTTAAAG 1594
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 486 MetLeuSerSerPheLeuSerGluAspValPheLysGlnGlyLeuAlaSerTyrLeuHis 505
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 1595 AAGTTTCAGCTATAGAAATGCTAAGAAATGATGACTTGTGGAGCAGTCTG----- 1642
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 506 ThrPheAlaTyrGlnAsnThrIleTyrLeuAsnLeuTrpAspHisLeuGlnLalaVal 525
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 1643 TCAATAGTGTGTTAGAAAGTATTTTACATCTGTGGAGTTGTTCATTCGGATCCCAAG 1702
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 526 AsnAsnArgSerIleGlnLeuProThr----- 535
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 1703 ATGCAAGTAACATGCTCGCTTTCTGGGGGAAATGCAGAGTCAAGAGATGATGACT 1762
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 536 -----ValArgAspIleMetAsn 541
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 1763 ACATGGAATCTCCAGAAAGGAATCCCTCTGCTGGTGTAAACAAGAGCGGGTTCATCTC 1822
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 542 ArgTrpThrLeuGlnMetGlyPheProValIleThrVal-----AspThrSerThrGly 559
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 1823 CGATGCAACAGAGAGCGTTCCTCCAGGGGGTTTTCCAGGAAGACCCCTGAA----- 1873
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 560 ThrLeuSerGlnGluHisPheLeuLeu-----AspProAspSerAsnVal 574
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 1874 TGGAGGGCCCTCAGAGAGGTACCTGTGGCATATCCCATTCACC----- 1918
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 575 ThrArgProSerGluPheAsnTyrValTrpIleValProIleThrSerIleArgAspGly 594
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 1919 -----TACTCCACG 1927
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 595 ArgGlnGlnAspTyrTrpLeuIleAspValArgAlaGlnAsnAspLeuPheSerThr 614
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 1928 AGTTCTTCTTAATGTGATCCACAGACACATTTCAAAATCAAGACAGATCTCTGGATCTA 1987
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 615 SerGlyAsn----- 617
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 1988 CCTGAAAGACACAGTTGGGTGAAATTTAATGTGGACTCAATGGTTTACTACATCGTTCCAC 2047
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 618 -----GluTrpValLeuLeuAsnLeuAsnValThrGlyTyrTyrArgValAla 633
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 2048 TATGAGGGTCATGGATGGGCAACTCATTTACACAGCTGGAATCAGAACACACACTTCTC 2107
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 634 TyrAspGluLysAsnTrpArgLysIleGlnThrGlnLeuGlnArgAspHisSerAlaIle 653
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 2108 AGACCTAAGGACAGATAGGTCATGATGATGTTTTCAGCTAGTTTGGTGCAGGGAGA 2167
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 654 ProValIleAsnArgAlaGlnIleIleAsnAspAlaPheAsnLeuAlaSerAlaHisLys 673
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 2168 CTGACCCCTAGACAAAGCTTTCACATGACTTACTACTCTCCACATGAAACAGAGCGCCC 2227
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 674 ValProValThrLeuAlaLeuAsnAsnThrLeuPheLeuIleGluGluArgGlnTyrMet 693
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 2228 GCATCTCTCGAAGGTCGAGTTTACTTGGAAATCGTTTACCACATGATGCAGAGAGGAAT 2287
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 694 ProTrpGluAlaLeuSerSerLeuSerTyrPheLysLeuMetPheAspArg----- 711
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
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QY 2288 ATTTCCAGATATCTCTGAAACCTCAGCGTTTACCTTCTTCCAGTATTTTAAACCAGTGATT 2347
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 712 ---SerGluValTyrGlyProMetLysAsnTyrLeuLysLysGlnValThrProLeuPhe 730
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 2348 -----GACAGGCAAGCTGGAGTGAC---AAGGGCTCAGTCTGGGACAGG 2389
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 731 IleHisPheArgAsnAsnThrAsnAsnTrpArgGluIleProGluAsnLeuMetAspGln 750
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 2390 ATGTCCTCGCTCGGCTCTCTTGAAGCTGGCCCTGTGCACCTGAAACCATGCTCTTGCATCCAG 2449
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 751 TyrSerGluValAsnAlaIleSerThrAlaCysSerAsnGlyValProGluCysGluGlu 770
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 2450 AAAGCTGCTGAACCTTCTCTCCAGTGGATGAAATCCAGTGAATAATTAATATACCAACA 2509
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 771 MetValSerGlyLeuPheLysGlnTrpMetGluAsnProAsnAsnAsnProIleHisPro 790
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 2510 GATGTTTAAAGATTGTGTAT-----TCTGTGGTGTCTCAGACAACAGCAGGATGGAAT 2563
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 791 AsnLeuArgSerThrValTyrCysAsnAlaIleAlaGlnGlyGlyGluGluGluTrpAsp 810
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 2564 TACCTTTTAGAGCAATATGAATCTGTCAATGCTCAAGTCTGAACAAACAAATTTCTGTAT 2623
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 811 PheAlaTrpGluGlnPheArgAsnAlaThrLeuValAsnGluAlaAspLysLeuArgAla 830
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 2624 GCTTTGCAACGACGACGATCAGAAAGTACTGAAGTAAATTAAGAACTAGGAATGGAA 2683
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 831 AlaLeuAlaCysSerLysGluLeuTrpIleLeuAsnArgTyrLeuSerTyrThrLeuAsn 850
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 2684 GGAAAGGTTATCAGACACAGAACTTGGCAGCTCTCTTCATGCGATTGCCAGACGTCCA 2743
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 851 ProAspLeuIleArgLysGlnAspAlaThrSerThrIleIleSerIleThrAsnAsnVal 870
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 2744 AAGGGCAGCAACTAGCATGGGATTTTGTAAAGAAATTTGGACCCCATCTTCTGAAAAA 2803
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 871 IleGlyGlnGlyLeuValTrpAspPheValGlnSerAsnTrpLysLeuPheAsnAsp 890
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 2804 TTTGACTTGGCTCATATGACATAAGGATGATCATCTCTGCGCACACAGCTCCTTTTCT 2863
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 891 TyrGlyGlySerPheSerPheSerAsnLeuIleGlnAlaValThrArgArgPheSer 910
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 2864 TCCAAGGATAGTGGCAAGAGTGCAAACTATTTTGAATCTCTTGAGGCTCAA----- 2917
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 911 ThrGluTyrGluLeuGlnGlnLeuGlnPheLysLysAspAsnGluGluThrGlyPhe 930
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 2918 GGATCACATCTGGATATTTTTCAAACTGTTCTGGAACGATAACCAAAAAATATAAAATGG 2977
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 931 GlySerGlyThrArgAlaLeuGluAlaLeuGluLysThrLysAlaAsnIleLysTrp 950
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 2978 CTGGAGAGAATCTTCGACTCTCGAGCTCTGAGGACTTGGCTAATGGTTAATACT 3025
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 951 ValLysGluAsnLysGluValValLeuGlnTrpPheThrGluAsnSer 966
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||

RESULT 10
TI0052
aminopeptidase (EC 3.4.11.-) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: TI0052
R;Constam, D.B.; Tobler, A.R.; Rensing-Ehl, A.; Kemler, I.; Hersh, L.B.; Fontana, A.
J;Biol. Chem. 270, 26931-26939, 1995
A;Title: Puromycin-sensitive aminopeptidase sequence analysis, expression, and functiona
A;Reference number: 216922; MUID:96070789; PMID:7592939
A;Accession: TI0052
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-920 <CON>
A;Cross-references: UNIPROT:Q11011; EMBL:U35646; NID:g1184160; PIDN:AAC52409.1; PID:g118
A;Note: puromycin-sensitive
C;Superfamily: membrane alanyl aminopeptidase
C;Keywords: aminopeptidase; metalloprotein; zinc

Alignment Scores: 1.48e-74 Length: 920
Pred. No.: 1
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Score:	1214.00	Matches:	305
Percent Similarity:	49.84%	Conservative:	167
Best Local Similarity:	32.21%	Mismatches:	353
Query Match:	20.53%	Indels:	122
DB:	2	Gaps:	26
US-10-039-073-2 (1-3366) x T10052 (1-920)			
QY	308	GTAGCACTAATGGGAACGATTTCTTGGCAGGAGCTAAGCTCCCGAGTGTGCTCAT	367
DB	43	LeuAlaAlaMetProGluLysArgProPheGlu-----ArgLeuProAlaGluValSer	60
QY	368	CCTCTCCATTATGACCTCTTTGTCCACCCCAATCTCACCTCTCTGGACTTTGTTCATCT	427
DB	61	ProIleAsnTyrSerLeuCysLeuLysProAspLeu-----LeuAspPheThrPheGlu	78
QY	428	GAGAAGTCGAAGCTTGG-----GTGAGCAATGCTACCCAGTATTATCATCTTCGACAGC	481
DB	79	GlyLysLeuGluAlaAlaAlaGlnValArgGlnAlaThrAsnGlnIleValMetAsnCys	98
QY	482	AAAGATCTTGAAATCACGAATGCCACCTTCAGTCAGAGGAAGATTCAAGATACATGAA	541
DB	99	AlaAspIleAspIleIleThrAlaSerTyrAlaProGluGlyAspGluGluIleHisAla	118
QY	542	CCAGGA-----AAAGAACTGAAAGTTTGTAGTTACCCCTGCTCATGAA	583
DB	119	ThrGlyPheAsnTyrGlnAsnGluAspGluLysValThrLeuSerPheProSerThrLeu	138
QY	584	CAATTCGACCTGCTGTTCCAGAGAACTTACGCTCACCTGAAATACATATGTGGCTATG	643
DB	139	GlnThrGly-----ThrGlyThrLeuLys-----Ile	147
QY	644	GACTTCCAAAGCTTAGGTGATGGCTTTGAAGGTTTATATAAAGCACATACAGAACT	703
DB	148	AspPheValGlyGluLeuAsnAspLysMetLysGlyPheTyrArgSerArgTyrThrThr	167
QY	704	CTTGGTGGTGAACAAGAATTTCTGCAGTAACAGATTTTGAGCCAAACCCAGGACGCATG	763
DB	168	ProAlaGlyGluValAlaGlyTyrAlaAlaValThrGlnPheGluAlaThrAspProArgArg	187
QY	764	GCTTTCCCTTGTGATGAACCGTTGTTCAAGCCAACTTTTCAATCAAGATACGAGA	823
DB	188	AlaPheProCysTrpAspGluProAlaIleLysAlaThrPheAspIleSerLeuValVal	207
QY	824	GAGAGCAGGCATATTGCATCTCAACATGCACAAAGGTT-----AAGACAATTGAAC	877
DB	208	ProLysAspArgValAlaLeuSerAsnMetAsnValIleAspArgLysProTyrProAsp	227
QY	878	GAAGAGGCTCTTTGGGAAGATCACTTTGAAACTACTGTAAATAGTACATACCTTGTA	937
DB	228	AspGluAsnLeuValGluValLysPheAlaArgThrProValMetSerThrTyrLeuVal	247
QY	938	GCCTACATAGTTTGTGATTTCCATCTCTGAGTGGCTTCACTTCATCAGGGGTCAAGGTG	997
DB	248	AlaPheValValGlyGluTyrAspPheValGluThrArgSerLysAspGlyValCysVal	267
QY	998	TCCATCTATGCATCCCCAGACAAACGGAATCAACACATATGCTTTGACGGCATCACTG	1057
DB	268	ArgValTyrThrProValGlyLysAlaGluGlnGlyPheAlaLeuGluValAlaAla	287
QY	1058	AAGTACTTGAATTTTATGAAGTACTTTGTATATCTACTATCTCCACTCTCCAACTGGAT	1117
DB	288	LysThrLeuProPheTyrLysAspTyrPheAsnValProTyrProLeuProLysIleAsp	307
QY	1118	TTAATTCGATTCTGACTTTCACCTGGAGCCATGGAATAATTTGGGGCTCATATCAT	1177
DB	308	LeuIleAlaIleAlaAspPheAlaAlaGlyAlaMetGluAsnTrpGlyLeuValThrTyr	327
QY	1178	AGGAGAGCTGCTGCTTTTGGCCCCAAGACCTCTTCTGCTCCGATAAAGTGGGTC	1237
DB	328	ArgGluThrAlaLeuLeuIleAspProLysAsnSerCysSerSerArgGlnTrpVal	347
QY	1238	ACCAGATCATAGCCCATGAACCTGGCGCACCGAGTGGTTTGGCAACCTGGTCACAATGGA	1297
DB	348	AlaLeuValValGlyHisGluLeuAlaHisGlnTrpPheGlyAsnLeuValThrMetGlu	367
QY	1298	TGTTGGAATGATATTTGGCTTAAGAGGGTTTTCGAAAATACATGAGAACTTATCGTGT	1357
DB	368	TrpTrpThrHisLeuTrpLeuAsnGluGlyPheAlaSerTrpIleGluTyrLeuCysVal	387
QY	1358	AATGCTACATATCCAGAGCTGCAATTTGATGACTATTTTGAATGTGTGTTTGAAGTA	1417
DB	388	AspHisCysPheProGluTyrAspIleTrpThrGlnPheValSerAlaAspTyrThrArg	407
QY	1418	ATTACAAA---GATTCATTGAATTCATCCCGCTTATCTCCAAACCCAGCGAAACCCCG	1474
DB	408	AlaGlnGluLeuAspAlaLeuAspAsnSerHisProIleGluValSerValGlyHisPro	427
QY	1475	ACTCAAAATACAGAAATGTTTGTATGAAGTTTCTTATAACAGGGAGCTGTATTTGAAT	1534
DB	428	SerGluValAspGluIlePheAspAlaIleSerTyrSerLysGlyAlaSerValIleArg	447
QY	1535	ATGCTCAAGGATTTCTGGGTGAGGAGAAATCCAGAAAGGAATAATTCAGTACTTAAAG	1594
DB	448	MetLeuHisAspTyrIleGlyAspLysAspPheLysGlyMetAsnMetTyrLeuThr	467
QY	1595	AAGTTTCAGCTATAGAAATGCTAAGAAATGATGACTTGTGGAGCAGTCTGTCAAATAGTGT	1654
DB	468	LysPheGlnGlnLysAsnAlaAlaThrGluAspLeuTrpGluSerLeuGluSerAla---	486
QY	1655	TTAGAAAGTGATTTTACATCTGTGTGAGTGTTCATTCGGATCCCAAGATGACAAGTAAC	1714
DB	486	-----	486
QY	1715	ATGCTCGCTTCTCGGGGAAAATGCAGAGGTCAAGAGATGATGACTACATGAGCTCTC	1774
DB	487	-----SerGlyLysProIleAlaAlaValMetAsnThrTrpThrLys	500
QY	1775	CAGAAAGGAATCCCTCGCTGCTGGTGGTTAAA-----CAAGACGGGTCTTCACCT	1822
DB	501	GlnMetGlyPheProLeuIleTyrValGluAlaGluGlnValGluAspArgValLeu	520
QY	1823	CGACTCCAAACAGAGCGCTTC---CTCCAGGGGGTTTC-----CAGAAAGACCTGAA	1873
DB	521	LysLeuSerGlnLysLysPheCysAlaSerGlyProTyrGlyGlyLysCysProGln	540
QY	1874	TGAGGGCCCTGCAGGAGAGGTACCTGTGCGCATATCCCATTTGACCTACCTCCACAGTCT	1933
DB	541	TrpMet-----ValProIleThrIleSerThrSerGlu	551
QY	1934	TCT---AATGTGATCCACAGACACATTTCTAAATCAAAGACAGAT-----ACTCTG	1981
DB	552	AspProAsnGlnAlaLysLeuLysIleLeuMetAspLysProGluMetSerValValLeu	571
QY	1982	GATCTACCTGAAAGACCAAGTGGTGAATTTATGTGGACTCAATAGTGTACTACATC	2041
DB	572	LysAsnValLysProAspGlnTrpValLysLeuAsnLeuGlyThrValGlyPheTyrArg	591
QY	2042	GTTTCATGAGGGTTCATGGATGGGACCAACTCATTACACAGCTGAATCAGAACCCACA	2101
DB	592	ThrGlnTyrSerSerAlaMetLeuGluSerLeuLeuProGlyIleArgAsp-----Leu	609
QY	2102	CTTCTCAGACCTTAAGACAGAGTAGTCTGTGATTCATGATGTGTTCAGTGTGTGCA	2161
DB	610	SerLeuProValAspArgLeuGlyLeuGlnAsnAspLeuPheSerLeuAlaArgAla	629
QY	2162	GGGAGACTACCTTAGACAAAGCTCTTGACATGACTTACTACTCTCAACATGAAACAAGC	2221
DB	630	GlyIleIle-----	632
QY	2222	AGCCCGCAGCTTCTCGAAGGTCTGAGTTACTTGGAAATCGTTTACCACATGTGGACAGA	2281
DB	633	-----SerThrValGluValLeuLysValMetGluAlaPheValAsnGluProAsnTyr	650
QY	2282	AGGAATATTTCAGATATCTCT-----	2302

Db 270 IleValLeuAenGluLeuHisSerValMetAlaValAlaLeuAaSerSerHisPro 289
Qy 1451 ATCTCCAAACAGCGGAA-----ACCCGACTCAATACAGGAAATGTTTGATGAA 1501
Db 290 LeuSerSerProAlaAaspGluValAsnThrProAlaGlnIleSerGluLeuPheAaspSer 309
Qy 1502 GTTTCCTATACAAGGAGCTGTGATTGTAATAGTCTCAAGGATTTTCTGGGTGAGGAG 1561
Db 310 IleThrTyrSerLysGlyAlaSerValLeuArgMetLeuSerSerPheLeuThrGluAasp 329
Qy 1562 AAATTCAGAAAGAAATTCAGTACTTAAGAAGTTTCAGCTATAGAAATGCTAAGAAT 1621
Db 330 LeuPheLysGluGlyLeuAlaSerTyrPheAlaTyrGlnAsnThrIleTyr 349
Qy 1622 GATGACTTGTGGAGCAGCTCTGCAATAGTTGTTTGAAGAGTGATTTTACATCTGGTGA 1681
Db 350 LeuAaspLeuThrGluHisLeuGlnGlnAlaVal----- 360
Qy 1682 GTTTGTCTATCCGATCCCAAGATGACAAAGTAACTGCTCGCTTCTGGGGGAAATGCA 1741
Db 361 -----AsnSerGlnSerAlaIleGlnLeuProAla 370
Qy 1742 GAGTCAAGAGATGATGACTACATGGAATCTCAGAAAGAAATCCCTGCTGGTGGTT 1801
Db 371 SerValArgAaspIleMetAaspArgTrpIleLeuGlnMetGlyPheProValValThrVal 390
Qy 1802 AAA---CAAGACGGGTGTTCACTCCGACTCGCAACAGGAGCGCTTCCTCCAGGGGTTTTC 1858
Db 391 AsnThrThrAsnGlyIle-----IleSerGlnHisPheLeuLeu----- 404
Qy 1859 CAGGAAGACCCCTGAA-----TGGAGGCGCTCGCAGGAGGTTACCTGTGGCATATC 1909
Db 405 -----AaspProThrSerAsnValThrArgProSerAaspPheAsnTyrLeuTrpIleVal 422
Qy 1910 CCATTGACCTACTCCAGAGTCTCTTAATGTGATCCACAGACAC----- 1954
Db 423 ProVal-----SerSerMetArgAsnGlyValGlnGlnGlnGluPheTrpLeuGlu 439
Qy 1955 ---ATTCTAAATCAAGACAGATACTCTGGATCTACTGTAAGACAGCAGTTGGTGAA 2011
Db 440 GlyValGluGlnThrGlnAsnSerLeuPheArgValGluGlyAaspAsnAsnTrpIleLeu 459
Qy 2012 TTTAATGTGGACCAATGTTTACTACATGCTTCATGAGGCTCATGGATGGGACCAA 2071
Db 460 AlaAsnLeuAenValThrGlyTyrTyrGlnValAsnTyrAaspGluGlyAsnTrpLysLys 479
Qy 2072 CTCATTACAGCTGAATCAGAACACACACTTCTCAGACCTTAAGGACAGTAGTCTG 2131
Db 480 LeuGlnThrGlnLeuGlnThrAsnProSerValIleProValIleAsnArgAlaGlnIle 499
Qy 2132 ATTCATGATGTTTTCAGTGTGTTGGTCAGGGAGACTGACCTCAGCAAGGCTCTTGAC 2191
Db 500 IleHisAaspAlaPheAsnLeuAlaSerAlaGlnLysValProValThrLeuAlaLeuAasp 519
Qy 2192 ATGACTTACTACTCCCAACATGAACAGCAGCGCCCGCCTCTTCGAAAGTCTCAGTTAC 2251
Db 520 AsnThrLeuPheLeuIleArgGluThrGluTyrMetProTrpGlnAlaAlaLeuSerSer 539
Qy 2252 TTGGAATCGTTTACCACATGATCGACAGAGGAAATATTCAGATATCTCTGAAACCTC 2311
Db 540 LeuAsnTyrPheLysLeuMetPheAaspArg-----SerGluValTyrGlyProMet 556
Qy 2312 AAGCGTTACCTTCTTCAGTATTTTAAGCCAGTATTTCAGCAGG-----CAA 2356
Db 557 LysAsnTyrLeuSerLysGlnValArgProLeuPheGluHisPheLysAsnIleThrAsn 576
Qy 2357 AGCTGGAGTGAACAAG---GGCTCAGCTGGGACAGGATGCTCCGCTCGCTCTTTGAAG 2413
Db 577 AspTrpThrArgAaspProAaspThrLeuMetAaspGlnTyrAsnGluIleAsnAlaIleSer 596
Qy 2414 CTGGCCTGTGACCTGAACCATGCTCTTGCATCCAGAAAGCTGCTGAACCTCTCTCCAG 2473
Db 597 ThrAlaCysSerAsnGlyIleGlnGluCysGluThrLeuValSerAaspLeuPheLysGln 616

Qy 2474 TGGATGAATCCAGTGGAAAAATTAATATACCAACAGATGTTTAAAGATTGTGTAT--- 2530
Db 617 TrpMetAaspAaspProSerAsnAsnProIleHisProAsnLeuArgThrThrValTyrCys 636
Qy 2531 -----TCTGTGGTGTCTCAGACACAGCAGGATGGAAATTCCTTTTAGACCAATAT 2581
Db 637 AsnAlaIleAlaLeuGlyGlyGluArgGlu-----TrpAaspPheAlaTyrGluGlnPhe 654
Qy 2582 GAAGTGTCAATGTCAAGTGTCAAGCAAAACAAATTTCTGTATGCTTTGTCAACGACCAAG 2641
Db 655 ArgAsnAlaThrLeuValAsnGluAlaAaspLysLeuArgSerAlaLeuAlaCysSerAsn 674
Qy 2642 CATCAGCAAAAGTGTCTGAAGTTAATTAAGTAGGAATGGAAGGTTATCAAGACA 2701
Db 675 GluValTrpIleLeuAsnArgTyrLeuSerTyrThrLeuAsnProAaspTyrIleArgArg 694
Qy 2702 CAGAACTTGGCAGCTCTCTTCATGCGATGTCAGAGCTGCCAAGGGGACCAACTAGCA 2761
Db 695 GlnAaspAlaThrSerThrIleAsnSerIleAlaSerAsnValIleGlyGlnThrLeuVal 714
Qy 2762 TGGGATTTGTAGACAAAATTTGGACCCCATCTCTGAAAAAATTTGACTTGGGCTCATAT 2821
Db 715 TrpAaspPheValGlnSerAsnTrpLysLysLeuPheGluAaspPheGlyGlySerPhe 734
Qy 2822 GACATAAGGATGATCATCTCTGGCACAACAGCTCAGCTTTTCTTCCAAAGGATAAGTTGCAA 2881
Db 735 SerPheAlaAsnLeuIleArgAlaValThrArgArgPheSerThrGluTyrGluLeuGln 754
Qy 2882 GAGGTGAACACTATT---TTTGAATCTCTTGGAGCTCAA---GGATCAGCATCTGGATATT 2935
Db 755 GlnLeuGluGlnPheArgLeuAsnAsnLeuAaspThrGlyPheGlySerGlyThrArgAla 774
Qy 2936 TTTCAAACTGTTCTGCAACGATAACCAAAAATATAAATGGCTGGGAGAGATCTTCCG 2995
Db 775 LeuGluGlnAlaLeuGluGlnThrArgAlaAsnIleLysTrpValGlnGluAsnLysGlu 794
Qy 2996 ACTCTGAGCACTTGGCTAATGGTTAATACT 3025
Db 795 AlaValLeuAlaTrpPheThrAlaAsnSer 804

RESULT 12
T29637
hypoetical protein F49E8.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29637
R;Murray, J.; Wohlmann, P.
A;Description: The sequence of C. elegans cosmid F49E8.
A;Reference number: Z20657
A;Accession: T29637
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-884 <MUR>
A;Cross-references: UNIPROT:Q20627; EMBL:U61949; PIDN:AAB03152.1; GSPDB:GN00022; CESP:F4;
A;Experimental source: strain Bristol N2; clone F49E8
C;Genetics:
A;Gene: CESP.F49E8.3
A;Map position: 4
A;Intons: 35/2; 248/2; 326/3; 636/2; 856/3
C;Superfamily: membrane alanyl aminopeptidase

Alignment Scores:
Pred. No.: 2,81e-70 Length: 884
Score: 151.00 Matches: 300
Percent Similarity: 49.73% Conservative: 157
Best Local Similarity: 32.64% Mismatches: 362
Query Match: 19.47% Indels: 100
DB: 2 Gaps: 25

US-10-039-073-2 (1-3366) x T29637 (1-884)

Db 676 AlaArgAlaGlyHisGlnProThrIleAspLysPheThrGlnMetPheAsnAspPheLeu 695
Qy 2480 GAATCCAGTGAAATAATATAACACATGTTTAAAGATTGTGTTATCTGTCGGGT 2539
Db 696 GilyysGlyThrProIleHis-----ProAspIleArgLeuAlaThrPheGlyValVal 713
Qy 2540 GCTCAG-----ACAACAGCAGGATGAATACCTTTAGAGCAATATGAACTGCTCAATG 2593
Db 714 AlaArgTyrGlyGlyLysGluGlyPheAspLysLeuMetAsnLeuArgGluThrThr 733
Qy 2594 TCAAGTGTCTGAACAAACAAATCTGTATGCTTTGTGTCAGCAGCAAGCATCAGGAAAG 2653
Db 734 PheGlnGluIleGluArgGlnThrMetValAlaMetSerGlnThrProGluGluSerLeu 753
Qy 2654 TTAAGTGAAGTTAATGAACTAGGATGAGGAAGGTTATCAAGACACAGAACTTGGCA 2713
Db 754 LeuAlaGlnLeuPheGluTyrGlyPheGluLysAsnLysValArgProGlnAspGlnLeu 773
Qy 2714 GCTCTCTTCATCGATTGCCAGACGCTCCAAAGGGCAGCAACTAGCATGGATTTTGTGA 2773
Db 774 TyrLeuPheLeuGlyThrGlyAlaThrHisMetGlyGlnGlnTyrAlaTyrLysTyrPhe 793
Qy 2774 AGAGAAATGGAGCCCATCTCTGAAATAATTT---GACTTGGCTCATATGACATAAGG 2830
Db 794 CysGluHisIleLysGluPheLeuAspLysTyrGlyGlyAlaAsnSerSerLeuPheGln 813
Qy 2831 ATGATCATCTCTGGCACACACAGCTCCTTTCTTCCAGGATAGTTGCCAGAGGTGAAA 2890
Db 814 ArgCysLeuLysPheAlaGlyGluSerPheGlyAsnGluLysArgAlaValGluPheGln 833
Qy 2891 CTATTTTTT-----GAATCTCTTGAGGCTCAAGGATCAGATCCTGGAT 2932
Db 834 AspPhePheCysAsnCysAsnValLeuSerAspThrAspArgGlnThrLeuAlaArgPro 853
Qy 2933 ATTTTCAACTGTTCTGGAAACGATACCAAAATATATAAATGGCTGGAGAGAT 2989
Db 854 IleGlyGlnThrVal---GluAlaIleArgLeuAsnAlaArgLeuLeuGluSerAsn 871
RESULT 13
S37794
aminopeptidase yscII (EC 3.4.11.-) - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YKL157w; protein YKL61
C:Species: Saccharomyces cerevisiae
C:Date: 03-May-1994 #sequence revision 03-May-1994 #text_change 09-Jul-2004
R:Vandenbol, M.; Bolle, P.; Dion, C.; Portetelle, D.; Hilger, F.
submitted to the EMBL Data Library, September 1993
A:Description: DNA sequencing of a 36.2 kb fragment located between the FAS1 and LAP4 loci
A:Reference number: S37786
A:Accession: S37794
A:Molecule type: DNA
A:Residues: 1-844 <VAN>
A:Cross-references: UNIPROT:P32454; EMBL:Z26877; NID:g407482; PIDN:CAA81497.1; PID:g4074
R:Vandenbol, M.; Bolle, P.A.; Dion, C.; Portetelle, D.; Hilger, F.
submitted to the Protein Sequence Database, March 1994
A:Reference number: S37976
A:Accession: S37987
A:Molecule type: DNA
A:Residues: 1-844 <VA2>
A:Cross-references: EMBL:Z28157; NID:g486272; PIDN:CAA81999.1; PID:g486273; MIPS:YKL157w
R:Vandenbol, M.; Bolle, P.A.; Dion, C.; Portetelle, D.; Hilger, F.
Yeast 10, 35-40, 1994
A:Title: DNA sequencing of a 36.2 kb fragment located between the FAS1 and LAP4 loci of
A:Reference number: S44563
A:Accession: S44571
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-844 <VA3>
A:Cross-references: EMBL:Z26877; NID:g407482; PIDN:CAA81497.1; PID:g407491
A:Experimental source: strain S288C
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1993

R;Garcia-Alvarez, N.; Cueva, R.; Suarez-Renduelles, P.
Eur. J. Biochem. 202, 993-1002, 1991
A:Title: Molecular cloning of soluble aminopeptidases from Saccharomyces cerevisiae. Seq
A:Reference number: S19642; MUID:92111552; PMID:1765107
A:Accession: S19642
A:Molecule type: DNA
A:Residues: 1-163, 'V', 165-441, 'E', 443-843, 'VNRDRDVVNKYLKNGYV' <GAR>
A:Cross-references: EMBL:X63998; NID:g3367; PIDN:CAA45403.1; PID:g3368
C:Genetics:
A:Gene: SGD:APE2; LAP1
A:Cross-references: SGD:S0001640; MIPS:YKL157w
A:Map position: 11L
C:Superfamily: membrane alanyl aminopeptidase
C:Keywords: aminopeptidase; glycoprotein; metalloprotein; zinc
F:290,622/Binding site: carboxylate (Asn) (covalent) #status predicted
F:305,309/Binding site: zinc (His) #status predicted
F:306/Active site: Glu #status predicted
Alignment Scores:
Pred. No.: 6,65e-68 Length: 844
Score: 1116.00 Matches: 281
Percent Similarity: 50.45% Conservative: 171
Best Local Similarity: 31.36% Mismatches: 372
Query Match: 18.88% Indels: 72
DB: 2 Gaps: 24
US-10-039-073-2 (1-3366) x S37794 (1-844)
Qy 332 CTTTGGCAGAGTAAGCTCCACAGTGGTGTCATTCCTCTCCATATGACCTCTTTGTC 391
Db 6 ProAsnArgGluIle---LeuProAspAsnValValProLeuHisTyrAspLeuThrVal 24
Qy 392 CACCCCAATCTCACCTCTCTGGACTTTTGTGATCTGAGAAGATCGAAGCTTTGGTCAGC 451
Db 25 GluProAspPheLysThrPheLysPheGluGlySerValLysIleGluLeuLysIleAsn 44
Qy 452 AAT---GCTACCCAGTTTATCATCTTGCACAGCAAAAGATCTTGAAATCAGAAATGCCACC 508
Db 45 AsnProAlaIleAspThrValThrLeuAsnThrValAspThrAspIleHisSerAlaLys 64
Qy 509 CTTCACTCAGAGGAAGATTCAAGATACATGAACACAGGAAGAACTGAAGTTTGTAGT 568
Db 65 IleGlyAspValThrSerSer-----GluIleIleSer 75
Qy 569 TACCTGCTCATGAACAAATTCACCTGCTGTTTCCAGAGAAACTTACGCTCACCTGAAA 628
Db 76 GluGluGluGlnValThrPheAlaPheProLysGlyThrMetSerSerPheLys 95
Qy 629 TACTATGTGGCTATGAC-----TTCCAAGCCCAAGTTAGGTGATGGCTTTGAAGGGTTT 682
Db 96 GlyAsnAlaPheLeuAspIleLysPheThrGlyIleLeuAsnAspAsnMetAlaGlyPhe 115
Qy 683 TATAAAGCACATACAGA---ACTCTGTGTGTAACAAAGAAATTTCTTCAGTAACAGAT 739
Db 116 TyrArgAlaLysTyrGluAspLysLeuThrGlyGluThrLysTyrMetAlaThrThrGln 135
Qy 740 TTTGAGCCCAACCCAGCAGCATGGCTTCCCTTGTCTTGTATGATGAAACCGTTTGTCAAGCC 799
Db 136 MetGluProThrAspAlaArgAlaPheProCysPheAspGluProAsnLeuLysAla 155
Qy 800 AACTTTTCAATCAAGATACAGAGAGACGAGCATATTGCATCTCCAACTCCCAAG 859
Db 156 SerPheAlaIleThrLeuValSerAspProSerLeuThrHisLeuSerAsnMet---Asp 174
Qy 860 GTTAAAGCAATGAACCTGAGAGAGCTTTTGGGAAGATCAGCTTTGAAACTACTGTAA 919
Db 175 ValLysAsnGluTyrValLysAspGlyLysValThrLeuPheAsnThrThrProLys 194
Qy 920 ATGAGTACATCTCTGTAGCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACT 979
Db 195 MetSerThrTyrLeuValAlaPheIleValAlaGluLeuLysTyrValGluSer---Lys 213
Qy 980 TCATCAGGGGTCAAGGTGTCTCATCTATGATCCCAAGACAAAGGAAATCAACACATTAT 1039

A:Accession: S46750
A:Molecule type: DNA
A:Residues: 1-856 <DUA>
A:Cross-references: UNIPROT:P37898; EMBL:U00062; NID:g488162; PIDN:AAB68919.1; PID:g488162
R:Caprioglio, D.R.; Padilla, C.; Werner-Washburne, M.
J. Biol. Chem. 268, 14310-14315, 1993

A:Title: Isolation and characterization of AAP1. A gene encoding an alanine/arginine aminopeptidase
A:Reference number: S48291; MUID:93300827; PMID:8100228

A:Accession: S48291
A:Molecule type: DNA
A:Residues: 107-549,570-645,'E',647-652 <CAP>
A:Cross-references: EMBL:L12542

C:Genetics:
A:Gene: SGD:AAP1
A:Cross-references: SGD:S0001089; MIPS:YHR047c
A:Map position: 88
C:Superfamily: membrane alanyl aminopeptidase
C:Keywords: aminopeptidase

Alignment Scores:
Pred. No.: 1,42e-64 Length: 856
Score: 1067.00 Match: 282
Percent Similarity: 48.46% Conservative: 159
Best Local Similarity: 30.99% Mismatches: 381
Query Match: 18.05% Indels: 88
DB: 2 Gaps: 23

US-10-039-073-2 (1-3366) x S46750 (1-856)

QY 350 CTCCTCCAGTGGTGCATTCCTCTCATATGACCTCTTTGCCACCCCAATCTCACCTCT 409
Db 6 LeuProAsnValThrProLeuHisTyrAspIleThrLeuGluProAsnPheArgAla 25
QY 410 CTGACACTTGTGTCATCTGAGAAATCAAGTCTTGTGTCAGC-----AATGCT 457
Db 26 PheThrPheGluGlySerLeuLysIleAspLeuGlnIleAsnAspHisSerIleAsnSer 45
QY 458 ACCCAGTTT-----ATCATCTGTCACAGCAAAAGATCTTGAATCACCAGATGCC 505
Db 46 ValGlnIleAsnTyrLeuGluIleAspPheHisSerAlaArgIleGluGlyValAsnAla 65
QY 506 ACCCTTCAGTCAGGAGATTCAGATACATGAATCAACAGCAAGAAAGAACTGAAAGTTTG 565
Db 66 IleGluValAsnLysAsnGluAsnGln----- 74
QY 566 AGTTACCTGCTCATGAACAAATTGCATGCTGCTGCTCA-----GAGAACTT 613
Db 75 -----GlnLysAlaThrLeuValPheProAsnGlyThrPheGluAsnLeu 89
QY 614 ACGCTCACCTGAAATACTATGTGGCTATGACCTTCCAAAGCCAAAGTTAGGTGATGGCTTT 673
Db 90 GlyProSerAlaLysLeuGluIle-----PheSerGlyIleLeuAsnAspGlnMet 107
QY 674 GAAGGGTTTATAAAGCACATACAGA---ACTCTTGGTGGTGAACAAGAAATCTTGGCA 730
Db 108 AlaGlyPheTyrArgAlaLysTyrThrAspLysValThrGlyGluThrLysTyrMetAla 127
QY 731 GTAACAGATTTTGACCAACCCAGCAGCATGCTTCCCTGCTTTGTGATGAACCGTTG 790
Db 128 ThrThrGlnMetGluAlaThrAspAlaArgArgAlaPheProCysPheAspGluProAsn 147
QY 791 TTCAAGCCCACTTTTCAATCAAGATACGAAGAGAGAGCAGGCATATTGCACTATCCAAAC 850
Db 148 LeuLysAlaThrPheAlaValThrLeuValSerGluSerPheLeuThrHisLeuSerAsn 167
QY 851 ATGCCAAAGGTTAAGCAATTTGAACCTTGAAGAGAGGTCTTTTGGGAAGATCACTTTGAACT 910
Db 168 Met---AspValArgAsnGluThrIleLysGluGlyLysTyrThrThrPheAsnThr 186
QY 911 ACTGTAAAATGAGTACATCTTGTAGCCCTACATAGTTTGTGATTTCCACTCTCTCAGT 970
Db 187 ThrProLysMetSerThrTyrLeuValAlaPheIleValAlaAspLeuArgTyrValGlu 206

QY 971 GGCTTCACCTTCATCAGGGGTCAAAGGTGCTCATCTATGATCCCTCCAGACAAACGGAATCAA 1030
Db 207 Ser---AsnAsnPheArgIleProValArgValTyrSerThrProGlyAspGluLysPhe 225
QY 1031 ACACATTATGCTTTGAGGAGTCACTGAGCTACTTGTATTTTATGAAAAGTACTTTTGAT 1090
Db 226 GlyGlnPheAlaAlaAsnLeuAlaArgThrLeuArgPhePheGluAspThrPheAsn 245
QY 1091 ATCTACTATCCACTCTCCAACTGGATTAATTTGCTATTCTCTGACTTTGACCTGGAGCC 1150
Db 246 IleGluTyrProLeuProLysMetAspMetValAlaValHisGluPheSerAlaGlyAla 265
QY 1151 ATGGAATAATTGGGCGCTCATATATAGGAGACGCTCACTGTCTTTTGAACCCCAAGACC 1210
Db 266 MetGluAsnTrpGlyLeuValThrTyrArgValIleAspLeuLeuAspIleGluAsn 285
QY 1211 TCTTCGCTTCCGATAAATGCTGGGTCCACAGAGTCAATGATCCCATGAGCTGGGCGACAG 1270
Db 286 SerSerLeuAspArgIleGlnArgValAlaGluValIleGlnHisGluLeuAlaHisGln 305
QY 1271 TGGTTTGGCAACCTGCTCAATGGAATGCTGAATGATATTTGGCTTTAAGGAGGGTTTT 1330
Db 306 TrpPheGlyAsnLeuValThrMetAspTyrTrpGluGlyLeuTrpLeuAsnGluGlyPhe 325
QY 1331 GCAAAATACATGGAACCTTATCGCTGTTAATGCTTACATATCCAGAGCTGCAA---TTTGAT 1387
Db 326 AlaThrTrpMetSerTrpTyrSerCysAsnLysPheGlnProGluTrpLysValTrpGlu 345
QY 1388 GACTATTTTGAATGTGCTTTTGAAGTAATTAACAAAGATTCATTGAATTCATCCCGC 1447
Db 346 GlnTyrValThrAspAsnLeuGlnArgAlaLeuAsnLeuAspSerLeuArgSerHis 365
QY 1448 CCTATCTCCAAACCCAGCGGAAACCCCGACTCAATACAGGAAATGTTTGAAGTTTCC 1507
Db 366 ProIleGluValProValAsnAsnAlaAspGluIleAsnGlnIlePheAspAlaIleSer 385
QY 1508 TATAACAAGGAGCTTGTATTTTGAATATGCTCAAGGATTTTCTGGGTGAGGAAATTC 1567
Db 386 TyrSerLysGlySerSerLeuLeuArgMetIleSerLysTrpLeuGlyGluThrPhe 405
QY 1568 CAGAAAGGAATAATTCAGTACTTTAAAGAGTTTCAAGTATAGAAATGCTAAGATGATGAC 1627
Db 406 IleLysGlyValSerGlnTyrLeuAsnLysPheLysTyrGlyAsnAlaLysThrGlyAsp 425
QY 1628 TTCTGAGCAGCTGCTCAAAATAGTTTGTAGAAAGTATTTTACATCTGCTGGAGTTGT 1687
Db 426 LeuTrpAspAlaLeu-----AlaAspAlaSerGlyLysAspValCys 439
QY 1688 CATTCGGATCCCAAGATGACAAAGTAACATGCTCCCTTTCTGGGGGAAAAATGCAGAGTC 1747
Db 439 ----- 439
QY 1748 AAGAGATGATGACTACATGGACTCTCCAGAAAGGAATCCCTGCTGGTGGTTAAACAA 1807
Db 440 ---SerValMetAsnIleTrpThrLysArgValGlyPheProValLeuSerValLysGlu 458
QY 1808 GACGGGTGTTCTACTCCGACTGCAACAGAGCGCTTCTCCAG---GGGGTTTCCAGAA 1864
Db 459 HisLysAsnLysIleThrLeuThrGlnHisArgTyrLeuSerThrGlyAspValLysGlu 478
QY 1865 GACCTCTGAATGGAGGCGCTTCAGGAGAGGTACTCTGTGGCATATCCATTGACTACTCC 1924
Db 479 GluGluAspThrThrIle-----TyrProIleLeuLeuAlaLeuLysAspSer 494
QY 1925 ACAGATGCTTCTTAATGTGATCCACAGACATCTTAAATCAAGACAGATACTCTGGAT 1984
Db 495 ThrGlyIleAspAsnThrLeu-----ValLeuAsnGluLysSerAlaThrPheGlu 511
QY 1985 CTACCTGAAAAGACCAAGTGGGTGAAATTTAATGTGACCTCAAAATGGTTACTACATCGTT 2044
Db 512 Leu---LysAsnGluGluPhePheLysIleAsnGlyAspGlnSerGlyLysIlePheIleThr 530
QY 2045 CACTATGAGGGTTCATGGATGGGACCAACTCATTTACAGCTGAATCAGAAACCAACACTT 2104

Db 531 SerTyrSerAspGluArgTirpAlaLysLeuSerLysGlnAlaAsn-----Leu 546
QY 2105 CTCAGACCTTAAGCAGAGTAGTCTGATTTCATGATGTGTTTCAGCTAGTTGGTGCAGGG 2164
Db 547 LeuSerValGluAspArgValGlyLeuValAlaAspAlaLysAlaLeuSerAlaSerGly 566
QY 2165 AGACTGACCTAGACAAAGCTCTTGACATGCTTACTACTCTCCACATCAAGAAACAGCAGC 2224
Db 567 TyrThrSerThrAsnPheLeuAsnLeuLeuSerAsnTrpLysAsnGluAspSerPhe 586
QY 2225 -----CCGCGACTCTCGAAGCTCTGAGTACTTGGAACTGTTTACCACATGATG 2275
Db 587 ValValTrpGluGlnIleLeuSerLeuSerAlaLeuLysSerThrTrpValPhe--- 605
QY 2276 GACAGAAGGAATPATTTCAGATATCTCTGAAAACCTCAAGCGTTACCTTCTTCAGTATTTT 2335
Db 606 -----GluProGluAspIleLeuAsnAlaLeuAspLysPheThrLeuAspLeuVal 622
QY 2336 AAGCCAGTGATTGACAGGCAAGCTGGAGT-----GACAAGGGCTCAGCTGGGACAGG 2389
Db 623 LeuAsnLysLeuSerGluLeuGlyTrpAsnIleGlyGluAspAspSerPheAlaIleGln 642
QY 2390 ATGCTCCGCTCGGCTCTCTGAAGCTGGCTGTGACCTGAACCATGCTCTTGATCCAG 2449
Db 643 ArgLeuLysValThrLeuPheSerAlaAlaCysThrSerGlyAsnGluLysMetGlnSer 662
QY 2450 AAAGCTGCTGAACTCTCTCCAGTGGATGGAATCCAGTGGAAATTAATAATATACCAACA 2509
Db 663 IleAlaValGluMetPheGluGluTyr---AlaAsnGlyAsnLysGlnAlaIleProAla 681
QY 2510 GATGTTTAAAGATTGTGTATTCTGTGGTGTCTGACACAAACAGCAGGATGGAATTAC--- 2566
Db 682 LeuPheLysAlaValPheAsnThrValAlaArgLeuGlyGlyGluAsnAsnTyrGlu 701
QY 2567 ---CTTTAGACCAATATGAACTGTCAATGTCAAGTGTGACACAAACAAATTCGTAT 2623
Db 702 LysIlePheAsnIleTyrGlnAsnProValSerSerGluGluLysIleAlaLeuArg 721
QY 2624 GTTTGTCTCAACGACGATCAGGAAAGTTACTGAAATTAATTTGAATAGGAATGGAA 2683
Db 722 AlaLeuGlyArgPheGluAspLysGluLeuLeuGluArgThrLeuSerTyrLeuLeuAsp 741
QY 2684 GGAAGGTTATCAAGACACAGAACTTGGCAGCTCTCTTCATGCGATTGCCAGAGCTCCA 2743
Db 742 GlyThrValLeu---AsnGlnAspPheTyrIleProMetGlnGlyIleArgValHisLys 760
QY 2744 AAGGGCAGCACTAGCATGGGATTTTGTAAAGAAATTTGACCCATCTTCTGAAAAA 2803
Db 761 LysGlyIleGluArgLeuTrpAlaTrpMetGlnGluHisTrpAspGluIleAlaLysArg 780
QY 2804 TTTGACTTTGGGCTCATATGACATAGGATGATCATCTCTGGCACAACAGCTCCTTTCT 2863
Db 781 LeuGlnProGlySerProValLeuGlyValLeuThrLeuGlyLeuThrAsnPheThr 800
QY 2864 TCCAGGATTAAGTTCAAGAGGTGAACATATTTTGAATCTCTTTGAGGCTCAAGGATCA 2923
Db 801 SerPheGluAlaLeuGluLysIleSerAlaPheTyrSerArgLysValThrLysGlyPhe 820
QY 2924 CATCTGGATATTTTCAAACTGTTCTGGAACGATAACCAAAATATATAAATGGCTGGAG 2983
Db 821 AspGlnThrLeuAlaGln---AlaLeuAspThrIleArgSerLysAlaGlnTrpValSer 839
QY 2984 AAGAATCTTCCGACTCTGAGGACTTGGCTA 3013
Db 840 ArgAspArgGluIleValAlaThrTyrLeu 849

RESULT 15

T39789

aminopeptidase - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: T39789

R:Seeger, K.; Harris, D.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1999
A:Reference number: Z21816
A:Accession: T39789
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-882 <SSE>
A:Cross-references: UNIPROT:Q9USX1; EMBL:AL122033; PIDN:CAB58971.1; GSPDB:GN00067; SPDB:
A:Experimental source: strain 972h-; cosmid c1921
C:Genetics:
A:Gene: SPDB:SPBIC1921.05
A:Map position: 2
C:Superfamily: membrane alanyl aminopeptidase

Alignment Scores:

Pred. No.:	3.03e-63	Length:	882
Score:	1047.50	Matches:	277
Percent Similarity:	47.67%	Conservative:	162
Best Local Similarity:	30.08%	Mismatches:	391
Query Match:	17.72%	Indels:	91
DB:	2	Gaps:	24

US-10-039-073-2 (1-3366) x T39789 (1-882)

QY 350 CTCCCAGTGTGTCATTCCTCTCCATTATGACCTCTTTGTCCACCCCAATCTCACCTCT 409
Db 20 LeuProLysAsnValLysProIleHisTyrAspLeuSerLeuTyrProAspLeuGluThr 39
QY 410 CTGGACTTTGTTGTCATCTGAGAGATCGAAGCTCTTGTGTCAGCAATGCTTACCAGCTTTATC 469
Db 40 PheThrTyrGlyGlyLysValValThrLeuAspValLeuGluAspSerAsnSerIle 59
QY 470 ATCTTGACACCAAGATCTTGAATCAGCAATGCCACCTTTCAGTCTCAGAGGAAGATTCA 529
Db 60 ThrLeuHisGlyIleAsnLeuArgIleLeuThrAlaAlaLeuGluTrpGlySerGlnThr 79
QY 530 AGATACATGAACACAGGAAAGAACTGAAAGTTTGTGTTTACCTGTCTCATGACAAAT 589
Db 80 ValTrpAlaSerGlu-----ValSerTyr---GlyAspGluArgIle 92
QY 590 GCATGTGTGTTCCAGAGAACTTACGCTCACCTGAAATACTATGTGGCTATGGACTTC 649
Db 93 ValLeuGlnPheProSerThrValProAlaAsnSerValAlaValLeuThrLeuProPhe 112
QY 650 CAAGCCAAAGTTAGTGTGCTTTGAAGGGTTTATAAAGCACATACAGAACTCTTGGT 709
Db 113 ThrAlaArgIleSerSerGlyMetGluGlyPheTyrArgSerSerTyrValAspSerAsp 132
QY 710 GGTGAACAAGAAATCTTGCAAGTAAACAGATTTTGAGCCAAACCCAGGACGATGGCTTTC 769
Db 133 GlyAsnThrLysTyrLeuAlaThrThrGlnMetGluProThrSerAlaArgArgAlaPhe 152
QY 770 CTTGTCTTGTGAACCGTGTCTTCAAAGCCAACTTTTCAATCAAGATACGAGAGAGAGC 829
Db 153 ProCysTrpAspGluProAlaLeuLysAlaThrPheThrIleAspIleThrAlaLysGlu 172
QY 830 AGGCATATTCAGCTATCCACATGCCAAAGGTTTAAGCAATTTGAATTTGAAGGAGGCTT 889
Db 173 AsnTyrThrIleLeuSerAsnMetAsnAlaValGluGlu---ThrValLysAspGlyLeu 191
QY 890 TTGGAAGATCACTTTGAACACTCTGTAATAATAGTACATACCTTGATGCTTACATAGTT 949
Db 192 LysThrAlaArgPheAlaGluThrCysArgMetSerThrTyrThrLeuLeuAlaTrpIleVal 211
QY 950 TGTGATTTCCACTCTCTGAGTGGCTTCATCTTCATCA-----GGGGTCAAGGTG 997
Db 212 AlaGluLeuGluTyrValGluTyrPheThrProGlyLysHisCysProArgLeuProVal 231
QY 998 TCCATCTATCATCCCGACAGACAAACGGAATCAAAACACATATTATGCTTTTGAGGATCACTG 1057
Db 232 ArgValTyrThrThrProGlyPheSerGluGlnGlyLysPheAlaAlaGluLeuGlyAla 251
QY 1058 AAGTACTTGATTTTATGAAAGAAAGTACTTTTGATATCTACTACTTCCACTCTCCAAATGGAT 1117

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 26, 2005, 06:07:35 ; Search time 527.604 Seconds
(without alignments)
6533.911 Million cell updates/sec

Title: US-10-039-073-2
Perfect score: 5912
Sequence: 1 cccgcgtccgcatgattt.....aaaaaaaaaaaaaaaaaaaa 3366

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-O=/cgn2.1/USPTO spoal_p/US10039073/runat_26092005_070409_21306/app query.fasta_1.6606
-DB=UniProt -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPT=0 -LOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODES=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10039073 @CGN 1 1 1214 @runat_26092005_070409_21306 -NCPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=10 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5052	85.5	960	Q9HBX2	Q9hb22 homo sapien
2	5047	85.4	960	Q7Z5K1	Q7z5k1 homo sapien
3	4789.5	81.0	915	Q6P179	Q6p179 homo sapien
4	2768	46.8	532	Q8TD32	Q8td32 homo sapien
5	2516.5	42.6	929	ART1_HUMAN	Q9nz08 h adipocyte
6	2512.5	42.5	941	Q6UWY6	Q6uw66 homo sapien
7	2480	41.9	930	ART1_MOUSE	Q9eqh2 mus musculus
8	2430	41.1	930	ART1_RAT	Q9ij22 rattus norv
9	2034.5	34.4	1003	Q6PE23	Q6pe23 brachydanio
10	2027	34.3	1025	LCAP_RAT	P9f629 r leucyl-cy
11	2022	34.2	1025	Q8C129	Q8ci29 mus musculus
12	1999	33.8	1025	LCAP_HUMAN	Q9uiq6 homo sapien
13	1883	31.9	694	Q8C9W5	Q8c9w5 mus musculus
14	1853.5	31.4	997	Q6PCG5	Q6pcg5 xenopus lae
15	1690	28.6	350	Q8WVJ4	Q8wvj4 homo sapien
16	1564	26.5	549	Q8C4S7	Q8c4s7 mus musculus

17	1455.5	24.6	942	1	AMPE_PIG	Q95334 sus scrofa
18	1444	24.4	957	1	AMPE_HUMAN	Q07075 homo sapien
19	1391.5	23.5	1012	2	Q9VFW7	Q9vfw7 drosophila
20	1391	23.5	945	1	AMPE_RAT	P50123 rattus norv
21	1390.5	23.5	945	1	AMPE_MOUSE	P16406 mus musculu
22	1389.5	23.5	1036	2	Q86P55	Q86p55 drosophila
23	1373.5	23.2	994	2	Q86NQ5	Q86ng5 drosophila
24	1371.5	23.2	991	2	Q7PQR3	Q7pqr3 anopheles g
25	1367	23.1	903	2	Q8INH5	Q8inh5 drosophila
26	1367	23.1	1025	2	Q8INH6	Q8inh6 drosophila
27	1361.5	23.0	988	2	Q9VFX0	Q9vfx0 drosophila
28	1347	22.8	885	2	Q8IHC5	Q8ihc5 drosophila
29	1344	22.7	942	2	Q9VFW9	Q9vfw9 drosophila
30	1343	22.7	885	2	Q9VFW8	Q9vfw8 drosophila
31	1329.5	22.5	691	2	Q8BZ14	Q8bz14 mus musculu
32	1329.5	22.5	862	2	Q8IGR1	Q8igr1 drosophila
33	1327	22.4	1025	1	THDE_RAT	Q10836 rattus norv
34	1322	22.4	1024	2	Q6UWJ4	Q6uwj4 homo sapien
35	1320	22.3	1024	1	THDE_HUMAN	Q9ukue homo sapien
36	1312	22.2	964	1	AMPN_RAT	P15684 rattus norv
37	1310	22.2	1025	1	THDE_MOUSE	Q8K093 mus musculu
38	1298	22.0	966	1	AMPN_FELCA	P79171 felis silve
39	1290.5	21.8	1007	2	Q9U0D1	Q9u0d1 aplysia cal
40	1280.5	21.7	866	2	Q9W0E4	Q9w0e4 drosophila
41	1280.5	21.7	1053	2	Q8IRH0	Q8irh0 drosophila
42	1280.5	21.7	1075	2	Q8IRH1	Q8irh1 drosophila
43	1275	21.6	997	2	Q7QAHS	Q7qahs anopheles g
44	1274	21.5	965	1	AMPN_RABIT	P15541 oryctolagus
45	1272.5	21.5	866	2	Q9GPG3	Q9gpg3 drosophila

ALIGNMENTS

RESULT 1
Q9HBX2 PRELIMINARY; PRT; 960 AA.
AC Q9HBX2;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE AminoPeptidase.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Schomburg L.;
RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF191545; AAG28383.1; -.
DR MEROPS; M01.024; -.
DR GO; GO:0004177; F:aminopeptidase activity; IEA.
DR GO; GO:0004179; F:membrane alanyl aminopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001930; Peptidase_M1.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF01433; Peptidase_M1; 1.
DR PRINTS; PR00756; ALADIPTASE.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW AminoPeptidase.
SQ SEQUENCE 960 AA; 110461 MW; 261EFC06870D644E CRC64;

Alignment Scores:
Pred. No.: 0 Length: 960
Score: 5052.00 Matches: 960
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.45% Indels: 0
DB: 2 Gaps: 0

US-10-039-073-2 (1-3366) x Q9HBX2 (1-960)

QY 146 ATGTTCCATCTTCTGCAATGTTAATTCACAGAAAACCAATGTTTACATTTCACAGA 205

Db 1 MetPheHisSerSerAlaMetValAsnSerHisArgLysProMetPheAsnIleHisArg 20
QY 206 GGATTTTACTGCTTAACAGCCATCTTGCCCAATATGCAATTTGCTTCAGTCTCAGTG 265
Db 21 GlyPheTyrCysLeuThrAlaIleLeuProGlnIleCysIleCysSerGlnPheSerVal 40
QY 266 CCATCTAGTATTACTTCACCTCAGAGATCCTGGGCTTTCCAGTAGGCACCTAAATGGGGAA 325
Db 41 ProSerSerTyrHisPheThrGluAspProGlyAlaPheProValAlaIleAsnGlyGlu 60
QY 326 CGATTTCCCTGGCAGGAGCTAAGGCTCCCAAGTGTGGTCAFTCTCTCCATTATGACCTC 385
Db 61 ArgPheProTTPGlnGluLeuArgLeuProSerValValIleProLeuHisTyrAspLeu 80
QY 386 TTTGTCCACCCCAATCTCACCCTCTCTGGACTTTGTCATCTGAGAAGATCGAAGTCTTG 445
Db 81 PheValHisProAsnLeuThrSerLeuAspPheValAlaSerGluLysIleGluValLeu 100
QY 446 GTCAGCAATGCTACCCAGTTTATCATCTTGACAGCAAAAGATCTTGAATCCACGAATGCC 505
Db 101 ValSerAsnAlaThrGlnPheIleIleLeuHisSerLysAspLeuGluIleThrAsnAla 120
QY 506 ACCCTTCAGTCAGGAGGATTTCAAGATACATGAATGAACCAAGAAAGAACTCAAGTTTG 565
Db 121 ThrLeuGlnSerGluGluAspSerArgTyrMetLysProGlyLysGluLeuLysValLeu 140
QY 566 AGTTACCCCTGCATGAACAAATTCACACTGCTGCTGCTCCAGAGAACTTAGCCCTCAGCTG 625
Db 141 SerTyrProAlaHisGluGlnIleAlaLeuLeuValProGluLysLeuThrProHisLeu 160
QY 626 AAATACTATGTGGCTATGGACTTCCAAGCCAAAGTTAGGTGATGCTTTGAAGGTTTAT 685
Db 161 LysTyrTyrValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTyr 180
QY 686 AAAAGCACATACAGAACTCTTGGTGGTGAACAAGAAATTTCTGCAGTAACAGATTTTGAG 745
Db 181 LysSerThrTyrArgThrLeuGlyGlyGluThrArgIleLeuAlaValThrAspPheGlu 200
QY 746 CCAACCCGAGCAGCATGGCTTTCCCTTCTGCTTGAATGAACCGTTGTTCAAGCCCACTTT 805
Db 201 ProThrGlnAlaArgMetAlaPheProCysPheAspGluProLeuPheLysAlaAsnPhe 220
QY 806 TCAATCAAGATACCAAGAGAGAGCAGCATATTCACCTATCCAACTGCACCAAGGTTAAG 865
Db 221 SerIleLysIleArgArgGluSerArgHisIleAlaLeuSerAsnMetProLysValLys 240
QY 866 ACAATTGAATGAAGGAGGTCTTTTGAAGATCACCTTTGAACTACTGTAAAAAATGAGT 925
Db 241 ThrIleGluLeuGluGlyGlyLeuLeuGluAspHisPheGluThrThrValLysMetSer 260
QY 926 ACATACCTTGTAGCTACATAGTTGTGATTTCCACTCTCTGAGTGGCTTCACCTCATCA 985
Db 261 ThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThrSerSer 280
QY 986 GGGGTCAAGGTGTCCATCTATGCATCCCAAGCAAAACGGAATCAACACATATGCTTTG 1045
Db 281 GlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyrAlaLeu 300
QY 1046 CAGGCATCACATGAAGCTACTTGAATTTTATGAAAAGTACTTTGATATCTACTATCCACTC 1105
Db 301 GlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyrProLeu 320
QY 1106 TCCAACTGGATTAATGCTATTCTGACTTTCCACTTTCACCTGGAGCCATGGAATTTGGGC 1165
Db 321 SerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsnTrpGly 340
QY 1166 CTCATTACATATAGGAGACGTCACTGCTTTTTCACCCCAAGACCTCTCTGCTTCGGAT 1225
Db 341 LeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAlaSerAsp 360
QY 1226 AAATGTGGGTACACAGATCATGCCATGAATCGGCCACCAAGTGGTTTGGCAACCTG 1285

Db 361 LysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeu 380
QY 1286 GTCAACATCGAATGGTGGATGATATTTGCTTTAAGAGGGTTTCCAAATACATCGAA 1345
Db 381 ValThrMetGlnTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyrMetGlu 400
QY 1346 CTTATCGCTGTTAATGCTACATATCCAGAGCTCAATTTGATGACTATTTTGAATGTG 1405
Db 401 LeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeuAsnVal 420
QY 1406 TGTTTGAAGTAATTAACAAAGATTCATTGAATTCATCCCGCCTATCTCCAAACACGCG 1465
Db 421 CysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLysProAla 440
QY 1466 GAAACCCGACTCAAAATACAGGAATGTTTGTAGTAAGTTTCTTATACAGGGAGCTGTG 1525
Db 441 GluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGlyAlaCys 460
QY 1526 ATTTTGAATATGCTCAAGGATTTTCTGGGTGAGGAGAAATTCAGAAAGGAATAATTTCAG 1585
Db 461 IleLeuAsnMetLeuLysAspPheLeuGlyGluGluLysPheGlnLysGlyIleGln 480
QY 1586 TACTTAAAGAGTTCAGCTATAGAAATGCTAAGAAATGATGACTTGTGGAGCAGTCTGTCA 1645
Db 481 TyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspAspLeuTrpSerSerLeuSer 500
QY 1646 AATAGTGTGTTAGAAATGATTTTACATCTGGTGGAGTTTGTTCATTCGGATCCCAAGATG 1705
Db 501 AsnSerCysLeuGluSerAspPheThrSerGlyValCysHisSerAspProLysMet 520
QY 1706 ACAAGTAAACATGCTCCGCTTTCTGGGGGAAAAATGCAGAGGTCAAGAGATGATGACTACA 1765
Db 521 ThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGluValLysGluMetThrThr 540
QY 1766 TGACTCTCCAGAAAGAAATCCCTCTGCTGGTGGTAAACAAGACGGGTGTTCACTCCGA 1825
Db 541 TrpThrLeuGlnLysGlyIleProLeuLeuValLysGlnAspGlyCysSerLeuArg 560
QY 1826 CTGCACAGGAGCGCTTCCTCCAGGGGTTCACAGAGACCTCAATGGAGGGCCCTG 1885
Db 561 LeuGlnGlnArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArgAlaLeu 580
QY 1886 CAGGAGAGTACCTGTGGCATATCCCATCTGACCTACTCCACGAGTCTTCTTAATGTGATC 1945
Db 581 GlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerThrSerSerSerAsnValIle 600
QY 1946 CACAGACACATTCCTAAAAACAAGACAGATACCTCTGATCTACTGAAAAGACAGTTGG 2005
Db 601 HisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThrSerTrp 620
QY 2006 GTCAAAATTTAATGTGGACTCAAAATGGTTACTACATCGTTTCACTATCAGGGTCAATGG 2065
Db 621 ValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHisGlyTrp 640
QY 2066 GACCAACTCATTAACACAGCTGAATCAGAACACACACTTCTCAGACCTTAAGGACAGAGTA 2125
Db 641 AspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAspArgVal 660
QY 2126 GGTCTGAATCATGATGTGTTTACCTAGCTAGTTGGTGGAGGAGACTGACCTTAGACAAAGCT 2185
Db 661 GlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAspLysAla 680
QY 2186 CTTGACATCACTTACTACTCCAAATGAACAAAGCAGCCCGCTCTCTCGAAGGTCTG 2245
Db 681 LeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProAlaLeuLeuGluGlyLeu 700
QY 2246 AGTTACTTGAATCGTTTACCACTATGATGGACAGAAAGGAATAATTTCAGATATCTCTGAA 2305
Db 701 SerTyrLeuGluSerPheTyrHisMetMetAspArgArgAsnIleSerAspIleSerGlu 720
QY 2306 AACCTCAAGGTTCACCTTCTTCTAGTATTTTAAAGCAGTGTGATGACAGGCAAGCTGGAGT 2365
Db 721 AsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSerTrpSer 740

QY 2366 GACAAAGGCTCAGTCTGGGACAGGATGCTCCGCTCGGCTCTCTTGAAGCTGGCCCTGTGAC 2425
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Db 741 AspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAlaCysAsp 760
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QY 2426 CTGAACCATGCTCCTTGGATCCAGAAAGCTGCTGAACCTCTTCCACGCTGGATGGAATCC 2485
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Db 761 LeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMetGluSer 780
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QY 2486 AGTGAAATTAATATATACCAACAGATGTTTTAAAGATTGTGTATTTCTGTGGGTGCTCAG 2545
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Db 781 SerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrSerValGlyAlaGln 800
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QY 2546 ACAACAGCAGGATGGAATACCTTTTAGCAATATGAACCTGTCAATGTCAAGTGTGAA 2605
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Db 801 ThrThrAlaGlyTrpAsnTyrLeuLeuGluGlnTyrGluLeuSerMetSerSerAlaGlu 820
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QY 2606 CAAACAAATTTCTGTATGCTTTGTCAACGAGCAGCATCAGGAAAGCTTACTGAAGTTA 2665
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Db 821 GlnAsnLysIleLeuTyrAlaLeuSerThrSerLysHisGlnGluLysLeuLeuLysLeu 840
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QY 2666 ATTGAACTAGGAATGGAAGAAAGTTATCAAGACACAGAACTTGGCAGCTCTCTTCAT 2725
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QY 2726 GCGATTGCAGAGCTCCAAAGGGCAGCAACTAGCATGGGATTTTGTGAAGAGAAATGG 2785
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QY 2846 ACAACAGCTCACTTTTCTTCAAGAGTAAGTTGCAAGAGTGAAACTATTTTGAATCT 2905
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Db 901 ThrThrAlaHisPheSerSerLysAspLysLeuGlnGluValLysLeuPheGluSer 920
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QY 2906 CTTGAGGCTCAAGGATCACTCTGGATATTTTCAAACTGTTCTGGAAACGATACCAA 2965
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|
Db 921 LeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIleThrLys 940
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QY 2966 AATATAAATGGCTGAGAGAGATTTCCGACTCTGAGACTTGGCTTAATGGTTAACT 3025
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Db 941 AsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeuMetValAsnThr 960
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|
|
RESULT 2
Q725K1
ID Q725K1 PRELIMINARY; PRT; 960 AA.
AC Q725K1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Leukocyte-derived arginine aminopeptidase long form variant.
GN Name=l-rap;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12799365; DOI=10.1074/jbc.M305076200;
RA Taniooka T., Hattori A., Masuda S., Nomura Y., Nakayama H.,
RA Mizutani S., Tsujimoto M.;
RT "Human leukocyte-derived arginine aminopeptidase: the third member of
RT the oxytocinase subfamily of aminopeptidases.";
RL J. Biol. Chem. 278:32275-32283(2003).
DR EMBL; AB109031; BAC78818.1; -;
DR MEROPS; M01.024; -;
DR GO; GO:0004177; F:aminopeptidase activity; IEA.
DR GO; GO:0004179; F:membrane alanyl aminopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001930; Peptidase_M1.
DR InterPro; IPR006025; Pept_M_Zn_BS.

DR Pfam; PF01433; Peptidase_M1; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Aminopeptidase.
SQ SEQUENCE 960 AA; 110447 MW; 27898FE2107E814E CRC64;
Alignment Scores:
Pred. No.: 0 Length: 960
Score: 5047.00 Matches: 959
Percent Similarity: 99.90% Conservative: 0
Best Local Similarity: 99.90% Mismatches: 1
Query Match: 85.37% Indels: 0
Gaps: 2
US-10-039-073-2 (1-3366) x Q725K1 (1-960)
QY 146 ATGTTCCATCTCTCTGCAATGGTTAAATTCACACAGAAAAACCAATGTTTAAACATTCACAGA 205
|
|
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Db 1 MetPheHisSerSerAlaMetValAsnSerHisArgLysProMetPheAsnIleHisArg 20
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|
|
QY 206 GGATTTTACTGCTTAAACAGCCATCTTCCCCCAATATGCATTTGTTCTCAGTTCTCAGTG 265
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|
Db 21 GlyPheTyrCysLeuThrAlaIleLeuProGlnIleCysIleCysSerGlnPheSerVal 40
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|
QY 266 CCATCTAGTTATCACTTCACTGAGGATCCTGGGCTTTCCAGTAGCCACTAATGGGAA 325
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Db 41 ProSerSerTyrHisPheThrGluAspProGlyAlaPheProValAlaIleAsnGlyGlu 60
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QY 326 CGATTTCTTGGCAGGAGCTAAAGGCTCCCGAGTGTGCTCATTTCTCTCCATTTATGACCTC 385
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|
Db 61 ArgPheProTrpGlnGluLeuArgLeuProSerValValIleProLeuHisTyrAspLeu 80
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|
|
QY 386 TTTGTCCACCCCAATCACTCTCTGACCTTTGTCATCTTGACATCTGAGAGATCGAAGTCTTG 445
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Db 81 PheValHisProAsnLeuThrSerLeuAspPheValAlaSerGluLysIleGluValLeu 100
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|
QY 446 GTACAGCAATCTACCCAGTTATCATCTTCACAGCAAGAGATCTTGAATCACCAGATGCC 505
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QY 506 ACCCTTCAGTCACAGGAGATTTCAAGATACATGAACCAAGGAAAGAACTGAAAGTTTG 565
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QY 566 AGTTACCTCTCATGAACAAATTTGCACTGCTGGTCCAGAGAACTTACCCCTCACCTG 625
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Db 141 SerTyrProAlaHisGluGlnIleAlaLeuLeuValProGluLysLeuThrProHisLeu 160
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QY 626 AATATCTATGTGCTATGGACTTCCAAAGCCAAAGTTAGTGTATGCTTTGAAGGTTTAT 685
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Db 161 LysTyrTyrValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTyr 180
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QY 686 AAAAGCACATACAGAACTTTGGTGGTGAACCAAGAAATTTCTGCAGTAACAGATTTTGAAG 745
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Db 181 LysSerThrTyrArgThrLeuGlyGlyGluThrArgIleLeuAlaValThrAspPheGlu 200
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QY 746 CCAACCCAGGACCATGCTTTCCCTTGTGTTGATGAACCGTTGTTCAAGCCCACTTT 805
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QY 866 ACAATTGAACTTGAAGGAGGTCTTTTGGAAAGATCACCTTTTGAACACTACTGTAAAAATGAGT 925
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RESULT 3
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ID Q6P179
AC Q6P179; 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE LRAP protein.
GN Name-LRAP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshitoki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McWan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RA Strausberg R.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; SC065240; ANH5240.1; -;
 DR GO; GO:0004179; F:membrane ananyl aminopeptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPRO06025; Pept_M_Zn_BS.
 DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
 SQ SEQUENCE 915 AA; 105525 MW; 10075BE1C076377F CRC64;

 Alignment Scores:
 Pred. No.: 2,166-312 Length: 915
 Score: 4789.50 Matches: 915
 Percent Similarity: 95.31% Conservative: 0
 Best Local Similarity: 95.31% Mismatches: 0
 Query Match: 81.01% Indels: 45
 DB: 2 Gaps: 1

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 QY 266 CCATCTAGTTATCACTTCACTAGAGATCCTGGGCTTTCCAGTAGCCACCAATGGGAA 325
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 QY 446 GTCCAGCAATGTCACCGATTTATCATCTTGCACAGCAAGATCTTGAATACCGAATGCC 505
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 QY 506 ACCCTTTCAGTCAGAGAGATTCAAGATACATGAAACCCAGGAAGAACTGAAAGTTTTTG 565

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 DB 237 ----- 237
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 QY 1406 TGTGTTGCAAGTAAATTCACAAAGATTCATTTGAATTCATCCCGCCCTATCTCCAAACCCAGC 1465
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Qy	1766	TGGACTCTCCAGAAAGAAATCCCTGCTGTGTGTTAAACAAGACGGGTCTCACTCCGA	1825
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Qy	1826	CTGCAACAGGAGCCCTTCTCCAGGGGTTTCCAGGAAGACCCCTGAATGAGGGCCCTG	1885
Db	516	LeuGlnGlnLysArgPheLeuGlnGlyValPheGlnGluAspProGluLysPheArgAlaLeu	535
Qy	1886	CAGGAGAGTACCTGTGGCATATCCCATTTGACCTTCCACGAGTCTTCTTAATGTGATC	1945
Db	536	GlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerThrSerSerAsnValIle	555
Qy	1946	CACAGACACATCTCAAAATCAACACACATCTCTGGATCTACCTGAAAGACCCAGTGG	2005
Db	556	HisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThrSerTrp	575
Qy	2006	GTGAAATTTAATGTGGACTCAAAATGGTTACTACATCGTTCACTATGAGGGTCAATGGATGG	2065
Db	576	VallysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHisGlyTrp	595
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Db	596	AspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAspArgVal	615
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Db	616	GlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAspLysAla	635
Qy	2186	CTTGACATGACTTACTACTCCCAATCAACAGAGAGCCCGGACTTCTCGAAGGTCTG	2245
Db	636	LeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProAlaLeuLeuGluGlyLeu	655
Qy	2246	AGTTACTTGGAAATCGTTTTACCACATGATGACAGAGGAATATTTTCAGATATCTTGAA	2305
Db	656	SerTyrLeuGluSerPheTyrHisMetMetAspArgArgAsnIleSerAspLysGlu	675
Qy	2306	AACCTCAAGCGTTACTTCTTCACTATTTAAGCCAGTGTATGACAGGCAAGCTGCAGT	2365
Db	676	AsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSerTrpSer	695
Qy	2366	GACAAGGGCTCAGTCTGGGACAGGATGCTCCGCTCGGCTCTCTTGAAGCTGGCTGTGAC	2425
Db	696	AspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLysLeuAlaCysAsp	715
Qy	2426	CTGAACCATGCTCTTGATCCAGAAAGCTGCTGAATCTTCTCCAGTGGATGCCATCC	2485
Db	716	LeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMetGluSer	735
Qy	2486	AGTGGAAATTAATATATACCAACAGATGTTTAAAGATTGCTATTTCTGTGGGTGCTCAG	2545
Db	736	SerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrSerValGlyAlaGln	755
Qy	2546	ACAAACAGCAGGATGGAATTTACTTTTTAGACCAATATGAACTGTCAATGTCAAGTGTGAA	2605
Db	756	ThrThrAlaGlyTrpAsnTyrLeuLeuGluGlnTyrGluLeuSerMetSerSerAlaGlu	775
Qy	2606	CAAAACAAAATCTGTATGCTTTCTCAACGAGCAAGCATCAGGAAAAGTTACTGAATTA	2665
Db	776	GlnAsnLysIleLeuTyrAlaLeuSerThrSerLysHisGlnGluLysLeuLeuLysLeu	795
Qy	2666	ATTGAATCAGAAAGGAGGAAGGTTATCAAGACACAGACTGGCAGCTCTCCTTCAT	2725
Db	796	IleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaAlaLeuLeuHis	815

Qy	2726	GCATTTGCCACAGCTCCAAAGGGCGACCACTAGCATGGGATTTTGTAAAGAGAAATGG	2785
Db	816	AlaIleAlaArgArgProLysGlyGlnLeuAlaTrpAspPheValArgGluAsnTrp	835
Qy	2786	ACCATCTTCTGAAAAATTTGACTTGGGCTCATATGACATAAGGATGATCATCTCTGGC	2845
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Qy	2846	ACACAGCTCACCTTCTTCCCAAGGATAGTTCGCAAGAGGTGAAACTATTTTGAATCT	2905
Db	856	ThrThrAlaHisPheSerSerLysAspLysLeuGlnGluValLysLeuPhePheGluSer	875
Qy	2906	CTTGAGGCTCAAGGATCACATCTCGATATTTTCAAACTGTTCTGGAACGATAACCAAA	2965
Db	876	LeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrLys	895
Qy	2966	AATATAAATGGCTGGAGAGAATCTTCCGACTCTGAGGACTTGGCTAATGGTTAATCT	3025
Db	896	AsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeuMetValAsnThr	915
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AC	Q8TD32;		
DT	01-JUN-2002 (TrEMBLrel. 21, Created)		
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	Leukocyte-derived arginine aminopeptidase short form.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=213741137; PubMed=11481040;		
RA	Hattori A., Matsumoto K., Mizutani S., Tsujimoto M.;		
RT	"Genomic organization of the human adipocyte-derived leucine		
RT	aminopeptidase gene and its relationship to the placental leucine		
RT	aminopeptidase/oxycotinase gene.";		
RL	J. Biochem. 130:235-241(2001).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Tanioka T., Hattori A., Masuda S., Nomura Y., Nakayama H.,		
RA	Mizutani S., Tsujimoto M.;		
RT	"Human leukocyte-derived arginine aminopeptidase: The third member of		
RT	the oxycotinase subfamily of aminopeptidases.";		
RL	J. Biol. Chem. 278:10000-10003(2003).		
DR	EMBL; AY028805; AAK37776.1; -.		
DR	MEROPS; M01.024; -.		
DR	GO; GO:0004177; F:aminopeptidase activity; IEA.		
DR	GO; GO:0004179; F:membrane alanyl aminopeptidase activity; IEA.		
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.		
DR	InterPro; IPR001930; Peptidase_M1.		
DR	InterPro; IPR006025; Pept_M_zn_BS.		
DR	Pfam; PF01433; Peptidase_M1; 1.		
DR	PRINTS; PR00756; ALADIPRTASE.		
DR	PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.		
KW	Aminopeptidase.		
SQ	SEQUENCE 532 AA; 60937 MW; DA0F4F00AD9E0D71 CRC64;		
Alignment Scores:			
Pred. No.:	5,93e-177	Length:	532
Score:	2768.00	Matches:	523
Percent Similarity:	99.81%	Conservative:	1
Best Local Similarity:	99.62%	Mismatches:	1
Query Match:	46.82%	Indels:	0
DB:	2	Gaps:	0
US-10-039-073-2 (1-3366) x Q8TD32 (1-532)			
Qy	146	ATGTTCCATCTTCTGCAATGGTTAATTCACAGAAACCAATGTTTAACATTCACAGA	205
Db	1	MetPheHisSerSerAlaMetValAsnSerHisArgLysProMetPheAsnIleHisArg	20

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QY 206 GGATTTTACTGCTTAACAGCCATCTTGCCCAAAATATGATTTGTTCTCAGTTCCTCAGTG 265
Db 21 GlyPheTyrCysLeuThrAlaIleLeuProGlnIleCysIleCysSerGlnPheSerVal 40
QY 266 CCATCTAGTTATCACTTCACTGAGGAGTCTCTGGGGCTTCCAGTAGGACCACTAAATGGGAA 325
Db 41 ProSerSerTyrHisPheThrGluAspProGlyAlaPheProValAlaThrAsnGlyGlu 60
QY 326 CGATTTTCTTGCAGGAGTAAGGCTCCCGAGTGGTCAATTCCTCTCCATTAATGACCTC 385
Db 61 ArgPheProTrpGlnGluLeuArgLeuProSerValIleProLeuHisTyrAspLeu 80
QY 386 TTTGTCCACCCCAATCTCACTCTCTGGACTTTGTGGCATCTTGAGAGATCGAAGCTCTTG 445
Db 81 PheValHisProAsnLeuThrSerLeuAspPheValAlaSerGluLysIleGluValLeu 100
QY 446 GTCAGCAATGCTACCCAGTTTATCATCTTGACACGACCAAGATCTTGAATCACGAATGCC 505
Db 101 ValSerAsnAlaThrGlnPheIleIleLeuHisSerLysAspLeuGluIleThrAsnAla 120
QY 506 ACCCTTTCAGTCAGAGAAAGATTCAAGATACATGAACACGAGAAAGAACTGAAAGTTTGT 565
Db 121 ThrLeuGlnSerGluLysSerArgTyrMetLysProGlyLysGluLeuLysValLeu 140
QY 566 AGTTACCTGCTCATGAACAAATTCACCTGCTGTTCCAGAGAAACTTACGCTCACCTG 625
Db 141 SerTyrProAlaHisGluGlnIleAlaLeuLeuValProGluLysLeuThrProHisLeu 160
QY 626 AATACTATGTGCTATGGACTTCCAGCAAGTTAGGTGATGGCTTTGAAGGTTTTAT 685
Db 161 LysTyrTyrValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTyr 180
QY 686 AAAACACATACAGAACTCTTGCTGGTGAACAAAGAAATCTTGCAAGTAAACAGATTTGAG 745
Db 181 LysSerThrTyrArgThrLeuGlyGlyGluThrArgIleLeuAlaValThrAspPheGlu 200
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QY 806 TCATCAAGATACGAAGAGAGCAGGCATATTGCACTATCCACATCCCAAGGTTAAG 865
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Db 241 ThrIleGluLeuGluGlyGlyLeuLeuGluAspHisPheGluThrThrValLysMetSer 260
QY 926 ACATACCTTGTAGCCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACTTCATCA 985
Db 261 ThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThrSerSer 280
QY 986 GGGTCAGGTGTCATCTATGCATCCCGAGCAACCGAATCAACACATATGCTTTG 1045
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Db 321 SerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsnTrpGly 340
QY 1166 CTCATTACATATAGGAGACGTCACTGCTTTTGTAGCCCAAGACCTCTTCTGCTCCGAT 1225
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QY 1346 CTTATCCGCTGTAATGTGTACATATCCAGAGCTGCAATTTGATGACTATTTTGAATGTG 1405
Db 401 LeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeuAsnVal 420
QY 1406 TGTTTGAAGTAATTTACAAAAGATTTCATTTGAATTCATCCCGCCCTATCTCCAAACACG 1465
Db 421 CysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLysProAla 440
QY 1466 GAAACCCCGACTCAAAATACAGGAAATGTTTCATGAAGTTTCTTATACAAAGGAGCTTGT 1525
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QY 1526 ATTTTGAATGCTCAAGGATTTTCTGGTCAGAGAGAAATTCAGAAAGGAATTAATTCAG 1585
Db 461 IleLeuAsnMetLeuLysAspPheLeuGlyGluGluLysPheGlnLysGlyIleIleGln 480
QY 1586 TACTTAAAGAGTTTCAGCTATAGAAATGCTAAGAAATGATGATCTTGTGGAGCAGTCTGTC 1645
Db 481 TyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspAspLeuTrpSerSerLeuSer 500
QY 1646 AATAGTTGTTAGAAAGTATTTACATCTCGTGGAGTTTGTCTATCCGATCCCAAGATG 1705
Db 501 AsnSerCysLeuGluSerAspPheThrSerGlyGlyValCysHisSerAspProLysMet 520
QY 1706 ACAAGTAACATGCTC 1720
Db 521 ThrSerAsnMetVal 525
RESULT 5
ART1_HUMAN STANDARD: PRT: 929 AA.
AC Q9NZ08; Q60278; Q8NEL4; Q8TAD0; Q9UHF8; Q9UKY2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Adipocyte-derived leucine aminopeptidase precursor (EC 3.4.11.-) (A-
DE LAP) (ARPS-1) (Aminopeptidase PILS) (Puromycin-insensitive leucyl-
DE specific aminopeptidase) (PILS-AP) (Type 1 tumor necrosis factor
DE receptor shedding aminopeptidase regulator).
GN Name=ARTS1; Synonyms=APPILS, KIAA0525;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=White adipose tissue;
RX MEDLINE=99238715; PubMed=10220586;
RA Hattori A., Matsumoto H., Mizutani S., Tsujimoto M.;
RT "Molecular cloning of adipocyte-derived leucine aminopeptidase highly
RT related to placental leucine aminopeptidase/oxytocinase.";
RL J. Biochem. 125:931-938(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Leukocyte;
RX MEDLINE=2137413; PubMed=11481040;
RA Hattori A., Matsumoto K., Mizutani S., Tsujimoto M.;
RT "Genomic organization of the human adipocyte-derived leucine
RT aminopeptidase gene and its relationship to the placental leucine
RT aminopeptidase/oxytocinase gene.";
RL J. Biochem. 130:235-241(2001).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC Schomburg L.;
RT "Molecular characterization of human aminopeptidase PILS.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC Cui X., Alsaaty S., Lawrence M., Combs C.A., Rouhani F.N.,
```

RA Levine S.J.;
RT "Identification of an aminopeptidase regulator of type I tumor
RT necrosis factor receptor shedding";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND REVISION TO 718.
RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
RA Nomura N., Ohara O.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 62-929 FROM N.A. (ISOFORM 2).
RC TISSUE=Brain;
RX MEDLINE=98290545; PubMed=9628581;
RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
RA Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. IX.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro.";
RL DNA Res. 5:31-39(1998).
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Testis;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fanev J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krawczynski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RP SEQUENCE OF 25-37, AND CHARACTERIZATION.
RX MEDLINE=20512052; PubMed=11056387;
RA Hattori A., Kitatani K., Matsumoto H., Miyazawa S., Rogi T.,
RA Tsuruoka N., Mizutani S., Natori Y., Tsujimoto M.;
RT "Characterization of recombinant human adipocyte-derived leucine
RT aminopeptidase expressed in Chinese hamster ovary cells.";
RL J. Biochem. 128:755-762(2000).
CC -!- FUNCTION: May play a role in the inactivation of peptide hormones.
CC May be involved in the regulation of blood pressure through the
CC inactivation of angiotensin II and/or the generation of bradykinin
CC in the kidney.
CC -!- CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Xaa-|-
CC Xbb-, in which Xaa is preferably Leu, but may be other amino acids
CC including Met, Cys and Phe.
CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9NZ08-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9NZ08-2; Sequence=VSP_005450;
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- PTM: N-glycosylated.
CC -!- SIMILARITY: Belongs to the peptidase M1 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF106037; AAF07395.1; ALT_INIT.
DR EMBL; AY028806; AAK37777.1; ALT_INIT.
DR EMBL; AY028807; AAK37778.1; ALT_INIT.
DR EMBL; AF183569; AAF20384.1; ALT_INIT.
DR EMBL; AF222340; AAF34664.1; ALT_INIT.
DR EMBL; AB011097; BRA25451.2; ALT_INIT.
DR EMBL; BC030775; AAK30775.1; ALT_INIT.
DR IntAct; Q9NZ08; -;
DR MEROPS; M01.018; -;
DR H-InvDB; HIX0005052; -;
DR MIM; 606832; -;
DR GO; GO:0005829; C:cytosol; NAS.
DR GO; GO:0005783; C:endoplasmic reticulum; NAS.
DR GO; GO:0005576; C:extracellular; IDA.
DR GO; GO:0016021; C:integral to membrane; NAS.
DR GO; GO:0005138; F:interleukin-6 receptor binding; IPI.
DR GO; GO:0004178; F:leucyl aminopeptidase activity; IDA.
DR GO; GO:0004239; F:methionyl aminopeptidase activity; NAS.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IPI.
DR GO; GO:0008270; F:zinc ion binding; NAS.
DR GO; GO:0045444; P:adipocyte differentiation; NAS.
DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . .; NAS.
DR GO; GO:0006509; P:membrane protein ectodomain proteolysis; IDA.
DR GO; GO:0050714; P:positive regulation of protein secretion; IDA.
DR GO; GO:0008217; P:regulation of blood pressure; NAS.
DR GO; GO:0045088; P:regulation of innate immune response; NAS.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR001930; Peptidase_M1.
DR Pfam; PF01433; Peptidase_M1; 1.
DR PRINTS; PR00756; ALADIPPTASE.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Alternative splicing; Aminopeptidase; Direct protein sequencing;
KW Glycoprotein; Hydrolase; Metalloprotease; Polymorphism; Protease;
KW Signal; Zinc.
FT SIGNAL 1 24 Adipocyte-derived leucine aminopeptidase.
FT CHAIN 25 929 Zinc (catalytic) (By similarity).
FT METAL 341 341 By similarity.
FT ACT_SITE 342 342 Zinc (catalytic) (By similarity).
FT METAL 345 345 Zinc (catalytic) (By similarity).
FT METAL 464 464 Proton donor (Potential).
FT ACT_SITE 426 426 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 58 58 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 142 142 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 748 748 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 889 889 N-linked (GlcNAc. . .) (Potential).
FT VARSPLIC 928 929 RM -> HDPEADATG (in isoform 2).
FT VARIANT 115 115 FTId=VSP_005450.
FT VARIANT 115 115 R -> P (in dBSNP:26653).
FT VARIANT 264 264 FTId=VAR_012779.
FT VARIANT 264 264 I -> M (in dBSNP:26618).
FT VARIANT 334 334 FTId=VAR_012780.
FT VARIANT 334 334 G -> D (in dBSNP:27895).
FT VARIANT 337 337 FTId=VAR_012781.
FT VARIANT 337 337 M -> V (in dBSNP:2287987).
FT VARIANT 516 516 FTId=VAR_012782.
FT VARIANT 516 516 K -> R (in dBSNP:27434).
FT VARIANT 718 718 FTId=VAR_012783.
FT VARIANT 718 718 Q -> E (in dBSNP:27044).
FT CONFLICT 502 502 FTId=VAR_012784.
FT CONFLICT 563 563 G -> R (in Ref. 3).
FT CONFLICT 713 713 D -> N (in Ref. 2, 5 and 6).
FT CONFLICT 713 713 R -> Q (in Ref. 2, 5 and 6).
SQ SEQUENCE 929 AA; 105846 MW; 75C6AD58D0D70D51 CRC64;
Alignment Scores: 4.86e-160 Length: 929
Pred. No.:

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Db	334	GlyIleThrMetThrValAlaHisGluLeuAlaHisGlnIrrPheGlyAenLeuValThr	353
Qy	1292	ATGGAATGGTGGAAATGATATTTGGCTTTAAGAGAGGGTTTTGCAAAATACATGGAACATTATC	1351
Db	354	MetGluTrpIrrPheAenAspLeuTrpLeuAenGluGlyPheAlaIysPheMetGluPheVal	373
Qy	1352	GCTGTTAATGCTACATATCCAGAGCTGCAATTTTGATGATGATCTATTTTTTGAATGTGTGTTTT	1411
Db	374	SerValSerValThrHisProGluLeuLeuValGlyAepTyrPhePheGlyIysCysPhe	393
Qy	1412	GAAGTAATACAAAAGATTCAATGAATTCAATCCGCCCTATCTCCAAACACGACGGAAACC	1471
Db	394	AspAlaMetGluValAspAlaLeuAenSerHisProValGluAen	413
Qy	1472	CCGACTCAAAATACAGAAATATGTTGATGAAGTTTCTATAACAAAGGAGCTTGTATTTTG	1531
Db	414	ProAlaGlnIleArgGluMetPheAspAspValSerTyrAspIysGlyAlaCysIleLeu	433
Qy	1532	AATATGCTCAAGGATTTTCTGGGTGAGGAAATTCAGAAAGGAATAATTCAGTACTTA	1591
Db	434	AsnMetLeuArgGluTyrLeuSerAlaAspAlaPheIysSerGlyIleValGlnTyrLeu	453
Qy	1592	AAGAGTTTCAGCTATAGAATGCTTAAGATGATGACTTGTGGAGCAGTCTGTCAATAGT	1651
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Qy	1652	TGTTTGAAGAGTCATTTTACATCTGCT-----GGAGTTTGTCTCCGATCCCAAGATG	1705
Db	474	Cys---ProThrAspGlyValIysGlyMetAspGlyPheCys---SerArgSerGlnHis	491
Qy	1706	ACAAGTAACATGCTGCCTTTCTGGGGGAAAAATGCAAGAGTCAAAGAGATGATGACTACA	1765
Db	492	SerSerSerSerHisTrpHisGlnGluGlyValAspValIysThrMetMetAsnThr	511
Qy	1766	TGCAGTCTCCAGAAAGGAATCCCGCTGCTGGTGGTTAAACAGACGGGTTCACCTCCGA	1825
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Qy	1826	CTGCAACAGAGCGCTTCTCCAGGGGGTTTTCCAGGAAGACCTCAATGGAGGGCGCTG	1885
Db	532	MetIysGlnGluHisTyrMetIysGly-----SerAspGlyAlaPro	545
Qy	1886	CAGGAGAGGTACTCTGGGCATATCCCATTTGACTACTCCACGAGTTCTTCTAATGTGATC	1945
Db	546	AspThrGlyTyrLeuTrpHisValProLeuThrPheIleThrSerIysSerAspMetVal	565
Qy	1946	CACAGACACATTTCAATTAACAGACAGATCTCTGGATCTACCTCAAAAAGACCACTTGG	2005
Db	566	HisArgPheLeuLeuIysThrIysThrAspValLeuIleLeuProGluGluValGluTrp	585
Qy	2006	GTCAAAATTAATGTGACTCAAAATGGTTACTACATCGTTCACTATCAGGCTCATGGATGG	2065
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Qy	2066	GACCAACTATTACACAGCTGAATCAGAACCAACACACTTCTCAGACTTAAGGACAGAGTA	2125
Db	606	AspSerLeuThrGlyLeuLeuIysGlyThrHisThrAlaValSerSerAenAspArgAla	625
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Qy	2246	AGTTACTTGGAAATCGTTTACCACATGATGGACAGGAAGAAATATTTTCAGATATCTCTGAA	2305

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QY 2906 CTGAGGCTCAAGGATCACATCTGGATATTTTCAAACTGTTCTGGAACGATTAACCAA 2965
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QY 2966 AATATAAATGGCTGGAGCAAGAACTTCCGACTCTGAGACTTGGCTA 3013
Db 906 AsnIleGlyTrpMetAspLysAsnPheAspLysIleArgValTrpLeu 921

RESULT 6
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DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE ARTS-1.
GN ORFNames=UNQ584;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liso D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Wagts A.,
RA vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.H., Yansura D.,

RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2285-2270(2003).
DR EMBL; AY358590; AAQ88953.1; -.
DR GO; GO:0004179; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001930; Peptidase M1.
DR InterPro; IPR006025; Pept_Mn_Zn_BS.
DR Pfam; PF01433; Peptidase M1; I.
DR PRINTS; PR00756; ALADIP7ASE.
DR PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.
SQ SEQUENCE 941 AA; 107143 MW; C3DC8ACFCFB5BBCC CRC64;
Alignment Scores:
Pred. No.: 9,03e-160 Length: 941
Score: 2512.50 Matches: 477
Percent Similarity: 69.34% Conservative: 172
Best Local Similarity: 50.96% Mismatches: 268
Query Match: 42.50% Indels: 19
DB: 2 Gaps: 7
US-10-039-073-2 (1-3366) x Q6UWY6 (1-941)
QY 212 TACTGCTTAACAGCCATCTTGGCCCAATATGATGCTTCTCAGTCTCAGTGCATCT 271
Db 15 PheLeuLeuSerSerLeuLeuAlaLeuLeuThrVal-----SerThrProSer 30
QY 272 AGTTATCATCTTCACTCAGGATCCTGGGCTTCCAGTAGTCCACTAATGGGACGATTT 331
Db 31 TrpCysGlnSerThrGlu-----AlaSerProLysArgSerAspGlyThrProPhe 47
QY 332 CCTTGCAGGAGCTAAGCTCCAGCTGGTCTCTCTCCTCATATGACCTCTTTGTC 391
Db 48 ProTrpAsnLysIleArgLeuProGluTyrValIleProValHisTyrAspLeuLeu 67
QY 392 CACCCCAATCTCACTCTCTGGACTTTTGTGCACTCTGAGAGATCGAAGTCTTGGTCAGC 451
Db 68 HisAlaAsnLeuThrThrLeuThrPheTrpGlyThrLysValGluIleThrAlaSer 87
QY 452 AATGCTACCAGTTTATCATCTTTCACAGCAAGATCTTGAATACAGAAATGCACCTT 511
Db 88 GlnProThrSerThrIleLeuHisSerHisLeuGlnIleSerArgAlaThrLeu 107
QY 512 CAGTCAGAGGAAGATTCAAGATACATGAACACAGGAAAGAACTGAAAGTTTGGATTAC 571
Db 108 ArgLysGlyAlaGlyGluArgLeuSerGlu-----GluProLeuGlnValLeuGluHis 125
QY 572 CTGTCTCATGAACAAATTCACCTGTCTGGTTCCAGAGAAACTTACGCTCACCTGAAATAC 631
Db 126 ProProGlnGluGlnIleAlaLeuLeuAlaProGluProLeuLeuValGlyLeuProTyr 145
QY 632 TATGTGGCTATGGACTTCCAAAGCAAGTTAGTGGCTTTGAAAGGTTTATAAAGC 691
Db 146 ThrValValIleHisTyrAlaGlyAsnLeuSerGluThrPheHisGlyPheTyrLysSer 165
QY 692 ACATACAGAACTCTTGGTGGTGAACAGAACTTTCGAGTACAGATTTTGGAGCCAAAC 751
Db 166 ThrTyrArgThrLysGluGluLeuArgIleLeuAlaSerThrGlnPheGluProThr 185
QY 752 CAGGCACGATGGCTTTCCCTTGTGTAACCGTTGTTCAAAGCCAACTTTTCAATC 811
Db 186 AlaAlaArgMetAlaPheProCysPheAspGluProAlaPheLysAlaSerPheSerIle 205
QY 812 AGATACGAGAGAGAGCGGATATTGCATATCCAAATGCAAGGTTTATAGCAAT 871
Db 206 LysIleArgArgGluProArgHisLeuAlaIleSerAsnMetProLeuValLysSerVal 225
QY 872 GAATTTGAAGGAGTCTTTTGGAGATCACTTTGAACTACTCTGAAATAGTACATAC 931
Db 226 ThrValAlaGluGlyLeuIleGluAspHisPheAspValThrValLysMetSerThrTyr 245

Qy	932	CTTGTAGCCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACTTTCATCATCGGGCTC	991
Db	246	LeuValAlaPheIleIleSerAspPheGluSerValSerIysIleThrLysSerGlyVal	265
Qy	992	AAGGTGTCCATCTATGATCCCGACAGAACGGATCAACACATTATGCTTTGCGAGCA	1051
Db	266	LysValSerValTyrAlaValProAspLysIleAsnGlnAlaAspTyrAlaLeuAspAla	285
Qy	1052	TCACTGAAGCTACTTGATTTTATGAAAAAGTACTTTGTATATCTACTATCCACTCTCCAAA	1111
Db	286	AlaValThrLeuLeuGluPheTyrGluAspTyrPheSerIleProTyrProLeuProLys	305
Qy	1112	CTGATTTTAATTCCTATTCCTGACTTTGACCTCGAGCCATGGAAAATTTGGGGCTCATTT	1171
Db	306	GlnAspLeuAlaIleProAspPheGlnSerGlyAlaMetGluAenTrpGlyLeuThr	325
Qy	1172	ACATATAGGGAGACGTCACTGCTTTTGTACCCCAAGACCTTCTCTGCTCCGATAAACTG	1231
Db	326	ThrTyrArgGluSerAlaLeuLeuPheAspAlaGluLysSerAlaSerSerLysLeu	345
Qy	1232	TGGGTCCACGAGTCATAGCCCATGAATTCATGCGCACCCAGTGGTTGCAACCTGGTCACA	1291
Db	346	GlyIleThrValThrValAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeuValThr	365
Qy	1292	ATGAATTTGGTGAATGATATTTGGCTTAAGGAGGGTTTTGCAAAATACATGGAACTTATC	1351
Db	366	MetGluTrpTrpAsnAspLeuTrpLeuAsnGluGlyPheAlaLysPheMetGluPheVal	385
Qy	1352	GCTGTTAATGCTACATATCCAGACGCTGCAATTTGATGCATCTATTTTTTGAATGTGTGTTT	1411
Db	386	SerValSerValThrHisProGluLeuLysValGlyAspTyrPhePheGlyLysCysPhe	405
Qy	1412	GAAGTAATATCAAAAGATTCATTTGAATTCATCCCGCCCTATCTCCAAACAGCGGAAACC	1471
Db	406	AspAlaMetGluValAspAlaLeuAsnSerSerHisProValSerThrProValGluAsn	425
Qy	1472	CCGACTCAATACAGGAAATGTTTGTATGAAGTTTCTTATTAACAGGAGGCTTGTATTTTG	1531
Db	426	ProAlaGlnIleArgGluMetPheAspAspValSerTyrAspLysGlyAlaCysIleLeu	445
Qy	1532	AATATGCTCAAGGATTTTCTGGGTGAGAGAGAAATTCAGAAAGAAATAATTCAGTACTTA	1591
Db	446	AsnMetLeuArgGluTyrLeuSerAlaAspAlaPheLysSerGlyIleValGlnTyrLeu	465
Qy	1592	AAGAAGTTACGCTATAGAAATGCTPAAGAATGATGACTGTGGAGCAGCTCTGTCAAAATAGT	1651
Db	466	GlnLysHisSerTyrLysAsnThrLysAsnGluAspLeuTrpAspSerMetAlaSerIle	485
Qy	1652	TGTTTAGAAGTGAATTTTACATCTGGT-----GGAGTTTGTCAATTCGGATCCCAAGATG	1705
Db	486	Cys---ProThrAspGlyValLysGlyMetAspGlyPheCys---SerArgSerGlnHis	503
Qy	1706	ACAAGTAACATGCTCGCTTCTTCTGGGGGAAAAATCGACAGGTCAAGAGATGATGACTACA	1765
Db	504	SerSerSerSerHisTrpHisGlnGluGlyValAspValLysThrMetMetAsnThr	523
Qy	1766	TGGACTCTCCAGAAAGAAATCCCTCTGCTGGTGGTTAAACAAGACGGGTGTTCACCTCCGA	1825
Db	524	TrpThrLeuGlnArgGlyPheProLeuIleThrIleThrValArgIlyArgAsnValHis	543
Qy	1826	CTGCAAAGGAGCGCTTCCCTCCAGGGGGTTTTCCAGGAAGACCCTGAATGGAGGGCCCTG	1885
Db	544	MetLysGlnGluHisTyrMetLysGly-----SerAspGlyAlaPro	557
Qy	1886	CAGGAGAGGTCACCTGTGGCATATCCCATTTGACCTTACTCCAGAGTCTCTTAATGTGATC	1945
Db	558	AspThrGlyTyrLeuTrpHisValProLeuThrPheIleThrSerLysSerAsnMetVal	577
Qy	1946	CACAGACACATCTTAAATCAAGACAGATACTCTCGGATCTACTCTGAAAAGACCATGTGG	2005
Db	578	HisArgPheLeuLeuLysThrLysThrAspValLeuIleLeuProGluLysValGluTrp	597

RESULT 7		
ART1 MOUSE		
ID	ART1 MOUSE	STANDARD; PRT; 930 AA.
AC	Q9EQH2; Q9ET63;	
DT	28-FEB-2003 (Rel. 41, Created)	

QY 1031 ACACATTATGCTTGCAGGCATCACTGAAGCTACTTGATTTTATGAAAAGTACTTTGAT 1090
Db 268 AlaAspTyrAlaLeuAspAlaValThrLeuLeuGluPheTyrGluAspTyrPheAsn 287
QY 1091 ATCTACTATCCACTCTCCAAACTGATTTAAATGCTTATCTCCTGACTTTGACCTGAGCC 1150
Db 288 IleProTyrProLeuProLysGlnAspLeuAlaIleProAspPheGlnSerGlyAla 307
QY 1151 ATGGAAATATGGGGCTCATATACATATAGGAGAGCGTCACTCTCTTTTGGACCCCAAGACC 1210
Db 308 MetGluAsnTrpGlyLeuThrTyrArgGluSerSerLeuLeuTyrAspLysGluLys 327
QY 1211 TCTTCTGCTTCCGATTAATCTGGGTCCACAGAGTCATAGCCCACTGAGCCGACACAG 1270
Db 328 SerSerAlaSerSerLysLeuGlyIleThrMetIleValSerHisGluLeuAlaHisGln 347
QY 1271 TGGTTTGGCAACTCGTCAATGGAATGGAATGATATTTGGCTTAAGGAGGTTT 1330
Db 348 TrpPheGlyAsnLeuValThrMetGluTrpTrpAsnAspLeuTrpAsnGluGlyPhe 367
QY 1331 GCAAAATACATGAATCTATCCTGTTAATGCTACATATCCAGAGCTGCAATTTTGATGAC 1390
Db 368 AlaLysPheMetGluPheValSerValThrValThrHisProGluLeuLysValGluAsp 387
QY 1391 TATTTTGAATGCTGCTGTTTGAAGTAAATACAAAGATTCAATCAATTCATCCGCCCT 1450
Db 388 TyrPhePheGlyLysCysPheAsnAlaMetGluValAspAlaLeuAsnSerSerHisPro 407
QY 1451 ATCTCCAAACACGCGGAACCCGACTCAATACAGGAAATGTTTGAAGTTTCTTAT 1510
Db 408 ValSerThrProValGluAsnProAlaGlnIleArgGluMetPheAspAspValSerTyr 427
QY 1511 AACAGGGAGCTGTATTTTGAATATGCTCAAGGATTTTCTGGGTGAGAGGAAATTCAC 1570
Db 428 GluLysGlyAlaCysIleLeuAsnMetLeuArgAspTyrLeuSerAlaAspThrPheLys 447
QY 1571 AAAGAATAATTCAGTACTTAAGAAGTTCAGCTATAGAAATGCTAAGAATGATGACTTG 1630
Db 448 ArgGlyIleValGlnTyrLeuGlnLysTyrSerTyrLysAsnThrLysAsnGluAspLeu 467
QY 1631 TGGACAGTCTCTCAAAATAGTTGT--TTAGAAAGTGATTTTACATCTGGTGGAGTTGT 1687
Db 468 TrpAsnSerMetMetHisIleCysProThrAspGlyThrGlnThrMetAspGlyPheCys 487
QY 1688 CATTCGGATCCCAAGATCAAGTAAACATGCTCGCTTCTGGGGGAAATATGCAGAGTGC 1747
Db 488 ---SerArgSerGlnHisSerSerThrSerHisTrpArgGlnGluValValAspVal 506
QY 1748 AAAGAGATGATGACTACATGAGTCTCCGAAAGGAATCCCTCTGCTGGTGGTTAAACA 1807
Db 507 LysThrMetMetAsnThrTrpThrLeuGlnLysGlyPheProLeuIleThrVal 526
QY 1808 GACGGGTGTCTACGCTCGACTCAACAGAGCGCTTCTCCAGGGGGTTTCCAGGAAGAC 1867
Db 527 SerGlyArgAsnValIleMetLysGlnLysIleTyrMet-----Asn 540
QY 1868 CCTGAATGGAGCGCCCTCGAGAGAGGTACCTGTGGCATATCCCATTTGACCTACTCCACG 1927
Db 541 AlaSerGluArgPheProGluThrGlyTyrLeuTrpHisValProLeuThrPheIleThr 560
QY 1928 AGTTCTTCTAATGTGATCCACAGACACATTTCTAAATCAAGACAGATCTCTGATCTA 1987
Db 561 SerLysSerAspSerValGlnArgPheLeuLeuLysThrLysThrAspValLeuIleLeu 580
QY 1988 CCTGAAAGACCCAGTTGGTGAATTTAATGAGTCAATGAGTCAATGTTACTACATCGTTCAC 2047
Db 581 ProGluAlaValGlnTrpLysPheAsnValGlyMetAsnGlyTyrTrpIleValHis 600
QY 2048 TATGAGGGTCTATGGTGGACCAATCATTTACACAGCTGAATCAAGAACACACACTTCTC 2107
Db 601 TyrAlaAspAspGlyTyrAlaSerLeuSerGlyLeuLeuLysGluAlaHisThrIle 620
QY 2108 AGACCTAAGGACAGATAGTCTGATTCATGATGTTTTCAGTGTGTTGGTGCAGGGAGA 2167

RESULT 8

ARTL_RAT
-ID ARTL_RAT STANDARD; PRT; 930 AA.
AC Q9UJ22; Q9UJ23;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Adipocyte-derived leucine aminopeptidase precursor (EC 3.4.11.-) (A-
LAP) (ARTS-1) (Aminopeptidase Plus) (Puromycin-insensitive leucyl-
specific aminopeptidase) (PILS-AP).

Db 621 SerSerAsnAspArgAlaSerLeuIleAsnAsnAlaPheGlnLeuValSerIleGluLys 640
QY 2168 CTGACCCCTAGACAAAGCTCTTGACATGACTTACTACCTCCCAACATGAAAGACGACGCC 2227
Db 641 LeuSerIleGluLysAlaLeuAspLeuThrLeuTyrLeuLysAsnGluThrGluIleMet 660
QY 2228 GCATTTCTCGAAGTCTGAGTTACTTGGAAATCGTTTATACCATGATCGACAGAGGAAT 2287
Db 661 ProfilePheGlnAlaLeuAsnGluIleProMetTyrLysLeuMetGluLysArgAsp 680
QY 2288 ATTTTCAGATATCTCTGAAAACCTCAAGCGTTTACTCTTCTCAGTATTTTAAAGCCAGTATT 2347
Db 681 MetIleGluValGluThrGlnPheLysAspPheLeuLeuLysLeuLeuLysAspLeuIle 700
QY 2348 GACAGGCAAACTCGAGTGACAAAGGCTCACTCGGACAGAGTCTCCGCTCGGCTCTC 2407
Db 701 AspLysGlnThrTrpThrAspGluGlySerValSerGluArgMetLeuArgSerGlnLeu 720
QY 2408 TTGAAGCTGGCTGTGACCTGAACCATGCTCTTTCATCTCCAGAAAGCTGCTGAATCTTC 2467
Db 721 LeuLeuLeuAlaCysValArgAsnTyrGlnProCysValGlnArgAlaGluArgTyrPhe 740
QY 2468 TCCAGTGGATGGAAATCCAGTGGAAATTAATATACCAACAGATGTTTTAAAGATTGTG 2527
Db 741 ArgGluTrpLysSerSerAsnGlyAsnMetSerIleProIleAspValThrLeuAlaVal 760
QY 2528 TATTCGTGGGTGCTCAGACCAACAGAGAGTGAATTACCTTTTAGACCAATATGAACCTG 2587
Db 761 PheAlaValGlyAlaGlnAsnThrGluGlyTrpAspPheLeuTyrSerLysTyrGlnSer 780
QY 2588 TCAATGTCAAGTGTGACAAACAAATCTGTATGCTTTGTCAACGAGCAAGCATCAG 2647
Db 781 SerLeuSerSerThrGluLysSerGlnIleGluPheSerLeuCysThrSerLysAspPro 800
QY 2648 GAAAAGTTACTGAAGTTAATTGAAGTAGGAATGGAAGAAAGGTATATCAACACACAGAAC 2707
Db 801 GluLysLeuGlnTrpLeuLeuAspGlnSerPheLysGlyGluIleLysThrGlnGlu 820
QY 2708 TTGGCAGCTCTCTTCATCGATTCGACAGCTCCAAAGGGGCGACAACTAGCATGGGAT 2767
Db 821 PheProHisIleLeuThrLeuIleGlyArgAsnProValGlyTyrProLeuAlaTrpLys 840
QY 2768 TTCTTAAGAGAAAATTCGACCCCATCTTCTGAAAAATTTGACTTGGGCTCATATGACATA 2827
Db 841 PheLeuArgGluAsnTrpAsnLysLeuValGlnLysPheGluLeuGlySerSerSerIle 860
QY 2828 AGGATGATCATCTCTGCGACACAGCTCCTTTTCTTCCAGGATAAGTTCCAGAGGTG 2887
Db 861 AlaHisMetValMetGlyThrThrAspGlnPheSerThrArgAlaArgLeuGluGluVal 880
QY 2888 AAACATTTTGTGAATCTCTTGAAGCTCAAGGATCAATCTGGATATTTTCAAACCTGT 2947
Db 881 LysGlyPhePheSerSerLeuLysGluAsnGlySerGlnLeuArgCysValGlnGlnThr 900
QY 2948 CTGGAACGATAACCAAAAAATATAAAATGCGCTGGAGAGAAATCTTCCGACTCTCAGGACT 3007
Db 901 IleGluThrIleGluGluAsnIleArgTrpMetAspLysAsnPheAspLysIleArgLeu 920
QY 3008 TGGCTA 3013
Db 921 TrpLeu 922

GN Name=Artsel; Synonyms=Appils;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC STRAIN=Sprague-Dawley; TISSUE=Pineal gland;
RX MEDLINE=20285344; PubMed=10824104;
RA Schomburg L., Kollmus H., Friedrichsen S., Bauer K.;
RT "Molecular characterization of a puromycin-insensitive leucyl-specific
RL Eur. J. Biochem. 267:3198-3207(2000).
CC -!- FUNCTION: May play a role in the inactivation of peptide hormones.
CC May be involved in the regulation of blood pressure through the
CC inactivation of angiotensin II and/or the generation of bradykinin
CC in the kidney (By similarity).
CC -!- CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Xaa-|-
CC Xbb-, in which Xaa is preferably Leu, but Met is also acceptable.
CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9J22-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9J22-2; Sequence=VSP_005451, VSP_005452;
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- SIMILARITY: Belongs to the peptidase M1 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF148323; AAF73106.1; -;
DR EMBL; AF148324; AAF73107.1; -;
DR MEROPS; M01.018; -;
DR GO; GO:0005829; C:cytosol; ISS.
DR GO; GO:0005783; C:endoplasmic reticulum; ISS.
DR GO; GO:0005766; C:extracellular; ISS.
DR GO; GO:0016021; C:integral to membrane; ISS.
DR GO; GO:0005138; F:interleukin-6 receptor binding; ISS.
DR GO; GO:0004178; F:leucyl aminopeptidase activity; ISS.
DR GO; GO:0004239; F:methionyl aminopeptidase activity; ISS.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; ISS.
DR GO; GO:0008270; F:zinc ion binding; ISS.
DR GO; GO:0045444; P:adipocyte differentiation; ISS.
DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . . ; ISS.
DR GO; GO:0006509; P:membrane protein ectodomain proteolysis; ISS.
DR GO; GO:0050714; P:positive regulation of protein secretion; ISS.
DR GO; GO:0008217; P:regulation of blood pressure; ISS.
DR GO; GO:0045088; P:regulation of innate immune response; ISS.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR001930; Peptidase_M1.
DR Pfam; PF01433; Peptidase_M1; 1.
DR PRINTS; PR00756; ALADIPTASE.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Alternative splicing; Aminopeptidase; Glycoprotein; Hydrolase;
KW Metalloprotease; Protease; Signal; Zinc.
FT SIGNAL 1 20 Potential.
FT CHAIN 21 930 Adipocyte-derived leucine aminopeptidase.
FT METAL 342 342 Zinc (catalytic) (By similarity).
FT ACT SITE 343 343 By similarity.
FT METAL 346 346 Zinc (catalytic) (By similarity).
FT METAL 465 465 Zinc (catalytic) (By similarity).
FT ACT SITE 427 427 Proton donor (Potential).
FT CARBOHYD 59 59 N-linked (GlcNAc . . .) (Potential).
FT 143 143 N-linked (GlcNAc . . .) (Potential).

FT CARBOHYD	403	403	N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD	655	655	N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD	749	749	N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD	890	890	N-linked (GlcNAc . . .) (Potential).
FT VARSPLIC	883	884	FF -> CM (in isoform 2). /FTId=VSP_005451.
FT VARSPLIC	885	930	Missing (in isoform 2). /FTId=VSP_005452.
SQ SEQUENCE	930 AA;	106418 MW;	92BE7143CBD0BE7F CRC64;

Alignment Scores:			
Pred. No.:	3,05e-154	Length:	930
Score:	2430.00	Matches:	456
Percent Similarity:	68.90%	Conservative:	171
Best Local Similarity:	50.11%	Mismatches:	265
Query Match:	41.10%	Indels:	18
DB:	1	Gaps:	6

US-10-039-073-2 (1-3366) x ART1_RAT (1-930)

QY	299	GCCTTCCCAGTAGCCACTAATGGGAACGATTTCTTGGCAGGAGCTAAGGCTCCCCAGT	358
DB	26	AlaserProlysaAlaserAenGlyAlaserPheProTrpAsnMetArgLeuProGlu	45
QY	359	GTGGTCATTCCTCTCCATTATGACCTCTTTGTCCACCCCAATCTCACCTCTCTGGACTTT	418
DB	46	TyrIleThrProIleHisTyrAspLeuMetIleHisAlaAsnLeuSerThrLeuThrPhe	65
QY	419	GTTCATCTCGAAGATCGAGTCTGGTCAGCAATGCTACCCAGTTTATCATCTTGCAC	478
DB	66	TrpGlyThrGluValGluIleThrValSerGlnProThrSerThrIleIleMetHis	85
QY	479	AGCAAGATCTTCAAAATCACGAATGCCACCTTCAG-----TCAGAGGAGGATTCAGA	532
DB	86	SerHisGlnLeuGlnIleSerLysAlaThrLeuArgGlyAlaGlu-----	102
QY	533	TACATGAACACAGAAAGAAATCGAAGTTTTCAGTTTACCTCTCATGAACAAATGCA	592
DB	103	---MetLeuProGluGluProLeuLysLeuMetGluTyrSerAlaHisGluInValAla	121
QY	593	CTGCTGGTCCAGAGAACTTACGCTCACCTCACTGAAATACCTATGCTGGCTATGCATCCAA	652
DB	122	LeuLeuThrAlaGlnProLeuLeuAlaGlySerValTyrThrValIleIleThrTyrAla	141
QY	653	GCCAAAGTTAGTGATGGCTTTGAAGGGTTTATAAAGACACATACAGAACTCTTGGTGGT	712
DB	142	AlaAsnLeuSerGluAsnPheHisGlyPheTyrLysSerThrTyrArgThrGlnGluGly	161
QY	713	GAACAAGAAATCTTCAGTAAACAGATTTCAGCCCAACCCAGCAGCATGGCTTCCCT	772
DB	162	GluArgGileLeuAlaAlaThrGlnPheGluProThrAlaAlaArgMetAlaPhePro	181
QY	773	TGCTTTGATGAACCGTTGTTCAAGCCAACTTTTCATCAAGATACGAGAGAGAGAGAGG	832
DB	182	CysPheAspGluProAlaLeuLysAlaSerPheSerIleLysIleLysArgAspProArg	201
QY	833	CATATGTCATCTTCCAAATGCGCAAGTTTGAAGCAACTTCAACTGAAGAGGCTCTTTTG	892
DB	202	HisLeuAlaIleSerAsnMetProLeuValLysSerValThrValAlaGluGlyLeuIle	221
QY	893	GAAGATCATCTTGAAGAACTACTGTAAATAATGAGTACATACCTGTAGCCTCATAGTTGT	952
DB	222	GluAspHisPheAspIleThrValLysMetSerThrTyrLeuValAlaPheIleIleSer	241
QY	953	GATTTCCACTCTCTGAGTGCCTTCACTTCATCAGGGGTCAAGGTCCATCTATGCATCC	1012
DB	242	AspPheLysSerValSerLysMetThrLysSerGlyValLysValSerValTyrAlaVal	261
QY	1013	CCAGACAAACGGATCAACACATATTATGCTTTCAGGCATCATCTAGAGCTACTTGTATTT	1072
DB	262	ProAspLysIleAsnGlnAlaAspTyrAlaLeuAspAlaAlaValThrLeuLeuGluPhe	281
QY	1073	TATGAAAAGTACTTTTGATGATCTACTATCTCACTCTCCAAACTGGATTTAATGCTATTCCT	1132

Db	633	PheGlnLeuValSerIleGlyLyLeuSerIleGluLyAlaLeuAspLeuIleuTyr	652
Qy	2204	CTCAACATGAAACAAAGCAGCCCGCACTTCTCGAAGGTCGTGATTTACTTTGAGTAACTCGTTT	2263
Db	653	LeuLyAsnGluThrGluIleMetProIlePheGlnGlyLeuAenGluLeuIleProMet	672
Qy	2264	TACCACATGATGACAGAGGAATATTTCAGATATCTCTGAAAAACCTCAAGCGTTTACCTT	2323
Db	673	TyrLyLeuMetGluLyArgAspMetValGluValGluThrGlnPheLyAspPheLeu	692
Qy	2324	CTTCAGTATTTTAAAGCCAGTGATTGACAGCAAGCTGGAGTCACAAAGGCTCAGTCTGG	2383
Db	693	LeuArgLeuLeuLyAspLeuIleAsnLyGlnThrTrpAspGluGlySerValSer	712
Qy	2384	GACAGATGTCGCGCTCGGCTCTCTTGAAGCTGGCCTGTCACCTGAACCATGCTCTCTGTC	2443
Db	713	GluArgMetLeuArgSerGlnLeuLeuLeuLeuAlaCysValHisArgTyrGlnLeuCys	732
Qy	2444	ATCCAGAAAGCTCTCTGAATCTTCTCCAGTGATGGAATCCAGTCGGAAATTAATATA	2503
Db	733	ValGlnArgAlaGluArgTyrPheArgGluTrpLyAlaSerAsnGlyAsnMetSerLeu	752
Qy	2504	CCACAGATGTTTTAAAGATCTGTATTCTGTGGTGCTCAGACACACAGCAGCATGGAAT	2563
Db	753	ProIleAspValThrLeuAlaValPheAlaValGlyAlaGlnAsnThrGluGlyTrpAsp	772
Qy	2564	TACCTTTTGAAGCAATATGAACCTGTCAATGTCAAGTGTGAAACAAACAAATTCGTAT	2623
Db	773	PheLeuTyrSerLySTyrGlnSerSerLeuSerSerThrGluLySerGlnIleGluPhe	792
Qy	2624	GCCTTTCTCAACGACGACATCAGGAAAGTTACTGAAGTTTAATGAATCTAGGAATGGAA	2683
Db	793	SerLeuCysIleSerGlnAspProGluLyLeuGlnTrpLeuLeuAspGlnSerPheLyS	812
Qy	2684	GGAAAGGTTATCAAGACACAGAACTTGGCAGCTCTCTTCATCGCATTCGCCAGCTCCA	2743
Db	813	GlyGluIleIleLySThrGlnGluPheProHisIleLeuThrLeuIleGlyArgAsnPro	832
Qy	2744	AAGGGCGACCACTAGCATGGGATTTTGTGAAGAGAAATTTGGACCCATCTCTCGAAAAA	2803
Db	833	ValGlyTyrProLeuAlaTrpLySLeuLySLeuAsnTrpAsnLySLeuValGlnLyS	852
Qy	2804	TTTGACTTGGGCTCATATGACATPAGGATGATCATCTCTGGCAACAACAGCTCACTTTTCT	2863
Db	853	PheGluLeuGlySerSerSerIleAlaHisMetValMetGlyThrThrAsnGlnPheSer	872
Qy	2864	TCCAAGATAAGTTGCAAGGTGAACTATTTTTTGAATCTCTTGAGGCTCAAGGATCA	2923
Db	873	ThrArgAlaArgLeuGluValLySLeuGlyPhePheSerSerLeuLySLeuAsnGlySer	892
Qy	2924	CATCTCGATATTTTCAAACCTGTTCTGGAAACGATTAACCAAAATATAAAATGGCTGGAG	2983
Db	893	GlnLeuArgCysValGlnGlnThrIleGluThrIleGluLeuAsnIleArgTrpMetAsp	912
Qy	2984	AGAATCTTTCCGACTCTGAGGACTTGGCTA	3013
Db	913	LyAsnPheAspLySLeuArgLeuTrpLeu	922
RESULT 9			
Q6PE23	ID	Q6PE23	PRELIMINARY; PRT; 1003 AA.
AC	DT	Q6PE23;	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	DT	05-JUL-2004	(TrEMBLrel. 27, Last sequence update)
DT	DT	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)
DE	DE	Hypochemical protein zgc:66103.	
GN	GN	ORFNames=zgc:66103;	
OS	OS	Brachydanio rerio (Zebrafish) (Danio rerio).	
OC	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;	
OC	OC	Cyprinidae; Danio.	
OX	OX	NCBI_TaxID=7955;	
RN	RN	[1]	

mi;

WZO

RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC058317; AAHS8317.1; -;
DR ZFIN; ZDB-GENE-030131-1534; zgc:66103.
DR GO; GO:0004179; P:membrane alanyl aminopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001930; Peptidase_M1.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF01433; Peptidase_M1; 1.
DR PRINTS; PR007562; Peptidase_M1; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
DR KW Hypothetical protein.
SQ SEQUENCE 1003 AA; 114373 MW; E2209CE4B753E978 CRC64;

Alignment Scores:
Pred. No.: 1e-127 Length: 1003
Score: 2034.50 Matches: 421
Percent Similarity: 59.70% Conservative: 179
Best Local Similarity: 41.89% Mismatches: 307
Query Match: 34.41% Indels: 98
DB: 2 Gaps: 14

US-10-039-073-2 (1-3366) x Q6PE23 (1-1003)
QY 28 AATTCAATGTTAAATATTGTTTCAGACCCCATGTGACATACTGGAGCCAGTGCAGTG 87
DB 88 AsnSerCys
QY 88 CCATGAAGAACTACGAGATTAGCCCTGGATATTAATCTGCTCTTCTAGAGAAATAGATTTTCAT 147
DB 94 SerThrLysThrAlaValGlyValLeuLeuValLeuValSerMetPheMet 113
QY 148 GTTCCATCTTC-----TGCATGGTTAAATTCACAGAAACCAATGTTTAAACAT 198
DB 114 ValIleTyrPheValProSerCysThr-----PheThrLysLys----- 126
QY 199 TCACAGAGGATTTTACTGCTTAAACAGCATCTTGCCTCCCAATATGATTTGTTCTCAGTT 258
DB 127 -----Gly-CysGlnLysSerAsnSe 133
QY 259 CTCAGTGCCATCTAGTTATCATCTTCACTGAGGATCTCGGGCTTTCACAGTAGCCACTAA 318
DB 133 rSerMetSerSerIleTyr-----ProIleSerThrSe 144
QY 319 TGGGGAACGATTTCTTGGCAGGAGCTTAAGCTCCCGAGTGCTGCTCTCTCCCATTA 378
DB 144 rGlyGluLeuPheProThrThrAspLeuArgLeuProValSerValHisProValHis 164

379 TGACCTCTTTGTCACCCCAATCTCACCTCTCTGGACTTTGTTGTCATCTCAGAAGATCGA 438
DB 164 rAnIleSerLeuHisProAspLeuAsnSerMetThrPheGlnGlyAsnValSerIleVa 184
QY 439 AGTCTTGGTCAGCAATCTCTACCCAGTTTATCATCTTTCACAGCAAAAGATCTTGAATCAC 498
DB 184 lValLeuValValHisGluThrLysAsnIleValLeuHisSerSerAspMetAsnIleI 204
QY 499 GAATGCCACCTTCAGTCAGAGGAAGATTCAAGATCATCATGAAACACGAGGAAAGAACTGAA 558
DB 204 eLysValThrPheAspAsp-----LysGluTyrAr 214
QY 559 AGTTTGGAGTTCCTGCTCATCAACAAATTTGCACTGCTGTTCCAGAGAAACTTACGCC 618
DB 214 gPheLeuGluTyrLysProTrpGlnIleAlaIleLysPheProGluAspLeuLysLy 234
QY 619 TCACCTGAAATATCATATGTGGCTATGCACTTCCAAAGCAAGTATAGGTGATCGCTTTGAAG 678
DB 234 sGly---GlnTyr-ValLeuLysPheSerTyrLysAlaAsnLeuSerAsnSerTyrAspG 253
QY 679 GTTTTATAAAGCACATACAGAACTCTTGGTGTGAAACAGAAATTTCTTCAGTAAACAGA 738
DB 253 yPheTyrAsnSerSerTyrValAspThrAlaGlyThrLysArgValLeuAlaIleThrG 273
QY 739 TTTTGAGCCAAACCCAGCGCATGCTTCCCTTCTGCTTTGTGATGAACCGTTGTTCAAAGC 798
DB 273 nPheGluProLeuAlaAlaArgLysAlaPheProCysPheAspGluProAlaPheLysSe 293
QY 799 CAATCTTTCAATCAAGATACGAAGAGAGAGAGCGCATATTTGCACTATCCCAACATGCCAAA 858
DB 293 rThrPheValValLysMetThrArgGluAlaLysTyrIleSerLeuSerAsnMetProLy 313
QY 859 GGTAAAGACAAATTGAACCT---GAAGGAGGTCTTTTGGAGAGATCACTTTGAAACTACTGT 915
DB 313 sIleLysThrThrAspLeuAsnGluAsnGlyLeuGlnGluAspGluPheGluSerVa 333
QY 916 AAAATGAGTACATACCTTGTCCTACATAGTTTGTGATTTCCTCACTCTCTGAGTGCTT 975
DB 333 lLysMetSerThrTyrLeuValAlaPheIleValAlaGluPheSerSerHisSerLysAs 353
QY 976 CACTTCATCAGGGGTCAAGGTGTCATCTATGATCATCCCAAGCAAAACGGGAATCAACACA 1035
DB 353 nValSerLys---ThrThrValSerValTyrAlaValProAspLysLysAspGlnValHi 372
QY 1036 TTATGCTTTGCAGGCATCACTGAGCTACTTGTATTTTATGAAAGTACTTTCATATCTA 1095
DB 372 sTyrAlaLeuGluThrAlaCysLysLeuLysPheTyrAsnThrPhePheGluIleGl 392
QY 1096 CTATCCACTCTCCAAACTGGATTAAATTGCTATTCCTGACTTTGCACTCTGAGCCATCGGA 1155
DB 392 uTyrProLeuSerLysLeuAspLeuValAlaIleProAspPheLeuAlaGlyAlaMetGl 412
QY 1156 AAATGGGGCTCATATACATATAGGAGAGCGTCACCTGCTTTTTCAGCCCAAGACCTCTTC 1215
DB 412 uAsnTrpGlyLeuIleThrPheArgGluThrThrLeuLeuValGly---AsnGlnSerSe 431
QY 1216 TGCTTCGATAAATCTGGGTCCAGAGCTCATAGCCCATGAACTGGCGCAGCAGTGGTT 1275
DB 431 rArgPheAspLysGluLeuValThrSerValIleAlaHisGluLeuAlaHisGlnTrpPh 451
QY 1276 TGGCAACCTGGTCACCAATGGAATGGTGGATGATATTGGCTTTAAGAGAGGTTTTCGAAA 1335
DB 451 eGlyAsnLeuValThrMetArgTrpTrpAsnAspLeuTrpLeuAsnGluGlyPheAlaTh 471
QY 1336 ATACATGGAACCTTATCGCTGTTTAAATGCTACATATCCAGAGCTGCAATTTGATGACTATT 1395
DB 471 rTyrMetGlnTyrMetSerIleGluAsnValPheProAspLeuAspIleAspIleGluPh 491
QY 1396 TTTGAATGCTGTGTTTGAAGTAATTACAAAGATTCATTAATTCATCCGCCCTACTCTC 1455
DB 491 eLeuAsnValArgPheLysAlaLeuAlaLysAspAlaLeuAsnSerSerHisProValSe 511

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QY 1456 CAACCCAGCGGAAACCCGACTCAATATACAGGAATGTTGATGAAGTTTCTCTATAACAA 1515
Db 511 rThrPheValSerThrProGluGlnValGluMetPheAspSerValSerTyrGluLy 531
QY 1516 GGGAGCTTGTATTTTGAATATGCTCAAGGATTTCTGGGTGAGGAGAAATCCAGAAAGG 1575
Db 531 sGlyAlaSerIleLeuLeuMetLeuAsnAlaThrLeuArgaspGlyGluPheHisLysG 551
QY 1576 AATAATTCAGTACTTAAAGAGTTCAGCTATAGAAATGCTAAGAAATGATGTTGTGGAG 1635
Db 551 yValIleGluTyrLeuGlnAsnTyrAsnLeuSerAsnThrGluSerLysAspLeuTyrAs 571
QY 1636 CAGTCTGTCAATAGTGTGTTAGAAAGTGAATTTACATCTGGTGAGTTTGTCTCCGA 1695
Db 571 nSerLeuSerGlnValSerLysGlnSer----- 580
QY 1696 TCCCAAGATGACAAGTAAATGCTCGCCTTCTTGGGGGAAATGACAGAGGTCAAGAGAT 1755
Db 586 -----LeuAsnValSerGluMe 586
QY 1756 GATGACTACATGGACTCTCCAGAAAGGAATCCCTGCTGCTGGTGTAAACAGAGCGGTG 1815
Db 586 tMetAsnThrTrpThrValHisLysGlyPheProLeuValThrValLysArgAsnGlyPr 606
QY 1816 TTCACTCCGACTGCACAGAGGCGCTTCTCCAGGGGGTTCCTCCAGGAAGACCTGTAATG 1875
Db 606 oGlnValThrLeuSerGlnGluHisPheLeuLeuAsnAla-----G 620
QY 1876 GAGGCGCTCGAGGAGAGTACCTGTGCATATCCATTGACCTACTCCACGAGTTCCTC 1935
Db 620 uAsnGlyThrAspAspSerLeuTrpHisIleProLeuThrTyrValAsnAspSerCy 640
QY 1936 TAATGTGTATCCACAGA-----CACATTCTAAATCAAAACAGACAGATACTCT 1980
Db 640 sSerValLeuArgSerCysLysGlnValPheHis---LeuLysAspLysGluAlaThrLe 659
QY 1981 GGATCTACTGAAAGACAGTGGTGGTGAATTTAATGTGGACTCAAAATGTTACTACAT 2040
Db 659 uGlnLeuProGluGlnValLysTrpLeuLysPheAsnPheArgSerAspGlyPheTyrIl 679
QY 2041 CGTTCACATGAGGCTCATGATGGACCACTCAATACACAGCTGAAATCAGAACACACAC 2100
Db 679 eValHisTyrAspGluGlnGlyTrpSerAspLeuIleSerAlaLeuLysValAspValAs 699
QY 2101 ACTTCTCAGACCTAAGGACAGATAGTCTGATTCATGATGTTTTCAGTGTGTTGGTC 2160
Db 699 nValLeuProSerGluAspLysAlaAlaLeuIleAsnAsnIlePheAlaLeuSerArgLe 719
QY 2161 AGGAGACTGACCTAGACAAAGCTCTTGACATGACTTACTACCTCCAAATGAAACAG 2220
Db 719 uGlyLysValSerPheArgGlnValLeuAsnLeuMetAspTyrIleArgAsnGluThrGl 739
QY 2221 CAGCCCCGCACTTCTCGAAGCTCTGAGTTACTTGAATCGTTTACCACATGATGGACAG 2280
Db 739 uthAlaProLeuThrGluAlaLeuSerGlnLeuGlyGlnIleTyrArgLeuLeuAspLys 759
QY 2281 AAGGAATATTTTCAGATATCTCTGAAAACCTCAAGCGTTTACCTTCTTCAGTATTTTAAGCC 2340
Db 759 sArgSerAspLeuAsnLeuAlaSerSerMetThrThrTyrIleGluSerHisPheGlySe 779
QY 2341 AGTGATTCAGAGCGAACTGGATGACAGAGGCTCAGCTCGGGACAGGATGCTCCGCTC 2400
Db 779 rLeuMetGluSerGlnSerTrpGluValGluThrSerValSerLysMetThrLeuArgSe 799
QY 2401 GGCTCTCTTGAAGCTGGCTGTGACCTCAACCATGCTCTCTTGCATCCAGAAAGCTGCTGA 2460
Db 799 rAlaLeuLeuGluThrAlaCysAlaLeuAsnArgProAsnCysThrThrGlnAlaArgAr 819
QY 2461 ACTCTTCTCCAGCTGGATGGAATCCAGTGGAAAAATTAATATACCAACAGATGTTTAA 2520
Db 819 gLeuPheAspGlnTrpLeuAlaSerAsnLysThrLeuGlnIleProSerAspLeuMetAr 839
QY 2521 GATTGTGTATTTCTGTGGTGTCTCAGACAAACAGCAGGATGGAATTACCTTTTAGAGCAATA 2580

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Db 839 gThrValPheLysValAlaAlaLysThrAspGluGlyTrpSerLysLeuLeuGlySerTy 859
QY 2581 TGAAGTCTGTCAGAGTCTCAAGTCTGAAACAAACAAATCTGTATGCTTTGTCAACAGCAA 2640
Db 859 rLysHisSerIleTyrAspThrGluLysArgLysMetLeuGluAlaLeuAlaSerThrGl 879
QY 2641 GCATCAGAAAGTTACTGAAGTTAATGAACCTAGGAATGGAAGAAAGGTTTCAAGAC 2700
Db 879 nAspValArgLysIleIleTrpValLeuGlnLysSerLeuAspGlySerGluIleGlnAs 899
QY 2701 ACAGAACTTGGCACTCTCTTCATGCTGCTCCAGAGCTCCAAAGGGGACGAACTAGC 2760
Db 899 nGlnGluPheProLeuValIleHisThrValCysArgAspPheAlaGlyTyrLeuTyrAl 919
QY 2761 ATGGGATTTTGAAGAAATATGGACCCATCTCTGAAAAAATTTGACTTGGGCTCATA 2820
Db 919 aTrpAspPheMetLysGluAsnTrpGluLysIleThrGlnLysPheProIleGlySerPh 939
QY 2821 TGACATGAAGATGATCATCTCTGGCACAACAGCTCCTTTTCTCCAAAGGATAAGTTGCA 2880
Db 939 eAlaIleGlnSerIleIleThrSerThrTrpSerGlnPheSerThrLysThrHisLeuAl 959
QY 2881 AGAGTCAAACTATTTTGAATCTCTTGAAGCTCAAGGATCACATCTGGATATTTTCA 2940
Db 959 aGluValGlnAsnPheSerSerLeuGlyAlaLysGlySerGlnMetArgIleValGl 979
QY 2941 AACTGTTTGGAAACGATAACCAAAATATATAAATGCTGGAGAAAGATCTTCGCACTCT 3000
Db 979 nGluAlaIleGluThrIleLysHisAsnMetArgTrpMetGluLysAsnLeuAsnThrLe 999
QY 3001 GAGGACTTGGCTA 3013
Db 999 uGlnSerTrpLeu 1003

RESULT 10
LCAP_RAT
ID LCAP_RAT STANDARD; PRT; 1025 AA.
AC P97629; Q11009;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Leucyl-cystinyl aminopeptidase (EC 3.4.11.3) (Cystinyl aminopeptidase)
DE (Oxytocinase) (OTase) (Insulin-regulated membrane aminopeptidase)
DE (Insulin-responsive aminopeptidase) (IRAP) (Placental leucine
DE aminopeptidase) (P-LAP) (Vesicle protein of 165 kDa) (Vp165) (GP160).
GN Name=Irapp; Synonyms=Irapp, Otase;
OS Rattus norvegicus (Rat);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=Sprague-Dawley; TISSUE=Adipocyte;
RA MEDLINE=96007507; PubMed=7559527; DOI=10.1074/jbc.270.40.23612;
RA Keller S.R., Scott H.M., Mastick C.C., Abersold R., Lienhard G.E.;
RT "Cloning and characterization of a novel insulin-regulated membrane
RT aminopeptidase from Glut4 vesicles.";
RL J. Biol. Chem. 270:23612-23618(1995).
RN [2]
SEQUENCE OF 168-176; 387-399; 731-740 AND 893-905.
RX MEDLINE=94164972; PubMed=8119954;
RA Mastick C.C., Abersold R., Lienhard G.E.;
RT "Characterization of a major protein in GLUT4 vesicles. Concentration
RT in the vesicles and insulin-stimulated translocation to the plasma
RT membrane.";
RL J. Biol. Chem. 269:6089-6092(1994).
CC -1- FUNCTION: Release of an N-terminal amino acid, cleave before
CC cysteine, leucine as well as other amino acids. Degrades peptide
CC hormones such as oxytocin, vasopressin and angiotensin III, and
CC plays a role in maintaining homeostasis during pregnancy. May be
CC involved in the inactivation of neuronal peptides in the brain.
CC Cleaves Met-enkephalin and dynorphin. Binds angiotensin IV and may

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CC be the angiotensin IV receptor in the brain (By similarity).
 CC -I- CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Cys[-
 CC Xaa, in which the half-cystine residue is involved in a disulfide
 CC loop, notably in oxytocin and vasopressin.
 CC -I- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
 CC -I- SUBUNIT: Homodimer. Binds tankyrases 1 and 2 (By similarity).
 CC -I- SUBCELLULAR LOCATION: Type II membrane protein. Localized mainly
 CC in intracellular vesicles together with GLUT4. Relocalizes to the
 CC plasma membrane in response to insulin. The dileucine
 CC internalization motif and/or the interaction with tankyrases may
 CC be involved in intracellular sequestration.
 CC -I- TISSUE SPECIFICITY: Highly expressed in heart, brain, spleen,
 CC lung, kidney and white adipose tissue. Detected at lower levels in
 CC skeletal muscle and liver.
 CC -I- PTM: N-glycosylated.
 CC -I- SIMILARITY: Belongs to the peptidase M1 family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U76997; AAB19066.1; -;
 CC EMBL; U32990; AAB38021.1; -;
 CC PIR; I55441; I55441.
 CC MEROPS; M01.011; -;
 CC InterPro; IPR001930; Peptidase_M1.
 CC InterPro; IPR006025; Pept_M_Zn_BS.
 CC Pfam; PF01433; Peptidase_M1; 1.
 CC PRINTS; PR00756; ALADIPTASE.
 CC PROSITE; PS00142; ZINC_PROTEASE; 1.
 CC Amino-peptidase; Direct protein sequencing; Glycoprotein; Hydrolase;
 KW Metal-binding; Metalloprotease; Protease; Signal-anchor;
 KW Transmembrane; Zinc.
 FT DOMAIN 1 109 Cytoplasmic (Potential).
 FT TRANSMEM 110 131 Signal-anchor for type II membrane
 FT ACT_SITE 132 1025 Protein (Potential).
 FT SITE 53 54 Extracellular (Potential).
 FT SITE 76 77 Dileucine internalization motif
 FT SITE 96 101 Dileucine internalization motif
 FT METAL 464 464 Tankyrase binding (By similarity).
 FT ACT_SITE 465 465 Zinc (catalytic) (By similarity).
 FT METAL 468 468 By similarity.
 FT METAL 487 487 Zinc (catalytic) (By similarity).
 FT CARBOHYD 145 145 Zinc (catalytic) (By similarity).
 FT CARBOHYD 184 184 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 215 215 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 256 256 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 266 266 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 368 368 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 374 374 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 447 447 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 525 525 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 578 578 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 664 664 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 682 682 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 695 695 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 758 758 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 834 834 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 850 850 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 989 989 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 909 916 LMKSLDQ -> YGTTQRAW (in Ref. 1;
 FT AAB38021).
 FT CONFLICT 916 1025 Missing (in Ref. 1; AAB38021).
 SQ SEQUENCE 1025 AA; 117201 MW; 8AD3BA3A446FB5EF CRC64;

. Alignment Scores:

	Pred. No.:	3.2e-127	Length:	1025
Score:	2027.00	Matches:	402	
Percent Similarity:	61.81%	Conservative:	158	
Best Local Similarity:	44.37%	Mismatches:	310	
Query Match:	34.29%	Indels:	36	
DB:	1	Gaps:	5	
US-10-039-073-2 (1-3366) x LCAP_RAT (1-1025)				
QY	305	CMAGTAGCCACTAATGGGAACGATTTCTTGGCAGAGCTAAGGCTCCCACTGGTGGTC	364	
DB	153	ProilleAlaThrAsnGlyLysValPheProTrpAlaGlnIleArgLeuProThrAlaIle	172	
QY	365	ATTCTCTCCATTATGACCTCTTTGTCCACCCCAATCTCACCTCTCTGGACTTGTGCA	424	
DB	173	IleProGlnArgTyrGlyLeuSerLeuHisProAsnLeuThrSerMetThrPheArgGly	192	
QY	425	TCGTAGAAGATCGAAGCTCTTGGTCAGCAATGCTACCCAGTTTATCATCTTGCACAGCAA	484	
DB	193	SerValThrIleSerLeuGlnAlaLeuGlnAspThrArgAspIleIleLeuHisSerThr	212	
QY	485	GATCTTGAATATCAGTAATGCCACCTTTCAGTCAGAGGAAGATTCAGATACATGAAACCA	544	
DB	213	GlyHisAsnIleSerValThrPheMetSerAlaValSerSerGln	228	
QY	545	GGAAAGAACTGAAGCTTTTGGATTACCTGCTCATGAACAATTCACCTGCTGGTTCCA	604	
DB	229	GluLysGlnValGluIleLeuGluTyrProTyrHisGluGlnIleAlaValAlaPro	248	
QY	605	GAGAACTTACCGCTCACCTGAAATACTATGTGGCTATGAGCTTCCAAGCCAAAGTTAGGT	664	
DB	249	GluSerLeuLeuThrGlyHisAsnTyrThrLeuLysIleGluTyrSerAlaAsnIleSer	268	
QY	665	GATGGCTTGAAGGGTTTATTAAGACCATACAGAACTCTTGGTGGTGAACAGAAAT	724	
DB	269	AsnSerTyrTyrGlyPheTyrGlyIleThrTyrThrAspLysSerAsnGluLysAsn	288	
QY	725	CTTGCAAGTAACAGATTTCAGCCCAACCCAGGCAAGCTGCTTCCCTGCTTTGATGAA	784	
DB	289	PheAlaAlaThrGlnPheGluProLeuAlaAlaArgSerAlaPheProCysPheAspGlu	308	
QY	785	CGTTGTTTCAAGCCCAACTTTTCAATCAAGATACAGAGAGAGAGAGGATATTCACCTA	844	
DB	309	ProAlaPheLysAlaThrPheIleLysIleThrArgAspGluHisThrAlaLeu	328	
QY	845	TCCAACTGCAAGAGGTTAAGCAATTCAGAGGAGGCTTTTGGAGAGTCACTTT	904	
DB	329	SerAsnMetProLysLysSerSerValProThrGluGluGluLeuGlnAspGluPhe	348	
QY	905	GAAACTACTGTAAATAAGTACATACCTTGTAGCCCTACATAGTTTGTGATTTCCACTCT	964	
DB	349	SerGluSerValLysMetSerThrTyrLeuValAlaPheIleValGlyGluMetArgAsn	368	
QY	965	CTGAGTGGTCTTCACTTCATCAGGGGTCAAGGTGTTCATCATGATCCCAAGCAACGG	1024	
DB	369	LeuSerGln---AspValAsnGlyThrLeuValSerValTyrAlaValProGluLysIle	387	
QY	1025	AATCAACACATTTATGCTTTTGGAGGATCCTGAGGAGGATCTTATTTTGAAGAGTAC	1084	
DB	388	AspGlnValTyrHisAlaLeuAspThrThrValLysLeuGluGluPheTyrGlnAsnTyr	407	
QY	1085	TTTGATATCTACTATCTCTCTCAAACTGGATTTAATTTGCTATTCTGCTTTGACCT	1144	
DB	408	PheGluIleGlnTyrProLeuLysLysLeuAspLeuValAlaIleProAspPheGluAla	427	
QY	1145	GGAGCCATGGAATTTGGGCGCTCATATTATAGGAGACGCTACTGCTTTTGCACCC	1204	
DB	428	GlyAlaMetGluAsnTrpGlyLeuLeuThrPheArgGluGluThrLeuLeuTyrAspAsn	447	
QY	1205	AGACCTCTTCTCTTCCGATAACTGTGGGTACACAGAGTACATAGCCATGAGTGGCG	1264	
DB	448	AlaThrSerSerValAlaAspArgLysLeuValThrLysIleIleAlaHisGluLeuAla	467	

QY 1265 CACCAAGTGGTTGGCAACTGGTCAATGGAATGGTGAATGATATTTGGCTTAAGGAG 1324
Db 468 HisGlnTrpPheGlyAsnLeuValThrMetGlnTrpAsnAspLeuTrpLeuAsnGlu 487
QY 1325 GGTTTGGCAAAATACATGAACTTATCGCTGTTAATGCTACATATCCAGAGCTCAATTT 1384
Db 498 GlyPheAlaThrPheMetGluTyrrPheSerValGluLysIlePheLysGluLeuAsnSer 507
QY 1385 GATGACTATTTTGAATGTGTTTGAAGTAATTACAAAAGATTCATTGAATTCATCC 1444
Db 508 TyrGluAspPheLeuAspAlaArgPheLysThrMetArgLysAspSerLeuAsnSerSer 527
QY 1445 CGCCCTATCTCCAAACCGGAAACCCGAGCTCAAAATACAGGAATGTTTGATCAAGTT 1504
Db 528 HisProIleSerSerValGlnSerSerGluGlnIleGluGluMetPheAspSerLeu 547
QY 1505 TCCTATAACAAGGAGCTGTGATTGTAATGCTCAAGGATTTTCTGGGTGAGGAGAA 1564
Db 548 SerTyrrPheLysGlyAlaSerLeuLeuMetLeuLysSerTyrrLeuSerGluAspVal 567
QY 1565 TTCCAGAAGGAATAATTCACTGACTTAAGAAGTTTCAGCTATAGAAATGCTAAGATGAT 1624
Db 568 PheGlnHisAlaIleLeuTyrrLeuHisAsnHisSerTyrrAlaAlaIleGlnSerAsp 587
QY 1625 GACTTGTGAGCAGCTCTGCTCAAAATAGTTGTTTAGAAAGTATTTTACATCTGGTGAGTT 1684
Db 588 AspLeuTrpAspSerPheAsnGlu----- 595
QY 1685 TGTCAATCGGATCCCAAGATGACAAGTAACATGCTCGCTTCTGGGGGAAATGCAGAG 1744
Db 596 -----ValThrGlyLysThrLeuAsp 602
QY 1745 GTCAAAGAGATGATGACTACATGACTCTCCAGAAAGGAATCCCTCTGCTGGTGTAAA 1804
Db 603 ValLysLysMetMetLysThrTrpThrLeuGlnLysGlyPheProLeuValThrValGln 622
QY 1805 CAAGACGGGTGTTCACTCGACTGCAACAGAGCGCTTCCTCCAGGGGGTTTTCCAGGAA 1864
Db 623 ArgLysGlyThrGluLeuLeuGlnGlnGluArgPhePheProSerMet----- 639
QY 1865 GACCTGATGAGGGCCCTGCAGGAGAGGTACCTGTCGCATATCCCATTCACCTACTCC 1924
Db 640 GlnProGluIleGlnAspSerAspThrSerHisLeuTrpHisIleProIleSerTyrrVal 659
QY 1925 ACGAGTCTCTTAATGTGATCCACAGACAC-----ATTCTAAATCAAGACAGAT 1975
Db 660 ThrAspGlyArgAsnTyrrSerGluTyrrArgSerValSerLeuLeuAspLysLysSerAsp 679
QY 1976 ACTCTGGATCTACCTGAAAGACCAAGTTGGGTGAAATTTAATGTGGACTCAATGGTTAC 2035
Db 680 ValIleAsnLeuThrGluGlnValGlnTrpValLysValAsnThrAsnMetThrGlyTyrr 699
QY 2036 TACATCGTTCACTATGAGGTCATGGATGGGACCAACTCATTACACAGCTCAATCAGAAC 2095
Db 700 TyrrIleValHisTyrrAlaHisAspGlyTrpAlaAlaLeuIleAsnGlnLeuLysArgAsn 719
QY 2096 CACACACTCTCCAGACCTTAAGACAGAGTAGTCTGATTTCATGTGTTTTCAGTACTT 2155
Db 720 ProTyrrValLeuSerAspLysAspArgAlaAsnLeuIleAsnAsnIlePheGluLeuAla 739
QY 2156 GGTGAGGAGAGTACGACCTAGACAAAGCTCTTGACATGACTTACTACTCCACATGAA 2215
Db 740 GlyLeuGlyLysValProIleGlnMetAlaPheAspLeuIleAspTyrrLeuArgAsnGlu 759
QY 2216 ACAACGACCCCGCACTCTCGAAGGTCGTGAGTTACTTGGAAATCGTTTACCATGATG 2275
Db 760 ThrHisThrAlaProIleThrGluAlaLeuPheGlnThrAspLeuIleTyrrAsnLeuLeu 779
QY 2276 GACACAGGAATATTTCAAGATATCTCTGAAAACCTCAAGCGCTTACTCTTCAGTATTTT 2335
Db 780 GluLysLeuGlyHisMetAspLeuSerSerArgLeuValThrArgValHisLysLeuLeu 799
QY 2336 AAGCCAGTGTGACAGGCAAGCTGGAGTGACAAAGGGCTCAGTCTGGGACAGGATGCTC 2395

Db 800 GlnAsnGlnIleGlnGlnGlnTrpThrAspGluGlyThrProSerMetArgGluLeu 819
QY 2396 CGCTCGGCTCTCTTGAAGCTGGCTGTGACCTGACCTGAACCACTGCTCTTGGCATCCAGAAAGCT 2455
Db 820 ArgSerAlaLeuLeuGluPheAlaCysAlaHisSerLeuGluAsnCysThrThrMetAla 839
QY 2456 GCTGAATCTCTTCCAGTGGATGGAATCCAGTCCGAAATTAATATATACCAACAGATGTT 2515
Db 840 ThrLysLeuPheAspGlyTrpMetAlaSerAsnGlyThrGlnSerLeuProThrAspVal 859
QY 2516 TTAAGATTGTTGTTTCTGGGTCTCAGACACAGCAGGATGGAATTAATCTTTAGAG 2575
Db 860 MetThrThrValPheLysValGlyAlaArgThrGluLysGlyTrpLeuPheLeuPheSer 879
QY 2576 CAATATCAACTGTCAATGTCAAGTCTGAAGCTGGAACAAACAAAATTTCTGTATGCTTTGTCAACG 2635
Db 880 MetTyrrSerSerMetGlySerGluAlaGluLysAspLysIleLeuGluAlaLeuAlaSer 899
QY 2636 AGCAAGCATCAGGAAAGTTACTGAAGTTAATGAATAGGAATGGAAGGAAGGTTATC 2695
Db 900 SerAlaAspAlaHisLysLeuTyrrTrpLeuMetLysSerSerLeuAspGlyAspIleIle 919
QY 2696 AAGACACAGAACTGGCAGCTCTCTTCATCGGATTGCCAGACGTCCTCAAGGGGCGACAA 2755
Db 920 ArgThrGlnLysLeuSerLeuIleIleArgThrValGlyArgGlnPheProGlyHisLeu 939
QY 2756 CTACATGGGATTTTGAAGAGAAATTTGGACCCATCTTCTGAAAAATTTGACTTTGGGC 2815
Db 940 LeuAlaTrpAspPheValLysGluAsnTrpAsnLysLeuValHisLysPheHisLeuGly 959
QY 2816 TCATATCACAATAAGATGATCATCTCTGGCACACAGCTCACTTTCTTCCAAAGGATAAG 2875
Db 960 SerTyrrThrIleGlnSerIleValAlaGlySerThrHisLeuPheSerThrLysThrHis 979
QY 2876 TTGCAAGAGGTGAACATATTTTGAATCTCTTGAGGCTCAAGGATCACATCTCGATATT 2935
Db 980 LeuSerGluValGlnGluPhePheGluAsnGlnSerGluAlaThrLeuGlnLeuArgCys 999
QY 2936 TTTCAAACTGTTCTGGAACGATAACCAAAAATATAAAATGGCTGGAGAAATCTTCCG 2995
Db 1000 ValGlnGluAlaPheGluValIleGluLeuAsnIleGlnTrpMetAlaArgAsnLeuLys 1019
QY 2996 ACTCTGAGGACTGGCTA 3013
Db 1020 ThrLeuThrLeuTrpLeu 1025
RESULT 11
Q8C129 PRELIMINARY; PRT; 1025 AA.
AC Q8C129;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched library, clone:473249D18 product:INSULIN-REGULATED MEMBRANE
DE AMINOPEPTIDASE IRAP homolog.
GN Name=Lnpep;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

Qy	1385	GATGACTATTTTGGAAATGTGTGTTTGAAGTAATTAACAAAGATTCAATTGAATTCATCC	1444
Db	508	TyrGluaspPheLeuAaspAlaAArgpPheLysThrMetArgLysAepSerLeuAenSerSer	527
Qy	1445	CGCCCTATCTCCAAACCAGCGGAAACCCGACTCAAATACAGGAAATGTTTGGATGAAGTT	1504
Db	528	HisProIleSerSerSerValGlnSerSerGluGlnIleGluGluMetPheAepSerLeu	547
Qy	1505	TCCTATAACAAGGGAGCTTGTTATTTTGAATATGCTCAAGGATTTTTCGGGTGAGGAGAA	1564
Db	548	SerTyrPheLysGlyAlaSerLeuLeuLeuMetLeuLysSerTyrLeuSerGluAepVal	567
Qy	1565	TTCCAGAAAGCAATAATTCAGTACTTAAGAGAGTTTCAGCTATAGAAATGCTAAGAATGAT	1624
Db	568	PheArgHisAlaValIleLeuTyrLeuHisAenHisSerTyrAlaIleGlnSerAep	587
Qy	1625	GACTTGTGGAGCAGCTGTCAAATAGTGTGTTAGAAAGTAGTATTTACATCTGGTGGAGTT	1684
Db	588	AspLeuTrpAepSerPheAen-----	594
Qy	1685	TGTCATTCGGATCCCAAGATGACAAGTAAACATGCTCGCCTTCTCGGGGAAAAATGCAGAG	1744
Db	595	-----GluValThrAepLysThrLeu-----	602
Qy	1745	GTCAAAGAGATGATGACTACATGCACTCTCCAGAAAGGAATCCCCCTGCTGGTGGTTAAA	1804
Db	603	ValLysLysMetMetLysThrTrpThrLeuGlnLysGlyPheProLeuValThrValGln	622
Qy	1805	CAAGACGGGTGTTCACTCCGACTCCAACAGGAGCGCTCTCCAGGGGGTTTCCAGGAA	1864
Db	623	ArgLysGlyThrGluLeuLeuLeuGlnGlnGluArgPhe-----	639
Qy	1865	GACCTGAATGGAGGGCCCTGCAGGAGGTACTGTGGCATATCCCAATTGCACTACTCC	1924
Db	640	GlnProGluSerGlnProSerAepThrSerHisLeuTrpHisIleProLysSerTyrVal	659
Qy	1925	ACGNGTTCCTTAATGTGATCCACAGACAC-----ATTCTAAATCAAGACAGAT	1975
Db	660	ThrAepGlyArgAenTyrSerGluTyrArgSerValSerLeuLeuAepLysLysSerAep	679
Qy	1976	ACTCTGATCTACCTGAAAGACACAGTGGGTGAAATTTAATGGAGCTCAAAATGGTTAC	2035
Db	680	ValIleAenLeuThrGluGlnValGlnTrpValLysValAenSerAenMetThrGlyTyr	699
Qy	2036	TACATCGTTCATATGAGGGTCATGGATGGGACCAACTCATATTACAGCTGAATCAGAAC	2095
Db	700	TyrIleValHisTyrAlaHisAepAepTrpThrAlaLeuIleAenGlnLeuLysAArgAen	719
Qy	2096	CACACACTTCTCAGACCTTAGGCAGAGTAGGCTCTGATTTCATGATGTTTTCAGCTAGTT	2155
Db	720	ProTyrValLeuSerAepLysAepArgAlaAenLeuIleAenAenIlePheGluLeuAla	739
Qy	2156	GGTCAGGGAGACTGACCCCTAGACAAAGCTCTTCACATGACTTACTACTCCCAACATGAA	2215
Db	740	GlyLeuGlyLysValProLeuAArgMetAlaPheAepLeuIleAepTyrLeuLysAenGlu	759
Qy	2216	ACAAGACGCCCCGACCTTCTCGAAGGTCTCAGATTACTTGGAAATCGTTTTACCACATGATG	2275
Db	760	ThrHisThrAlaProIleThrGluAlaLeuPheGlnThrAenLeuIleTyrAenLeuLeu	779
Qy	2276	GACAGAGGAATATTTCCAGATATCTCTGAAAACTCAAGCGTTTACCTTCTTCAGTATTTT	2335
Db	780	GluLysLeuGlyHisMetAepLeuSerSerArgLeuValAlaArgValHisLysLeuLeu	799
Qy	2336	AAGCCAGTGTATGACGCAAGCTGGAGTGACAAAGGGCTCAGTCTCGGGACAGAGTCCTC	2395
Db	800	GlnAenGlnIleGlnGlnThrTrpThrAepGluGlyThrProSerMetArgGluLeu	819
Qy	2396	CGCTCGGCTCTCTTGAAGCTGGCCCTGTGACCTGAAACCATGCTCTCTGCATCCAGAAAGCT	2455
Db	820	ArgSerAlaLeuLeuGluPheAlaCysAlaHisSerLeuGluAenCysThrThrMetAla	839

Qy	2456	GCTGAAC	TCTTCC	CCAGTGG	AAATTA	TATACCA	CAGATG	TT	2511			
Db	840	ThrAsn	LeuPhe	AspSer	TrpMet	AlaSer	AsnGly	ThrGln	SerLeu	ProThr	AspVal	859
Qy	2516	TTAAAG	ATTCGT	TATCTC	TGGGTG	CTCAG	CAACAC	GACGAG	TATGGA	TTACCT	TTT	2575
Db	860	MetVal	ThrVal	PheLys	ValGly	AlaArg	ThrGlu	LysGly	TrpLeu	PheLeu	PheSer	879
Qy	2576	CAATAT	GAACTG	CAATG	CTCAAG	TGCTGA	CAACAA	CAAAAT	TCTCTG	TATGCT	TTGTCA	2635
Db	880	MetTy	SerSer	MetGly	SerGlu	AlaGlu	LysAsn	LysIle	LeuGlu	AlaLeu	AlaSer	899
Qy	2636	AGCAG	CATCAG	GAAGA	TTTACT	GAAGTT	TAATTC	AACTAG	GATGG	AGAAAG	GTTC	2695
Db	900	SerGlu	AspVal	HisLys	LeuTy	TrpLeu	MetLys	SerSer	LeuAsp	GlyAsp	Ile	919
Qy	2696	AAGAC	ACAGAA	CTTGG	CAGCTC	CTCTTC	ATGCAT	TGCCAG	ATGCC	AGACGT	CCAAAG	2755
Db	920	ArgThr	GlnLys	LeuSer	LeuIle	IleArg	ThrVal	GlyArg	HisPhe	ProGly	HisLeu	939
Qy	2756	CTAGCA	TGGGAT	TTTCTG	TAAGAG	AAAAAT	TTGAC	CCCATC	TCTCTG	AAAAAA	TTTGAT	2815
Db	940	LeuAla	TrpAsp	PheVal	LysGlu	AsnTrp	AsnLys	LeuVal	HisLys	PheHis	LeuGly	959
Qy	2816	TCATAT	GACATAT	AGGATG	ATCATC	TCTCGG	CACAA	CAGCTC	ACTTTCT	TCTC	CAAGGAT	2875
Db	960	SerTy	ThrIle	GlnSer	IleVal	AlaGly	SerThr	HisLeu	PheSer	ThrLys	ThrHis	979
Qy	2876	TTGCAG	AGGCTG	AAACTAT	TTTTTGG	ATCTCT	TGAGG	CTCTTG	AGGCTC	CAAGNT	CACATC	2935
Db	980	LeuSer	GluVal	GlnAla	PhePhe	GluAsn	GlnSer	GluAla	ThrLeu	LysLeu	ArgCys	999
Qy	2936	TTTCAA	ACTGTT	CTGGA	ACGATA	ACCA	AAAAAT	TATAAA	TATGGCT	TGGAG	AGAAAT	2995
Db	1000	ValGln	GluAla	LeuGlu	ValIle	GlnLeu	AsnIle	GlnTrp	MetVal	ArgAsn	LeuLys	1019
Qy	2996	ACTCTG	AGGACT	TGGCTA	3013							
Db	1020	ThrLeu	SerGln	TrpLeu	1025							

RESULT 12

LCAP HUMAN

ID

LCAP HUMAN

STANDARD;

PRT; 1025 AA.

AC

Q9UIQ6; Q00769; Q15145; Q9UIQ7;

DT

28-FEB-2003 (Rel. 41, Created)

DT

28-FEB-2003 (Rel. 41, Last sequence update)

DT

25-OCT-2004 (Rel. 45, Last annotation update)

DE

Leucyl-cystinyl aminopeptidase (EC 3.4.11.3) (Cystinyl aminopeptidase) (Oxytocinase) (otase) (Insulin-regulated membrane aminopeptidase) (Insulin-responsive aminopeptidase) (IRAP) (Placental leucine aminopeptidase) (p-LAP).

GN

Name=LNPEP; Synonyms=OTASE;

OS

Homo sapiens (Human).

OC

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX

NCBI_TaxID=9606;

RN

[1]

RP

SEQUENCE FROM N.A., AND SEQUENCE OF 160-168; 319-332; 615-624;

RP

635-647; 798-814 AND 870-880.

RC

TISSUE=Placenta;

RC

MEDLINE=961132882;

RA

Rogi T., Tsujimoto M., Nakazato H., Mizutani S., Tomoda Y.;

RT

"Human placental leucine aminopeptidase/oxytocinase. A new member of type II membrane-spanning zinc metalloproteinase family.";

RL

J. Biol. Chem. 271:56-61(1996).

RN

[2]

RP

SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RC

TISSUE=Placenta;

RC

MEDLINE=97320624; PubMed=9177475; DOI=10.1016/S0167-4781(97)00036-5;

RA

Laustsen P.G., Rasmussen T.E., Petersen K., Pedraza-Diaz S.;

RA

Moestrup S.K., Gliemann J., Sottrup-Jensen L., Kristensen T.;

RT

"The complete amino acid sequence of human placental oxytocinase.";

RL

Biochim. Biophys. Acta 1352:1-7(1997).

[3] SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).
RP MEDLINE=20223264; PubMed=10759854;
RA Raamussen T.E., Pedraza-Diaz S., Hardre R., Lausteen P.G.,
RA Carrion A.G., Kristensen T.;
RT "Structure of the human oxytocinase/insulin-regulated aminopeptidase
RT gene and localization to chromosome 5q21.";
RL Eur. J. Biochem. 267:2297-2306 (2000).
[4]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RX MEDLINE=21286092; PubMed=11389728;
RA Matsunoto H., Nagaoka T., Hattori A., Rogi T., Tsuruoka N.,
RA Mizutani S., Tsujimoto M.;
RT "Expression of placental leucine aminopeptidase/oxytocinase in
RT neuronal cells and its action on neuronal peptides.";
RL Eur. J. Biochem. 268:3259-3266 (2001).
[5]
RP CHARACTERIZATION.
RX MEDLINE=92117646; PubMed=1731608;
RA Tsujimoto M., Mizutani S., Adachi H., Kimura M., Nakazato H.,
RA Tomoda Y.;
RT "Identification of human placental leucine aminopeptidase as
RT oxytocinase.";
RL Arch. Biochem. Biophys. 292:388-392 (1992).
[6]
RP FUNCTION.
RX MEDLINE=21623680; PubMed=11707427; DOI=10.1074/jbc.C100512200;
RA Albiston A.L., McDowell S.G., Matsacos D., Sim P., Clune E., L.M.,
RA Mustafa T., Lee J., Mendelsohn F.A., Simpson R.J., Connolly L.M.,
RA Chai S.Y.;
RT "Evidence that the angiotensin IV (AT(4)) receptor is the enzyme
RT insulin-regulated aminopeptidase.";
RL J. Biol. Chem. 276:48623-48626 (2001).
CC -I- FUNCTION: Release of an N-terminal amino acid, cleave before
CC hormones such as oxytocin, vasopressin and angiotensin III, and
CC plays a role in maintaining homeostasis during pregnancy. May be
CC involved in the inactivation of neuronal peptides in the brain.
CC Cleaves Met-enkephalin and dynorphin. Binds angiotensin IV and may
CC be the angiotensin IV receptor in the brain.
CC -I- CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Cys-|-
CC Xaa, in which the half-cystine residue is involved in a disulfide
CC loop, notably in oxytocin and vasopressin.
CC -I- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -I- SUBUNIT: Homodimer. Binds tankyrase 1 and 2.
CC During pregnancy serum levels are low in the first trimester, rise
CC progressively during the second and third trimester and decrease
CC rapidly after parturition. In brain only the membrane-bound form
CC is found. The protein resides in intracellular vesicles together
CC with GLUT4 and can then translocate to the cell surface in
CC response to insulin and/or oxytocin. Localization may be
CC determined by dileucine internalization motifs, and/or by
CC interaction with tankyrase.
CC -I- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Comment=Experimental confirmation may be lacking for some
CC isoforms;
CC Name=1;
CC IsoId=O9UIQ6-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O9UIQ6-2; Sequence=VSP_005448;
CC Name=3;
CC IsoId=O9UIQ6-3; Sequence=VSP_005449;
CC -I- TISSUE SPECIFICITY: Highly expressed in placenta, heart, kidney
CC and small intestine. Detected at lower levels in neuronal cells in
CC the brain, in skeletal muscle, spleen, liver, testes and colon.
CC -I- PTM: The pregnancy serum form is derived from the membrane-bound
CC form by proteolytic processing.
CC -I- PTM: N-glycosylated.
CC -I- SIMILARITY: Belongs to the peptidase M1 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D50810; BAA09436.1; ALT_INIT.
DR EMBL; U62768; AAB66672.1; -
DR EMBL; U62769; AAB66673.1; -
DR EMBL; AJ131023; CAB61646.1; JOINED.
DR EMBL; AJ131025; CAB61646.1; JOINED.
DR EMBL; AJ131026; CAB61646.1; JOINED.
DR EMBL; AJ131027; CAB61646.1; JOINED.
DR EMBL; AJ131028; CAB61646.1; JOINED.
DR EMBL; AJ131029; CAB61646.1; JOINED.
DR EMBL; AJ131030; CAB61646.1; JOINED.
DR EMBL; AJ131031; CAB61646.1; JOINED.
DR EMBL; AJ131032; CAB61646.1; JOINED.
DR EMBL; AJ131033; CAB61646.1; JOINED.
DR EMBL; AJ131034; CAB61646.1; JOINED.
DR EMBL; AJ131035; CAB61646.1; JOINED.
DR EMBL; AJ131036; CAB61646.1; JOINED.
DR EMBL; AJ131037; CAB61646.1; JOINED.
DR EMBL; AJ131038; CAB61646.1; JOINED.
DR EMBL; AJ131039; CAB61646.1; JOINED.
DR EMBL; AJ131025; CAB94753.1; -
DR EMBL; AJ131026; CAB94753.1; JOINED.
DR EMBL; AJ131027; CAB94753.1; JOINED.
DR EMBL; AJ131028; CAB94753.1; JOINED.
DR EMBL; AJ131029; CAB94753.1; JOINED.
DR EMBL; AJ131030; CAB94753.1; JOINED.
DR EMBL; AJ131031; CAB94753.1; JOINED.
DR EMBL; AJ131032; CAB94753.1; JOINED.
DR EMBL; AJ131033; CAB94753.1; JOINED.
DR EMBL; AJ131034; CAB94753.1; JOINED.
DR EMBL; AJ131035; CAB94753.1; JOINED.
DR EMBL; AJ131036; CAB94753.1; JOINED.
DR EMBL; AJ131037; CAB94753.1; JOINED.
DR EMBL; AJ131038; CAB94753.1; JOINED.
DR EMBL; AJ131039; CAB94753.1; JOINED.
DR PIR; A59383; A59383.
DR MEROPS; M01.011; -
DR Genew; HGNC:6656; LNRP.
DR MTM; 151300; -
DR InterPro; IPR001930; Peptidase M1.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF01433; Peptidase M1; 1.
DR PRINTS; PR00756; ALADIPTASE.
KW PROSITE; PS00142; ZINC PROTEASE; 1.
KW Alternative splicing; Aminopeptidase; Direct protein sequencing;
KW Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Polymorphism;
KW Protease; Signal-anchor; Transmembrane; Zinc.
FT DOMAIN 1 110 Cytoplasmic (Potential).
FT TRANSMEM 111 131 Signal-anchor for type II membrane
FT protein (Potential).
FT DOMAIN 132 1025 Extracellular (Potential).
FT SITE 53 54 Dileucine internalization motif
FT SITE 76 77 Dileucine internalization motif
FT SITE 96 101 Tankyrase binding.
FT SITE 154 155 Cleavage (in pregnancy serum form).
FT METAL 464 464 Zinc (catalytic) (By similarity).
FT ACT_SITE 465 465 By similarity.
FT METAL 468 468 Zinc (catalytic) (By similarity).
FT METAL 487 487 Zinc (catalytic) (By similarity).
FT CARBOHYD 145 145 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 184 184 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 215 215 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 256 256 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 266 266 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 368 368 N-linked (GlcNAc...) (Potential).

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FT CARBOHYD 374 374 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 448 448 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 525 525 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 578 578 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 598 598 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 664 664 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 682 682 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 760 760 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 834 834 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 850 850 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 999 999 N-linked (GlcNAc...) (Potential)
FT VARSPLIC 1 14 Missing (in isoform 2).
FT VARSPLIC 1 19 Missing (in isoform 3).
FT VARSPLIC 1 19 /FTIG=VSP 005449.
FT VARIANT 763 763 A -> T (in dbSNP:2303138).
FT CONFLICT 66 66 V -> D (in Ref. 2).
FT CONFLICT 386 386 N -> K (in Ref. 1).
FT CONFLICT 892 892 K -> Q (in Ref. 1).
FT CONFLICT 944 944 F -> L (in Ref. 1).
SQ SEQUENCE 1025 AA; 117318 MW; 0A2763F9CE62753A CRC64;

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Alignment Scores:

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Pred. No.: 2,418-125 Length: 1025
Score: 1999.00 Matches: 400
Percent Similarity: 61.81% Conservative: 160
Best Local Similarity: 44.15% Mismatches: 310
Query Match: 33.81% Indels: 36
DB: 1 Gaps: 6

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US-10-039-073-2 (1-3366) x LCAP_HUMAN (1-1025)

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QY 305 CAGTAGCCACTAAATGGGACGATTCTCTGGCAGGAGTAAGCTCCCGAGTGTGTC 364
DB 153 PropheAlaThrAsnGlyLysLeuPheProIleAlaGlnIleArgLeuProThrAlaVal 172
QY 365 ATTCTCTCCATATGACCTTTTCCACCCCAATCTCACCTCTCTGGAGTTGTCGA 424
DB 173 ValProLeuArgTyrGluLeuSerLeuHisProAsnLeuThrSerMetThrPheArgGly 192
QY 425 TCTGAGAGATCGAAGTCTTGTCAGCAATGTCACCGAGTTATCATCTTCGACAGCAAA 484
DB 193 SerValThrIleSerValGlnAlaLeuGlnValThrTrpAsnIleIleLeuHisSerThr 212
QY 485 GATCTTGAATCACCAGATGCCACCTTCAGTCAGAGGAAGATTCAAGATACATGAACCA 544
DB 213 GlyHisAsnIleSerArgValThrPheMetSerAlaValSerSerGln----- 228
QY 545 GGAAGAAGAACTGAAAGTTTGTAGTTTACCCTGCTCATGAACAAATTCGCTGCTTCCA 604
DB 229 GluLysGlnAlaGluLeuGluTyrAlaTyrHisGlyGlnIleAlaIleValAlaPro 248
QY 605 GAGAACTTACGCTCCTCAGCTGAATACATATGTCGCTATGAGCTTCCAGCCCAAGTAGT 664
DB 249 GluAlaLeuLeuAlaGlyHisAsnTyrThrLeuLysIleGluTyrSerAlaAsnIleSer 268
QY 665 GATGCTTTGAGGGTTTATAAAAGCACATACAGAACTCTTGGTGGTGAACAAAGAAATT 724
DB 269 SerSerTyrTyrGlyPheTyrGlyPheSerTyrThrAspGluSerAsnGluLysLysTyr 288
QY 725 CTTGAGTAACAGATTTTGTAGCCCAACCCAGGACGATGGCTTTCCCTTGTCTTGTGATGAA 784
DB 289 PheAlaAlaThrGlnPheGluProLeuAlaAlaArgSerAlaPheProCysPheAspGlu 308
QY 785 CGGTGTTCAAGCCCACTTTTCAATCAAGATACGAAGAGAGAGAGAGCATATTCACATA 844
DB 309 ProAlaPheLeuAlaThrPheIleIleIleIleIleIleIleIleIleIleIleIleIle 328
QY 845 TCCACATGCCCAAGGTTTAAAGCAATTCGAATTTGAAGGAGGTCTTTTGAAGATCATT 904
DB 329 SerAsnMetProLysSerSerValValLeuAspGlyLeuValGlnAspGluPhe 348

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QY 905 GAAACTACTGTAAATAAGTAGTACATACCTTGTAGCTTACATAGTTTGTGATTTCCACTCT 964
DB 349 SerGluSerValLysMetSerThrTyrLeuValAlaPheIleValGlyGluMetLysAsn 368
QY 965 CTGAGTGGCTTCACTTATCATCAGGGGTCAAGGTGTCATCATGATCCCAAGCAAAACGG 1024
DB 369 LeuSerGln----AspValAsnGlyThrLeuValSerIleTyrAlaValProGluAsnIle 387
QY 1025 AATCAAAACACATATTGCTTTTCAGGCATCACTCAAGCTACTTGTATTTTATGAAAGTAC 1084
DB 388 GlyGlnValHisTyrAlaLeuGluThrThrValLysLeuLeuGluPhePheGlnAsnTyr 407
QY 1085 TTTGATATCTACTATCACTCTCCAACTGATTAATTAATGCTATTCCTGACTTTGCCACT 1144
DB 408 PheGluIleGlnTyrProLeuLysLeuAspLeuValAlaIleProAspPheGluAla 427
QY 1145 GGAGCCATGGAAAATTGGGGCTCATATACATATAGGAGAGCTGACTCTTTTTCACCCC 1204
DB 428 GlyAlaMetGluAsnTrpGlyLeuLeuThrPheArgGluGluThrLeuLeuTyrAspSer 447
QY 1205 AAGACCTCTTCTGCTTCCGATAAACTGTGGGTCCACAGAGTCATAGCCCATCAACTGGCG 1264
DB 448 AsnThrSerSerMetAlaAspArgLysLeuValThrLysIleIleAlaHisGluLeuAla 467
QY 1265 CACCAGTGGTTGGCAACCTGTCACAAATGGAATGGTGGAAATGATATTTGGCTTAAGAG 1324
DB 468 HisGlnTrpPheGlyAsnLeuValThrMetLysTrpTrpAsnAspLeuTrpLeuAsnGlu 487
QY 1325 GGTTTTCCMAATACATGGAATCTATCGCTGTTAATGCTACATATCCAGAGTCGAATTT 1384
DB 488 GlyPheAlaThrPheMetGluTyrPheSerLeuGluLysIlePheLysGluLeuSerSer 507
QY 1385 GATGACTATTTTGAATGTGTGTTTGAAGTAATACAAAAGATTTCATTAATTCATCC 1444
DB 508 TyrGluAspPheLeuAspAlaArgPheLysThrMetLysLysAspSerLeuAsnSerSer 527
QY 1445 CGCCTATCTCCAAACAGCGGAAACCCCGACTCAATATACAGGAATATTTGTATGAAGTT 1504
DB 528 HisProIleSerSerSerValGlnSerSerGluGlnIleGluGluMetPheAspSerLeu 547
QY 1505 TCCTATAACAGGAGCTTGTATTTTGAATATGCTCAAGGATTTTCTGGGTGAGAGAAA 1564
DB 548 SerTyrPheLysGlySerSerLeuLeuMetLeuLysThrTyrLeuSerGluAspVal 567
QY 1565 TTCCAGAAAGAAATAATTTCAGTACTTAAAGAAAGTTTCAGTATAGAAATGCTAAGATGAT 1624
DB 568 PheGlnHisAlaValValLeuTyrLeuHisAsnHisSerTyrAlaSerIleGlnSerAsp 587
QY 1625 GACTTGTGGAGCAGCTGTGTCAAATAGTGTGTTTGAAGAGTATTTTACATCTGGTGGAGTT 1684
DB 588 AspLeuTrpAspSerPheAsn----- 594
QY 1685 TGTCTATTCGGATCCCAAGATGACAAGTAACATGCTCGCTTTTCTGGGGGAAAATGCACAG 1744
DB 595 -----GluValThrAsnGlnThrLeu-----Asp 602
QY 1745 GTCAAGAGAGATGATGACTTACATGCACTCTCCAGAAAAGAAATCCCTGCTGCTGTTAAA 1804
DB 603 ValLysArgMetMetLysThrTrpThrLeuGlnLysGlyPheProLeuValThrValGln 622
QY 1805 CAAGACGGGTGTTTCACTCCGACTGCAACAGAGAGCGCTTCTCCAGGGGGTTTTCCAGAA 1864
DB 623 LysLysGlyLysGluLeuPheIleGlnGlnIleArgPhePheLeuAsnMet----- 639
QY 1865 GACCTCAATGGAGGGCCCTGCAGGAGAGGTACTGTCGATATCCCATTTGACCTACTCC 1924
DB 640 LysProGluIleGlnProSerAspThrSerTyrLeuTrpHisIleProLysSerTyrVal 659
QY 1925 ACAGAGTTCTTCTTAATGTGATCCACAGACAC-----ATTCTTAAATCAAGACAGAT 1975
DB 660 ThrGluGlyArgAsnTyrSerLysTyrGlnSerValSerLeuLeuAspLysLysSerGly 679
QY 1976 ACTCTGATCTACTCTGAAAAGACCAGTGTGGTGAAATTTAATGTGGACTCAATGGTTTAC 2035

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Db	680	ValIleAsnLeuThrGluGluValLeuTrpValLysValAsnIleAsnMetAsnGlyTyr	699
Qy	2036	TACATCGTTCACATGAGGGTCATGGAGTGGGACCAACTCATATTACACAGCTGCAATCAGAAC	2095
Db	700	TyrIleValHisTyrAlaAspAspTrpGluAlaLeuIleHisGlnLeuLysIleAsn	719
Qy	2096	CACACACTTCACACACTTAGGCACAGAGTAGGTCTGATTCAATCATGATGTTCTTACGCTAGTT	2155
Db	720	ProTyrValLeuSerAspLysAspArgAlaAsnLeuIleAsnAsnIlePheGluLeuAla	739
Qy	2156	GGTCAGGAGACTGACCCCTAGACAAAGCTCTTGACATGACTTACTACTCTCCACATGAA	2215
Db	740	GlyLeuGlyLysValProLeuLysArgAlaPheAspLeuIleAsnTyrLeuGlyAsnGlu	759
Qy	2216	CAAAGCAGCCCCGACCTTCTCGAAGGTCCTGAGTTTACTTGGAAATCGTTTTTACCACATGATG	2275
Db	760	AsnHisThrAlaProIleThrGluAlaLeuPheGlnThrAspLeuIleTyrAsnLeuLeu	779
Qy	2276	GACAGAGGAATATTTCCAGATATCTCTGAAAACTCAAGCGTTTACCTTCTTCAGTATTTT	2335
Db	780	GluLysLeuGlyTyrMetAspLeuAlaSerArgLeuValThrArgValPheLysLeuLeu	799
Qy	2336	AAGCCACTGATTTCAGACGCAAGCTGGAGTGCACAAAGGGCTCAGTCTCGGCACAGGATGCTC	2395
Db	800	GlnAsnGlnIleGlnGlnThrTrpThrAspGluGlyThrProSerMetArgGluLeu	819
Qy	2396	CGCTCGGCTCTTTCGAAGCTGGCTGTGACCTGAAACCATGCTCTTCGATCTCCAGAAAGCT	2455
Db	820	ArgSerAlaLeuLeuGluPheAlaCysThrHisAsnLeuGlyAsnCysSerThrThrAla	839
Qy	2456	GCTGAACTCTTCTCCAGTGGATGGAATCCAGTGGAAAAATTAATATACCAACAGATGTT	2515
Db	840	MetLysLeuPheAspAspTrpMetAlaSerAsnGlyThrGlnSerLeuProThrAspVal	859
Qy	2516	TTAAAGATTGTGTAATCTGTGGGTGCTCAGACAAACAGACAGATGGAATTAACCTTTTAGAG	2575
Db	860	MetThrThrValPheLysValGlyAlaLysThrAspLysGlyTrpSerPheLeuLeuGly	879
Qy	2576	CAATATGAACTGTCAATGTCAAGTGTGAAACAAACAAAAATCTGTATGCTTTGTCAACG	2635
Db	880	LysTyrIleSerIleGlySerGluAlaGluLysAsnLysIleLeuGluAlaLeuAlaSer	899
Qy	2636	AGCAAGCATCAGGAAAAAGTTACTGAACTTAATTGAACTAGGAATGGAGGAAAGGTTATC	2695
Db	900	SerGluAspValArgLysLeuTyrTrpLeuMetLysSerSerLeuAsnGlyAspAsnPhe	919
Qy	2696	AAGCACAGAACTTGGCAGCTCTCTTCATCGCATTCGCCAGCGTCCAAAGGGCAGCAA	2755
Db	920	ArgThrGlnLysLeuSerPheIleIleArgThrValGlyArgHisPheProGlyHisLeu	939
Qy	2756	CTAGCATGGGATTTTGTAAAGAGAAAATGGACCCATCTCTCGAAAAAATTTGACTGGGC	2815
Db	940	LeuAlaTrpAspPheValLysGluAsnTrpAsnLysLeuValGlnLysPheProLeuGly	959
Qy	2816	TCATATGACATAAGGATGATCATCTTGGCACACACAGCTCACTTTTCTTCCAGGATTAAG	2875
Db	960	SerTyrThrIleGlnAsnIleValAlaGlySerThrTyrLeuPheSerThrLysThrHis	979
Qy	2876	TTGCAACAGGTGAACATATTTTGAATCTCTTGAGGCTCAAGGATCACATCTCGGATATT	2935
Db	980	LeuSerGluValGlnAlaPhePheGluAsnGlnSerGluAlaThrPheArgLeuArgCys	999
Qy	2936	TTTCAAACTGTCTTGGAAACGATAACCAAAAAATATAAAATAGCTGGGAGAGAATCTTCCG	2995
Db	1000	ValGlnGluAlaLeuGluValIleGlnLeuAsnIleGlnIleTrpMetGluLysAsnLeuLys	1019
Qy	2996	ACTCTGAGGACTTGGCTA 3013	
Db	1020	SerLeuThrTrpTrpLeu 1025	


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QY 2735 AGACGCTCAAGGGGCGAGCACTAGCATGGGATTTTGTAAAGAGAAAAATTCGACCCATCTT 2794
DB 594 ArgAsnProValGlyTyrProLeuAlaTrpLysPheLeuArgGluAsnTrpAsnLysLeu 613
QY 2795 CTGAAAAAATTTGACTTGGGCTCATATGACATAGGATGATCACTCTCGGCACACACAGCT 2854
DB 614 ValGlnLysPheGluLeuGlySerSerSerileAlaHisMetValMetGlyThrThrAsp 633
QY 2855 CACTTTTCTCCAGGATAGTTCGAAGAGTGGAACATATTTTGAATCTCTTGAGGCT 2914
DB 634 GlnPheSerThrArgAlaArgLeuGluGluValLysGlyPhePheSerSerLeuLysGlu 653
QY 2915 CAAGGATCACATCTGGATATTTTCAAACTGTTCTGGAAAGGATAACCAAAAATATAAAA 2974
DB 654 AsnGlySerGlnLeuArgCysValGlnGlnThrIleGluThrIleGluGluAsnIleArg 673
QY 2975 TGGCTGGAGAGAAATCTCCGACTCTGAGGACTTGGCTA 3013
DB 674 TrpMetAspLysAsnPheAspLysIleArgLeuTrpLeu 686
RESULT 14
Q6PCG5
ID Q6PCG5 PRELIMINARY; PRT; 997 AA.
AC Q6PCG5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE MG69084 protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Chordata; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Amphibia; Batrachia;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=23289257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
initiative.";
RL Dev. Dyn. 225:384-391 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX Klein S., Strausberg R.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC059334; AAHS9334.1; -;
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DR GO; GO:0004179; F:membrane alanyl aminopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001930; Peptidase.M1.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF01433; Peptidase.M1; 1.
DR PRINTS; PR00756; ALADIPTASE.
DR PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.
SQ SEQUENCE 997 AA; 113619 MW; 460E0EC8895D2A14 CRC64;

Alignment Scores:
Pred. No.: 1,35e-115 Length: 997
Score: 1853.50 Matches: 394
Percent Similarity: 57.52% Conservative: 176
Best Local Similarity: 39.76% Mismatches: 316
Query Match: 31.35% Indels: 105
DB: 2 Gaps: 19

US-10-039-073-2 (1-3366) x Q6PCG5 (1-997)
QY 137 ATAGATTTCATGTTCCATTCTCTGCAATGGTTAATTC-----CACAGAAA--- 184
DB 78 MetSerPheMetAsnArgSerSerGlyLeuArgAsnSerAlaThrAsnTyrArgGlnVal 97
QY 185 -----CNAATGTTTAACTTACAGAGAGATTTTACTGCTTAAACGCGCATC 229
DB 98 ArgAspGlyLeuCysProValSerProArgThrValIleValCysValValVal 117
QY 230 TTGCCCAATATGCAATTTGTTCTCAGTCTCAGTGCCCTAGTATATCACTTCACCTGAG 289
DB 118 IleIleAlaValSerLeuValThrValValValValValValValValValVal 137
QY 290 GAT-----CCTGGGCTTTCCAGTAGCAGTAAATGGGAA 325
DB 138 GluGlyCysHisGluLysLysAlaMetGluLeuValTyrProIleAlaArgAsnGlyLys 157
QY 326 CGATTTCTTGGCAGGAGCTTAAGCTCCCGAGTGGTGCTCATCTCTCCATTTATGACCTC 385
DB 158 ValPheProTrpAlaIleSerArgLeuProAsnSerIleLysProIleHisTyrIleLeu 177
QY 386 TTTGTCCACCCCAATCTCACTCTCTGGACTTTGTTGCATCTCAGAGAGATCGAAGTCTTG 445
DB 178 ThrLeuHisProAsnMetThrThrMetSerPheThrGlyThrValGlnIleAsnLeuAsn 197
QY 446 GTCAGCAATGCTACCCAGTTTATCATCTTCACAGCAAGAGATCTTGAAATCAGCAATGCC 505
DB 198 IleThAlaArgSerLysAsnIleValLeuHisSerSerAspLeuArgIleThrLysAla 217
QY 506 ACCCTTCAGTCAGAGGAGATTCAAGATACATCAAGAACCCAGGA-----AAGAAGCTG 556
DB 218 AsnVal-----LeuValProGlyGlyThrThrMetAspAla 229
QY 557 AAGTTTGTGAGTTACCTGCTCATGACAAATTTGCACTGCTGTTCCAGAGAACTTACG 616
DB 230 GluValLeuGluTyrProArgPheGluGluIleAlaIleIleSerProGluSerLeu--- 248
QY 617 CTTCACTGAAATACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 676
DB 249 ProLysGlyAsnCysLeuLeuThrIleGluTyrThrSerAsnPheSerSerSerTyrTyr 268
QY 677 GGGTTTTATAAAGCATACATACAACTCTTGGTGGTGAACAAAGAAATCTTTCGAGTAACA 736
DB 269 GlyPheTyrLysIleAspTyrMetAspLysGlySerLys---ArgSerLeuAlaIleThr 287
QY 737 GATTTTGGCCCAACCCAGGACCATGCTGCTTCCCTTGTTCATGAAACCGTTGTTCAAA 796
DB 288 GlnPheGluProThrAlaAlaArgLysAlaPheProCysPheAspGluProAlaPheLys 307
QY 797 GCCAACTTTTCAATCAAG---ATACGAAGAGAGAGAGGAGCATATTTGCACATCATCAACATG 853
DB 308 SerThrPheGlnIleAsnIleIleArgLysAspGluSerMetIleSerLeuSerAsnMet 327
QY 854 CCAAAGTTTAAGCAATTTGACTTGAAGGAGGCTTTTGGAGAGGCTTTTGGAGAGACTTACT 913
DB 854 CCAAAGTTTAAGCAATTTGACTTGAAGGAGGCTTTTGGAGAGGCTTTTGGAGAGACTTACT 913
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Db 328 ProLysAlaLysThrSerThrThrAsnAspGlyLeuLeuLeuAspGluPheSerThrSer 347
Qy 914 GTAAAAATGAGTACATACCTGTAGCCTACATAGTTTGTGATTTCCACTCTCTGAGTGGC 973
Db 348 ValLysMetSerThrTyrLeuValAlaPheIleValGlyAspIleLysAsnThrThrArg 367
Qy 974 TTCACCTTCATCAGGGGTCAAGGTGCTCCTATGCTATGCATCCCGACAGAACCGAATCAACA 1033
Db 368 GluThrAsnAspThrLeu---ValSerValTyrThrValProGluLysThrAspGlnVal 386
Qy 1034 CATTATGCTTTCAGGACCTACGAGTACTTGTATTTTATGAAAAGTACTTTCATATC 1093
Db 387 LysTyrAlaLeuAspSerAlaValLysLeuLeuAspPheTyrSerAsnTyrTyrGlyIle 406
Qy 1094 TACTATCCACTCTCCAACTCGATTAATTTGCTATTCCTGACTTTGACCTCGAGCCATG 1153
Db 407 LysTyrProLysLeuLysLeuAspLeuValAlaIleProAspPheGlnAlaAlaMet 426
Qy 1154 GAAATTTGGGGCTCATTACATATAGGAGAGCTCACTGCTTTTGTAGCCCAAGCCTCT 1213
Db 427 GluAsnTrpGlyLeuIleThrPheArgGluThrSerLeuLeuTyrAsnGluAspSerSer 446
Qy 1214 TCTGCTTCCGATAAACTGTGGGTCAACAGAGTCATAGCCCATCACTGGCGCACCAGTGG 1273
Db 447 SerIleLysAspLysGlnThrIleAlaIleAlaHisGluLeuThrHisGlnTrp 466
Qy 1274 TTGGCAACTGGTCACAATGGAATGGTGAATGATATTTGGCTTAAGAGAGGTTTGC 1333
Db 467 PheGlyAsnLeuValThrMetGluTrpTrpAsnAspLeuTrpLeuAsnGluGlyPheAla 486
Qy 1334 AAATACATGGAATTATCCGCTTAATGCTACATATCCAGAGCTGCAATTTGATCACTAT 1393
Db 487 ThrTyrMetGluTyrPheSerValSerSerLeuPheProGluLeuAsnSerGluAsnSer 506
Qy 1394 TTTTGTGAATGTGTGTGAAGTAAATACAAAAGATTCAATGAATTCATCCGCCCTATC 1453
Db 507 PheLeuLysMetArgPheMetAlaLeuLysLysAspSerLeuAsnAlaSerHisProIle 526
Qy 1454 TCCAAACGACGGAAACCCGACTCAATACAGGAAATGTTTGTAGTAAAGTTTCCTATAAC 1513
Db 527 SerThrAspIleArgSerProGluGlnIleGluMetPheAsnAspLysSerTyrIle 546
Qy 1514 AAGGAGCTGTATTTGTAATGCTCAAGGATTTTCTGGGTGAGAGAGAAATTCAGAAA 1573
Db 547 LysGlyAlaSerIleLeuLeuMetLeuLysThrPheLeuSerGluAspMetPheHisLeu 566
Qy 1574 GGAATAATTCAGTACTTAAAGAAGTTCAGCTATAGAAATGCTAAGAAATGATGACTTGTGG 1633
Db 567 SerIleArgSerTyrLeuGlnSerHisGlnTyrGlySerThrThrSerAspSerLeuTrp 586
Qy 1634 AGCAGCTGTCAATAGTTGTTTGAAGAAAGTATTTACATCTCGTGGAGTTTGTCAATCG 1693
Db 587 AspSerLeuAsn----- 590
Qy 1694 GATCCCAAGATGACAAGTAAACATGCTCGCTTCTGGGGGAAAATGACAGAGTCAAGAG 1753
Db 591 -----ValValThrLysGluAsnProAsnValLysAsn 601
Qy 1754 ATGATGACTACATGACTCTCCAGAAAGGAATCCCTGCTGGTGTGTTAAACAGACGGG 1813
Db 602 MetMetLysThrTrpThrGlnLysAlaGlyTyrProLeuValThrAlaLeuArgLysGly 621
Qy 1814 TGTTCACCTCCGACTGCAACAGGAGCGCTTCCTCCAGGGGGTTTTCCAGGAAGACCCCTGAA 1873
Db 622 GluGluIleThrValArgGlnGluArgPheLeuArgSerThr-----LysProAsp 638
Qy 1874 TGGAGGGCCCTCAGAGAGGTACTGCTGGGATATCCCATTTGACCTATCCACAGATTCT 1933
Db 639 ---HisAlaThrAsnAlaSerThrValTrpHisIleProLeuThrTyrValThrLysLys 657
Qy 1934 TCTAATGTGATCCACAGA-----CACATTCTAAATCAAGACAGATACT 1978
Db 658 CysAsnGlyValAspProAspCysAspLysValTyrLeuLeuLysAlaProThrGlyThr 677

Qy 1979 CTGATCTACCTGAAAAGACACGAGTGGTGAATTTTAATGTGGACTCAAAATGGTTACTAC 2038
Db 678 IleAsnValSerSerGluPheProTrpValLysPheAsnValAsnMetThrGlyTyrTyr 697
Qy 2039 ATCGTTCACTATGAGGGTCATGGATGGGACCAACTCATTACACAGCTGCAATCAGAACAC 2098
Db 698 IleValAspTyrGlyAlaAspGlyTrpAspAlaLeuIleGluGlnLeuHisGargAspHis 717
Qy 2099 ACATTTCTCAGACCTCAAGGACAGAGTAGTCTGATTTTCATATGATGTGTTTTCAGCTAGT 2158
Db 718 ThrValLeuHisSerSerAspArgAlaAsnLeuIleHisAspIlePheMetLeuAlaGly 737
Qy 2159 GCAGGAGACTGACCTTAGACAAAGCTCTTGACATGACTTACTCTCAACATCAAAACA 2218
Db 738 ValGlyLysValProLeuAlaLysAlaPheLysLeuLeuGlyTyrLeuValAsnGluThr 757
Qy 2219 AGCAGCCCGCAGCTTCTCGAAGGTCGTAGTTACTTGGAAATCGTTTTCACAC----- 2269
Db 758 AspSerAlaProIleIleGlnAla-----LeuHisGlnPheTyrHisIleArgGly 774
Qy 2270 ATGATGGACAGAGGAATATTTTCAGATATCTCTGAAAACCTCAAGCGTTACTCTTCAG 2329
Db 775 IleLeuLeuLysArgGlyLeuAspAspLeuSerAspLysLeuMetGluArgGlyLeuAsp 794
Qy 2330 TATTTTAAAGCCAGTGTGACAGCAAGCTGGAGTGACAAAGGCTCAGTCTGGGACAGG 2389
Db 795 LeuLeuAsnAsnThrLeuIleLysGlnThrTrpLysAspGluGlyThrLeuAlaGluArg 814
Qy 2390 ATGCTCCGCTCGGCTCTCTTGAAGCTGGCTGACCTGACCTGAACCATGCTCTTCGATCCAG 2449
Db 815 GluLeuArgThrSerLeuLeuAspPheAlaCysSerAsnGlyValLeuAsnCysLeuAsp 834
Qy 2450 AAAGCTGCTGAATCTCTCCAGTGGATGGAATCCAGTGGAAAATTAATATATACCAACA 2509
Db 835 ArgAlaThrGluLeuPheAsnSerTrp-----ArgPheAsnGluThrArgIleProSer 852
Qy 2510 GATCTTTTAAAGATTGTATTTCTGGGTGCTCAGACACAGCAGGATGGAATTTACCTT 2569
Db 853 AspValIleAsnIleValPheLysValGlyThrLysThrThrGluGlyTyrThrPheLeu 872
Qy 2570 TTAGAGCAATGAATGCTCAATGCTCAAGTCTCAACAAACAAATTTCTGTATGCTTTG 2629
Db 873 ArgArgArgTyrAspSerSerIleTyrGluSerGluLysSerLysIleLeuGluAlaLeu 892
Qy 2630 TCAACGAGCAAGCATCAGGAAAAGTTACTGAAGTTAATTAAGTGAATAGGAAAGAAAG 2689
Db 893 AlaSerThrAspAsnAlaLysAspLeuGlnGlyLeuMetGlnGluSerLeuAlaGlyGly 912
Qy 2690 GTTATCAAGACACAGAACTTGGCAGCTCTCTCTCATCGGATTCGACAGCTCCAAAGGG 2749
Db 913 SerIleArgSerGlnGluLeuProAsnValIleSerPheIleCysArgArgSerProGly 932
Qy 2750 CAGCAACTAGCATGGGATTTTGAAGAGAAAATTTGGACCCCATCTCTGAAAATAATTCAC 2809
Db 933 TyrLeuLeuAlaTrpAsnPheValLysGlnAsnTrpAsnLeuIleThrGlnLysLeu--- 951
Qy 2810 TTGGGCTCATATGACATAAGGATGATCATCTCTGGCACACAGCTCACTTT-----TCT 2863
Db 952 -----LeuHisPhePheAsnSer 957
Qy 2864 TCCAAGGATAAGTTGCAAGAGGTGAAACTATTTTGAATCTCTTTGAGGCTCAAGGATCA 2923
Db 958 ThrLysGluLysSerArgGluValTrpTyrValLysGluAla----- 971
Qy 2924 CATCTGGATATTTTCAAACTGTTCTGAAAACGATAACCAAAATATATAAATGCTCGAG 2983
Db 972 -----LeuGluThrIleLysLeuAsnIleLysTrpMetLys 983
Qy 2984 AAGAACTCTCCGACTCTGAGGACTTTGGCTAATG 3016
Db 984 AsnAsnLeuAspSerLeuLysThrTrpLeuLeu 994

RESULT 15

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Q8WVJ4
ID Q8WVJ4 PRELIMINARY; PRT; 350 AA.
AC Q8WVJ4;2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE LRAP protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RN SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017927; AAH17927.1; -.
DR MEROPS; M01.024; -.
DR GO; GO:0004179; F:membrane alanyl aminopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR PRINTS; PR00756; ALADIP756.
SQ SEQUENCE 350 AA; 40060 MW; 5234F40276A81253 CRC64;

Alignment Scores:
Pred. No.: 9.67e-105 Length: 350
Score: 1690.00 Matches: 322
Percent Similarity: 99.69% Conservative: 2
Best Local Similarity: 99.08% Mismatches: 1
Query Match: 28.59% Indels: 0
DB: 2 Gaps: 0

US-10-039-073-2 (1-3366) x Q8WVJ4 (1-350)
Qy 146 ATGTTTCATCTCTCGAATGGTTAAATTCACAGAAAACCAATGTTTAACTTCACAGA 205
Db 1 MetPheHisSerSerAlaMetValAsnSerHisArgLysProMetPheAsnIleHisArg 20
Qy 206 GGATTTTACTGCTTAACAGCCATCTGCCCCAATATGCAATTTGTTCTCAGTTCTCAGTG 265
Db 21 GlyPheTyrCysLeuThrAlaIleLeuProGlnIleCysIleCysSerGlnPheSerVal 40
Qy 266 CCATCTAGTTATCACTTCACTAGGATCCTGGGCGCTTTCAGTAGCCACTAATGGGGA 325
Db 41 ProSerSerTyrHisPheThrGluAspProGlyAlaPheProValAlaThrAsnGlyGlu 60
Qy 326 CGATTTCTGGCAGGAGCTAAGGCTCCCGAGTGTGTGCTATTCCTCCCAATTATGACCTC 385
Db 61 ArgPheProTyrGlnGluLeuArgLeuProSerValValIleProLeuHisTyrAspLeu 80
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Qy 386 TTTGTCCACCCCAATCTCACCTCTCTGGACTTTTGTTCATCTCAGAAAGATCGAAGTCTTG 445
Db 81 PheValHisProAsnLeuThrSerLeuAspPheValAlaSerGlnIleGluValLeu 100
Qy 446 GTCCAGCAATGCTACCCAGTTTATCATCTTTCACAGCAAAAGATCTTGAATACAGAAATGCC 505
Db 101 ValSerAsnAlaThrGlnPheIleIleLeuHisSerLysAspLeuGluIleThrAsnAla 120
Qy 506 ACCCTTCAGTCAGGAGAAATTCAAGATACATCAATAAACCAGGAAAAGAACTGAAAGTTTGG 565
Db 121 ThrLeuGlnSerGluGluAspSerLysTyrMetLysProGlyLysGluLeuLysValLeu 140
Qy 566 AGTTACCTCGCTCATCAACAAATTGACCTGCTGCTTCCAGAGAAACTTACGCTCCACTG 625
Db 141 SerTyrProAlaHisGluGlnIleAlaLeuValProGlnLysLeuThrProHisLeu 160
Qy 626 AAATACTATGTGGCTATGGACTTCCAAAGCCAAAGTTAGGTAGTGGCTTTGAAGGTTTAT 685
Db 161 LysTyrTyrValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTyr 180
Qy 686 AAAGACATACAGAACTCTTGTGTGTGTAACAGAAATCTTCCAGTAACAGATTTTGAG 745
Db 181 LysSerThrTyrArgThrLeuGlyGlyGluThrArgIleLeuAlaValThrAspPheGlu 200
Qy 746 CCAACCCAGGCGCATGGCTTTCCCTTGTGTTGATGAACCGTGTGTTCAAGGCCAACTTT 805
Db 201 ProThrGlnAlaArgMetAlaPheProCysPheAspGluProLeuPheLysAlaAsnPhe 220
Qy 806 TCAATCAAGATACGAAAGAGAGAGAGCGCATATTCGCACTATCCAAACATGCCAAAGGTTAAG 865
Db 221 SerIleLysIleArgArgGluSerArgHisIleAlaLeuSerAsnMetProLysValLys 240
Qy 866 ACATTTGAACTTGAAGAGGCTCTTTTGGAGAGATCACTTTGAAACTACTGTAAAAATGAGT 925
Db 241 ThrIleGluLeuGluGlyGlyLeuLeuGluAAspHisPheGluThrThrValLysMetSer 260
Qy 926 ACATACCTTGTAGCCTACATAGTTTCTGATTTCCACTCTCTGAGTGGCTTCACCTTCATCA 985
Db 261 ThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThrSerSer 280
Qy 986 GGGGTCAAGGTGTCCATCTATGCAATCCCGAGACAAACGGAATCAAAACACATTATGCTTTG 1045
Db 281 GlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyrAlaLeu 300
Qy 1046 CAGGCATCACTGAAGCTACTGATTTTATGAAAGTACTTTTCATATCTACTATCCACTC 1105
Db 301 GlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyrProLeu 320
Qy 1106 TCCAAAACCTGGATTTA 1120
Db 321 SerLysLeuGlyMet 325

Search completed: September 26, 2005, 07:43:04
Job time : 634.604 secs
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target for diagnosis and treatment in aminopeptidase-related disorders
and for identifying modulators of therapeutic use.

Claim 9; Fig 1; 92pp; English.

The invention relates to a novel human aminopeptidase, designated aminopeptidase 17867 (AAB60299) and to cDNA encoding aminopeptidase 17867 (AAB27148). Human aminopeptidase 17867 contains a neutral zinc metalloproteinase zinc-binding region signature motif at residues 367-376, and an M1 aminopeptidase signature motif at residues 334-338. The invention also relates to host cells comprising human aminopeptidase 17867 DNA, the preparation of the protein, an antibody which binds to the protein, methods of detection of the protein, methods of modulating activity of the protein, and methods of identifying modulators of protein activity. Aminopeptidase 17867 proteins and nucleic acids are useful as targets for diagnosis and treatment in aminopeptidase-related diseases. Such diseases include a wide variety of lung disorders (e.g., pulmonary embolism, pulmonary hypertension, emphysema, bronchial asthma) and colon disorders (e.g., diarrhoea, dysentery, Crohn's disease, ulcerative colitis). In particular, they may be used in the diagnosis and treatment of breast and colon carcinoma, lung carcinoma (especially squamous cell carcinoma), and insulin-related disorders such as diabetes. The aminopeptidase 17867 proteins are also useful in drug screening methods to identify modulators of activity, and for raising antibodies for use in diagnosis and treatment. The present sequence represents human aminopeptidase 17867

SQ Sequence 960 AA;

Alignment Scores:

Pred. No.: 0 Length: 960
Score: 5052.00 Matches: 960
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.45% Indels: 0
DB: 4 Gaps: 0

US-10-039-073-2 (1-3366) x AAB60299 (1-960)

QY 146 ATGTTCCGATCTTCTGCATGGTAAATTCACAGAAACCAATGTTAACTTCACAGA 205
Db 1 MetPheHisSerSerAlaMetValAsnSerHisArgLysProMetPheAsnIleHisArg 20
QY 206 GGATTTTACTGCTTAACAGCCATCTGCCCAATATATGCATTTGCTTCAGTCTCAGTG 265
Db 21 GlyPheTyrCysLeuThrAlaIleLeuProGlnIleCysIleCysSerGlnPheSerVal 40
QY 266 CCATCTAGTTATCACTTCACCTGAGGATCCTGGGCTTTCCAGTAGCCACTAAATGGGAA 325
Db 41 ProSerSerTyrHisPheThrGluAspProGlyAlaPheProValAlaThrAsnGlyGlu 60
QY 326 CGATTTCTTCGCGAGGAGCTAAGCTCCCGAGTGGTTCATCTCTCCATTATGACCTC 385
Db 61 ArgPheProTrpGlnGluLeuArgLeuProSerValValIleProLeuHisTyrAspLeu 80
QY 386 TTGTGCCACCCCAATCTCACCTCTGAGCTTTGTCATCTCGAAGAGATCGAAGTCTTG 445
Db 81 PheValHisProAsnLeuThrSerLeuAspPheValIleSerGluLysIleGluValLeu 100
QY 446 CTCAGCAATGTACCCAGTTTATCATCTTGTCAGCAGCAAGATCTTGAATCACGAATGCC 505
Db 101 ValSerAsnAlaThrGlnPheIleLeuHisSerLysAspLeuGluIleThrAsnAla 120
QY 506 ACCCTTCAGTCAGGAGGATTCAGATACATGAACCAAGAAAGAACTGAAAGTTTGTG 565
Db 121 ThrLeuGlnSerGluGluAspSerArgTyrMetLysProGlyLysGluLeuLysValLeu 140
QY 566 AGTTACCCCTGCTCATCAACAAATGCACTGCTGGTTCAGAGAACTTACGCCCTCAGCTG 625
Db 141 SerTyrProAlaHisGluGlnIleAlaLeuLeuValProGluLysLeuThrProHisLeu 160
QY 626 AAATACTATGTGGCTATGGACTTCCAGCCCAAGTTAGTGTAGTGGCTTTGAAGGTTTAT 685

Db 161 LysTyrTyrValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTyr 180
QY 686 AAAAGCAGCATACAGAACTCTTGGTGGTGAACAAAGAAATTTCTGCAGTAACAGATTTTGAG 745
Db 181 LysSerThrTyrArgThrLeuGlyGlyGluThrArgIleLeuAlaValThrAspPheGlu 200
QY 746 CCAACCCAGGACGACGATGGCTTCCCTTGTCTTGTAGTAACCGTGTGTTCAAGGCCAACTTT 805
Db 201 ProThrGlnAlaArgMetAlaPheProCysPheAspGluProLeuPheLysAlaAsnPhe 220
QY 806 TCAATCAAGATACGAAGAGAGACGACATATTGCATATCCAAACATGCCAAAGGTTAAG 865
Db 221 SerIleLysIleArgArgGluSerArgHisIleAlaLeuSerAsnMetProLysValLys 240
QY 866 ACATATGAATTCGAAGAGGTCTTTTGGAGATACACTTTGAAACTACTGTAAAAATCAGT 925
Db 241 ThrIleGluLeuGlyGlyLeuLeuGluAspHisPheGluThrThrValLysMetSer 260
QY 926 ACATACCTTGTAGCTACATAGTTTGTGATTTCACACTCTCTGAGTGGCTTCACTTCATCA 985
Db 261 ThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThrSerSer 280
QY 986 GGGGTCAAGGTGTCCATCTATGCATCCCAACAGAAACGGAAATCAACACATATGCTTTG 1045
Db 281 GlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyrAlaLeu 300
QY 1046 CAGGCATCACTGAGCTACTTGTGATTTTATGAAGTACTTTTCATATCTACTACTCCACTC 1105
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QY 1106 TCCAAACTCGATTAAATTTGCTATTCTGACCTTGTGCACCTCGAGCCATGGAATTTGGGC 1165
Db 321 SerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsnTrpGly 340
QY 1166 CTCATTACATATAGGAGACGTCACTGCTTTTGTGACCCCAAGACCTTCTTCGCTTCGAT 1225
Db 341 LeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAlaSerAsp 360
QY 1226 AAATGTTGGTCCACGAGCTAGCCCATGAAGTGGCGCACCGAGTGGTTGGCAACCTG 1285
Db 361 LysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeu 380
QY 1286 GTCACAAATGAATGGTGGAAATGATTTTGGCTTAAAGAGGGTTTGCAAAATACATGGAA 1345
Db 381 ValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyrMetGlu 400
QY 1346 CTTATCGCTGTTAATGCTACATATCCAGAGCTCCAAATTTGATGACTATTTTTTGAATGTG 1405
Db 401 LeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeuAsnVal 420
QY 1406 TGTGTTGAAGTAAATTAACAAAGATTCATTAATTCATCCCGCCTATCTCCAAACACGCG 1465
Db 421 CysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLysProAla 440
QY 1466 GAAACCCCGACTCAAGGAAATGTTTGTAGTAAGATTTCTTATTAACCAAGGGAGCTTGT 1525
Db 441 GluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGlyAlaCys 460
QY 1526 ATTTTGAATATGCTCAAGGATTTTTCGGGTGAGAGAAATTCAGAAAGGAATAATTCAG 1585
Db 461 IleLeuAsnMetLeuLysAspPheLeuGlyGluLysPheGlnLysGlyIleGln 480
QY 1586 TACTTAAAGAGTTCAGCTATAGAAATGCTAAGAATGACTTGTGGAGCAGTCTCTCA 1645
Db 481 TyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspLeuTrpSerSerLeuSer 500
QY 1646 AATAGTTGTTTGAAGAGTGAATTTTACATCTGGTGGAGTGTTCATTCGGATCCCAAGATG 1705
Db 501 AsnSerCysLeuGluSerAspPheThrSerGlyValCysHisSerAspProLysMet 520
QY 1706 ACAAGTAACTGCTCGCTTTCGGGGGAAATTCAGAGGTCAAGAGATGATGACTACA 1765
Db 521 ThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGluValLysGluMetMetThrThr 540

CC such as anorexia, dysphagia; cardiovascular disorder such as
 CC atherosclerosis, vasculitis; autoimmune/inflammatory disorder such as
 CC acquired immune deficiency syndrome (AIDS), asthma; cell proliferative
 CC disorder such as actinic keratosis, cirrhosis; developmental disorder
 CC such as epilepsy, anaemia; epithelial disorder such as allergic contact
 CC dermatitis, eczema; neurological disorder such as Alzheimer's disease,
 CC dementia and reproductive disorder such as infertility and teratogenesis.
 CC PRTS DNA is useful for creating 'knockin' humanised animals (pigs) or
 CC transgenic animals (mice or rats) to model human disease. PRTS DNA is
 CC also in use for gene therapy. PRTS and its immunogenic fragments are
 CC useful for screening libraries of compounds in several drug screening
 CC assays. PRTS is useful for analysing the proteome of a tissue or cell
 CC type

XX Sequence 960 AA;

Alignment Scores:
 Pred. No.: 0 Length: 960
 Score: 5052.00 Matches: 960
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 85.45% Indels: 0
 DB: 4 Gaps: 0

US-10-039-073-2 (1-3366) x AAE04879 (1-960)

QY 146 ATGTTCCATTCTTCGCAATGGTAAATTCACACAGAAAACCAATGTTTAAACATTCACAGA 205
 DB 1 MetPheHisSerSerAlaMetValAsnSerHisArgLysProMetPheAsnIleHisArg 20
 QY 206 GGATTTTACTGCTTAAACAGCCATCTGCCCCAAATATGCATTGTTCTTCAGTCTCAGTG 265
 DB 21 GlyPheTyrCysLeuThrAlaIleLeuProGlnIleCysIleCysSerGlnPheSerVal 40
 QY 266 CCATCTAGTTATCACTTCACGTAGAGCTCGGGCTTCCAGTAGCCATGACCAATATGGGGAA 325
 DB 41 ProSerSerTyrHisPheThrGluAspProGlyAlaPheProValAlaThrAsnGlyGlu 60
 QY 326 CGATTTCTCGCAGGAGCTAAGGCTCCCGAGTGGTGCATCTCTCCATTATGACCTC 385
 DB 61 ArgPheProThrGlnGluLeuArgLeuProSerValValIleProLeuHisTyrAspLeu 80
 QY 386 TTGTGCCACCCCAATCTCACCTCTCTGGACTTTGTGTCATCTGAGAGATCGAAGTCTTG 445
 DB 81 PheValHisProAsnLeuThrSerLeuAspPheValAlaSerGluLysIleGluValLeu 100
 QY 446 GTCAGCAATGCTACCCAGTTTATCATCTTGACAGCAAGATCTTGAATCACCAGATGCC 505
 DB 101 ValSerAsnAlaThrGlnPheIleLeuHisSerLysAspLeuGluIleThrAsnAla 120
 QY 506 ACCCTTCAGTCAGAGGAAGATTCAAGATACATGAATCAACAGGAAAAGAACTGAAAGTTTGT 565
 DB 121 ThrLeuGlnSerGluLysAspSerArgTyrMetLysProGlyLysGluLeuLysValLeu 140
 QY 566 AGTTACCTGCTCATGAACAAATTCGACTGCTGGTTCCAGAGAAACTTACGCCCTCACCTG 625
 DB 141 SerTyrProAlaHisGluGlnIleAlaLeuLeuValProGluLysLeuThrProHisLeu 160
 QY 626 AAATACTATGTGGCTATGACATTCACAGCCAGTAGGTAGTGATGGCTTTGAAGGGTTTAT 685
 DB 161 LysTyrTyrValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTyr 180
 QY 686 AAAAGACATACAGAACTCTTGGTGGTGAACAAGAATCTTTCAGTAAACAGATTTTGTAG 745
 DB 181 LysSerThrTyrArgThrLeuGlyGlyGluThrArgIleLeuAlaValThrAspPheGlu 200
 QY 746 CCAACCCAGGACGCATGGCTTTCCCTTGGCTTTGATGAACCGTGTGTTCAAAGCCAACTTT 805
 DB 201 ProThrGlnAlaArgMetAlaPheProCysPheAspGluProLeuPheLysAlaAsnPhe 220
 QY 806 TCATCAAGATACCAAGAGAGAGGAGCATATTCGACTATCCACATGCCCAAGGTTAAG 865
 DB 221 SerIleLysIleArgGluSerArgHisIleAlaLeuSerAsnMetProLysValLys 240

QY 866 ACAATTGAACTTGAAGGAGGTCTTTTGGAAAGATCACCTTTGAAACTACTGTAAAAATCAGT 925
 DB 241 ThrIleGluLeuGluGlyLeuLeuGluAspHisPheGluThrThrValLysMetSer 260
 QY 926 ACATACCTTGTAGCCTACATAGATTGTTGATTTTCCACTCTCTGAGTGGCTTCACATTCATCA 985
 DB 261 ThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThrSerSer 280
 QY 986 GGGGTCAAGTGTCCATCTATGATCCCCAGACAAACGGGAATCAACACACATTAATGCTTTG 1045
 DB 281 GlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyrAlaLeu 300
 QY 1046 CAGGCATCACTGAAGCTTACTTGTATTTTATGAAAGTACTTTTCATATCTACTACTCACTC 1105
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 QY 1166 CTCATTACATATAGGGAGAGCTCACTGCTTTTGGACCCCAAGACCTCTTCTGCTCCGAT 1225
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 QY 1226 AAACTGTGGGTCAACAGAGTCATAGCCCATGAACTGGCGCACAGTGGTTTGGCAACCTG 1285
 DB 361 LysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeu 380
 QY 1286 GTCACAAATGGAATGGTGAATGATATTTGGCTTTAAGAGGGTTTGCAAAATACATGGAA 1345
 DB 381 ValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyrMetGlu 400
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 DB 401 LeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeuAsnVal 420
 QY 1406 TGTTTTGAAGTAATTAACAAAGATTTCATGAAATTCATCCCGCCCTATCTCCAAACACAGCG 1465
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 QY 1466 GAAACCCCGACTCAATACAGGAAATGTTTGTGATGAAGTTTCCATTAAACAGGGAGCTTGT 1525
 DB 441 GluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGlyAlaCys 460
 QY 1526 ATTTTCAATATGCTCAAGGATTTTCTGGGTGAGGAGAAATTCAGAGAAAGAAATAATTCAG 1585
 DB 461 IleLeuAsnMetLeuLysAspPheLeuGlyGluGluLysPheGlnLysGlyIleIleGln 480
 QY 1586 TACTTAAAGAAAGTTTCAGCTATAGAAATGCTAAGAATGATGACTTGTGGAGCAGTCTGTCA 1645
 DB 481 TyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspAspLeuTrpSerSerLeuSer 500
 QY 1646 AATAGTTGTTTGAAGAGTGAATTTATCTGTTGGAGTTTGTTCATTCCGGATCCCAAGATG 1705
 DB 501 AsnSerCysLeuGluSerAspPheThrSerGlyValCysHisSerAspProLysMet 520
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 DB 521 ThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGluValLysGluMetMetThrThr 540
 QY 1766 TGGACTCTCCAGAAAGAAATCCCTCTGCTGGTGGTGGTGTGTTTAAACAAAGACGGGTTCACCTCGA 1825
 DB 541 TrpThrLeuGlnLysGlyIleProLeuLeuValLysGlnAspGlyCysSerLeuArg 560
 QY 1826 CTCGAACAGAGGCGCTTCTCCAGGGGGTTTTCAGAGAGACCCCTGATAGAGGGCCCTG 1885
 DB 561 LeuGlnGlnGluArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArgAlaLeu 580
 QY 1886 CAGGAGAGGTACCTGTGGCATATCCCACTTGCACCTACTCCACGAGTCTTCTTAATGTGATC 1945
 DB 581 GlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerThrSerSerAsnValIle 600

```
QY 1946 CACAGACACATCTTAAATCAAGACAGATACCTCGGATCTACCTGAAAAGACCAAGTTGG 2005
Db |||||||
QY 601 HieArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThrSerTrp 620
Db |||||||
QY 2006 GTGAATTTAATGTGACATCAAAATGTTACTACATCGTTCTACTATGAGGTCATGATGG 2065
Db |||||||
QY 621 VallysPheAsnValAspSerAsnGlyTrpTyrIleValHisIleGluGlyHisGlyTrp 640
Db |||||||
QY 2066 GACCAACTCATTTACACAGCTGAATCAGAACCAACACACTTCTCAGACCTAAAGACAGAGTA 2125
Db |||||||
QY 641 AspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAspArgVal 660
QY 2126 GGTCTGATTCATGATGTTTTCAGCTAGTGTGTGAGGAGACTGACCTAGACAAAGCT 2185
Db |||||||
QY 661 GlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAspLysAla 680
QY 2186 CTTGACATGACTTACTTACCTCAACATGAACAGCAGCCCGCACTTCTCGAAGGTCTG 2245
Db |||||||
QY 681 LeuAspMetThrTyrTrpLeuGlnHisGluThrSerSerProAlaLeuLeuGluGlyLeu 700
QY 2246 AGTTACTTTGGAATCGTTTACCACATGATGAGCAGAGGAATATTTTCAGATATCTCTGAA 2305
Db |||||||
QY 701 SerTyrLeuGluSerPheTyrHisMetMetAspArgArgAsnIleSerAspIleSerGlu 720
QY 2306 AACCTCAAGCGTTACCTTCTCAGTATTTTAAGCCAGTGTGACAGCAAGCTGGAGT 2365
Db |||||||
QY 721 AsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSerTrpSer 740
QY 2366 GACAAGGGCTCAGTCTGGACAGGATGCTCGGCTCTCTCAAGCTGGCCGTGCAC 2425
Db |||||||
QY 741 AspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAlaCysAsp 760
QY 2426 CTGAACCATCTCTTTCATCCAGAAAGCTGCTGAACTCTTCTCCAGTGGATGGAATCC 2485
Db |||||||
QY 761 LeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMetGluSer 780
QY 2486 AGTGAATAATTAATATATACCAACAGATGTTTAAAGATGTGTATTTCTGTGGGTCTCAG 2545
Db |||||||
QY 781 SerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrSerValGlyAlaGln 800
QY 2546 ACAACAGCAGAGTGAATTTACCTTTTACAGCAATATGAATCTCAATGTCAAGTCTCAA 2605
Db |||||||
QY 801 ThrThrAlaGlyTrpAsnTyrLeuLeuGluGlnTyrGluLeuSerMetSerSerAlaGlu 820
QY 2606 CAAACAAAATCTCTATGCTTTGTCAACGAGCAAGCATCAGAAAAGTTACTGAAGTTA 2665
Db |||||||
QY 821 GlnAsnLysIleLeuTyrAlaLeuSerThrSerLysHisGlnGluLysLeuLysLeu 840
QY 2666 ATTGAATAGGAATGGAAGGAAGTTATCAAGACACAGAACTTGGCAGCTCTCTTCAAT 2725
Db |||||||
QY 841 IleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaAlaLeuLeuHis 860
QY 2726 GCGATTGCCAGCTGCCAAGGGGCGACACTAGCATGGATTTTGTAAAGCAAAATGG 2785
Db |||||||
QY 861 AlaIleAlaArgProLysGlyGlnGlnLeuAlaTrpAspPheValArgGluAsnTrp 880
QY 2786 ACCATCTTCTGAAAATTTTCACTTGGGCTCATATGACATAAGATGATCATCTCTGGC 2845
Db |||||||
QY 881 ThrHisLeuLeuLysLysPheAspLeuGlySerTyrAspIleArgMetIleIleSerGly 900
QY 2846 ACAACAGCTCACTTTTCTTCCAGGATAGTTGCAAGAGGTGAACCTATTTTTTGAATCT 2905
Db |||||||
QY 901 ThrThrAlaHisPheSerSerLysAspLysLeuGlnGluValLysLeuPhePheGluSer 920
QY 2906 CTTGAGGCTCAGAGTCAATCTGATATTTTCAAACTGTCTCGAACCATACCAAA 2965
Db |||||||
QY 921 LeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIleThrLys 940
QY 2966 AATATAAATGCTGCGAGAGGAATCTTCCGACTCTCAGGACTTGGCTAATGTTAATACT 3025
Db |||||||
QY 941 AsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeuMetValAsnThr 960
```

RESULT 3

ABP69122
ID ABP69122 standard; protein; 960 AA.

XX AC ABP69122;

XX XX 20-JAN-2003 (first entry)

XX DE Human polypeptide SEQ ID NO 1169.

XX KW Human; genome mapping; gene therapy; food supplement; virus; fungus;
cell-proliferative disorder; neurodegenerative disease; bacterial;
Parkinson's disease; Alzheimer's disease; autoimmune disease;
multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
arthritis; cytostatic; immunomodulator; neoplastic; neuroprotective;
antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;
antiarthritic.

XX OS Homo sapiens.

XX PN WO200270539-A2.

XX PD 12-SEP-2002.

XX PF 05-MAR-2002; 2002WO-US005095.

XX PR 05-MAR-2001; 2001US-00799451.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;

PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;

PI Wehrman T, Wang J, Wang D, Drmanac RT;

XX DR WPI: 2002-759812/82.

XX DR N-PSDB; ABZ11339.

XX PT New polynucleotides comprising sequences assembled from expressed
sequence tags (ESTs), useful for treating cell-proliferative,
neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
or coagulation disorders.

XX PS Claim 9; SEQ ID NO 1169; 1012pp + Sequence Listing; English.

XX CC The invention relates to an isolated polynucleotide (I) comprising a
nucleotide sequence selected from any of 948 sequences (ABZ11119-
ABZ12066) or their mature protein coding portion, active domain coding
protein or complementary sequences. The polynucleotides are useful for
identifying expressed genes or for physical mapping of human genome. The
encoded polypeptides (ABP6902-ABP6949) are useful as molecular weight
markers, as a food supplement, for generating antibodies, in medical
imaging, screening and diagnostic assays and for treating cell-
proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
platelet or coagulation disorders, wound, burns, incision, ulcers, liver
or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
arthritis, etc. Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic format
directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 960 AA;

Alignment Scores:

Pred. No.:	0	Length:	960
Score:	5048.00	Matches:	959
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.90%	Mismatches:	0
Query Match:	85.39%	Indels:	0
DB:	5	Gaps:	0

US-10-039-073-2 (1-3366) x ABP69122 (1-960)

Qy	146	ATGTTCCATTCTTC	GCNATGGTTAA	TTCA	CACAGAAA	CCAA	TGTTTAA	CAATTCAC	AGA	205
Db	1	MetPheHisSerSerAlaMetValAsnSerHisArgLysProMetPheAsnIleHisArg	20							
Qy	206	GGATTTTACTGCTTAA	CACAGCCATCTG	CCCCAA	ATAATG	CA	TTTCTCT	CAGTTCTC	AGTCTC	265
Db	21	GlyPheTyrCysLeuThrAlaIleLeuProGlnIleCysSerGlnPheSerVal	40							
Qy	266	CCATCTAGTTATCACT	TGAGGATCCTGGG	GCTTTC	CAGTAG	CCACTAA	TG	GGGAA	325	
Db	41	ProSerSerTyrHisPheThrGluAspProGlyAlaPheProValAlaThrAsnGlyGlu	60							
Qy	326	CGATTTCTTGGCAGGAGCT	TAAGGCTCCCA	GTGTGTCAT	CTCTCT	CCATAT	TAC	CTC	385	
Db	61	ArgPheProTyrGlnGluLeuArgLeuProSerValIleProLeuHisTyrAspLeu	80							
Qy	386	TTTGTCCACCCCAATCT	CACCTCTCGAC	TTCTTGCAT	CTGAGAGAT	CGAGT	CTTG	445		
Db	81	PheValHisProAsnLeuThrSerLeuAspPheValAlaSerGluLysIleGluValLeu	100							
Qy	446	GTCAGCAATGCTAC	CCAGTTTATCAT	CTTGCACAGCA	AAAGATCTTGA	ATC	CACGAATGCC	505		
Db	101	ValSerAsnAlaThrGlnPheIleLeuHisSerLysAspLeuGluIleThrAsnAla	120							
Qy	506	ACCTTCAGTCAGAGGA	AGATTCAAGAT	ACATGAAAC	CAGGAA	AGAACTG	AAAGTTTG	565		
Db	121	ThrLeuGlnSerGluGluAspSerArgTyrMetLysProGlyLysGluLeuLysValLeu	140							
Qy	566	AGTTACCTGCTCAT	GACAAATTC	CACTGCTG	GTTCAGAG	AAAC	TTCGCCTC	625		
Db	141	SerTyrProAlaHisGluGlnIleAlaLeuLeuValProGluLysLeuThrProHisLeu	160							
Qy	626	AAATACTATGTGGCT	TATGGACTTCCA	AGCCAA	GTTAGTGAT	GCTTGA	AGGGGT	685		
Db	161	LysTyrTyrValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTyr	180							
Qy	686	AAAAGCACATAC	AGAACTCTTTGGT	GGTGAAACA	AGAATTC	TGCAGT	AAACA	745		
Db	181	LysSerThrTyrArgThrLeuGlyGlyGluThrArgIleLeuAlaValThrAspPheGlu	200							
Qy	746	CCAACCCAGGCAC	GCATGGCTTTCC	CTTGCTTTCAT	GAACCGT	TGTTCAA	AGCCAACTTT	805		
Db	201	ProThrGlnAlaArgMetAlaPheProCysPheAspGluProLeuPheLysAlaAsnPhe	220							
Qy	806	TCAATCAAGATAC	GAAGAGAGCAG	GCATATTC	CAC	TATCCA	CATG	865		
Db	221	SerIleLysIleArgArgGluSerArgHisIleAlaLeuSerAsnMetProLysValLys	240							
Qy	866	ACAATGAACTTGA	AGGAGGTCTTTT	GGAAGAT	CAC	TTTGA	AACTACTG	925		
Db	241	ThrIleGluLeuGluGlyLeuLeuGluAspHisPheGluThrThrValLysMetSer	260							
Qy	926	ACATACCTTGTAG	CGCTACATAG	TTTGTGATTT	CCACTCT	CTGAGT	GGCTTCA	985		
Db	261	ThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThrSerSer	280							
Qy	986	GGGTCAAGGTG	CCATCTATG	CATCCCC	CACAAAC	CGGAATCA	ACACAT	1045		
Db	281	GlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyrAlaLeu	300							
Qy	1046	CAGGCATC	CAC	TGAAGCTACT	GATTTTAT	GAAAAGT	ACTTTG	1105		
Db	301	GlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyrProLeu	320							
Qy	1106	TCCAAACTGG	ATTAATTG	CTTATTC	TGAC	TTTG	CACTGG	1165		
Db	321	SerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsnTrpGly	340							
Qy	1166	CTCATTCATAT	AGGAGAC	GTCACTG	CTTTTTC	GACCC	AGAC	1225		
Db	341	LeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAlaSerAsp	360							
Qy	1226	AAACTGTGGGT	CAC	CAGAGT	CATAG	CCCATG	CACTGG	1285		

Db	361	LysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeu	380
Qy	1286	GTCACAATGAATGGTGGCAATGATATTGGCTTAAGGAGGGTTTGGCAAAATACATCGAA	1345
Db	381	ValThrMetGluTrpTrpAsnAspIleTrpLeuysGluGlyPheAlaLysTyrMetGlu	400
Qy	1346	CTTATCGCTGTTAATGCTACATATCCAGAGCTGCAATTTCGATGACTATTTTTGAATGTG	1405
Db	401	LeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspPheLeuAsnVal	420
Qy	1406	TGTTTTGAAGTAATTACAAAAGATTCTTGAATTATCCCGCCCTATCTCCAAACCGCG	1465
Db	421	CysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLysProAla	440
Qy	1466	GAACCCCGCATCAAATACAGGAAATGTTTGATGAAAGTTTCCTATACAGGAGGAGCTTGT	1525
Db	441	GluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGlyAlaCys	460
Qy	1526	ATTTTGAATATGCTCAAGGATTTTCTGGGTGAGGAGAAATCCAGAAAGAAATAATTCA	1585
Db	461	IleLeuAsnMetLeuLysAspPheLeuGlyGluGluLysPheGlnLysGlyIleIleGln	480
Qy	1586	TACTTAAAGAGTTACGCTATAGAAATGCTAAGAAATGATGACTGTGGACGACTGTGTCA	1645
Db	481	TyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspLeuTrpSerSerLeuSer	500
Qy	1646	AATAGTTGTTTGAAGAGTGATTTTACATCTGGTGGAGTTTGTCATTCGGATCCCAAGATG	1705
Db	501	AsnSerCysLeuGluSerAspPheThrSerGlyGlyValCysHisSerAspProLysMet	520
Qy	1706	ACAAGTAACATGCTCGCTTCTCTGGGGGAAATGCGAGAGTCAAAGAGATGATGACTACA	1765
Db	521	ThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGluValLysGluMetMetThrThr	540
Qy	1766	TGGACTCTCCAGAAAGGAATCCCTCTGGTGGTTAAACAAGACGGGTGTTCACTCCGA	1825
Db	541	TrpThrLeuGlnLysGlyIleProLeuLeuValValLysGlnAspGlyCysSerLeuArg	560
Qy	1826	CTGCAACAGAGCGCTTCCTCCAGGGGGTTTCCAGGAAGACCCCTGAATGGAGGGCCCTG	1885
Db	561	LeuGlnGluArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArgAlaLeu	580
Qy	1886	CAGGAGAGGTACCTGTGGCATATCCCATTCACCTACTCCACGAGTGTCTTCTAATGTGATC	1945
Db	581	GlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerThrSerSerAsnValIle	600
Qy	1946	CACAGACACATTCTAAATCAAGACAGATATCTGTGATCTACTGAAAGACAGATGTG	2005
Db	601	HisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThrSerTrp	620
Qy	2006	GTGAAATTTAATGTGGACTCAATGGTTACTATCGTTCACCTATGAGGCTCATGATGG	2065
Db	621	ValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHisGlyTrp	640
Qy	2066	GACCACTCTATTACACAGCTGAATCAGAACACACACACTCTCCAGACTAAGGACAGATG	2125
Db	641	AspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAspArgVal	660
Qy	2126	GGTCTGATTATCATGTGTTTTCAGTATGTTGGTCAGGGAGATGACCCCTAGACAAAGCT	2185
Db	661	GlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAspLysAla	680
Qy	2186	CTTGACATGACTTACTACTCTCCAACATGAACAACAGAGCCCGCCACTTCTCGAGGCTCTG	2245
Db	681	LeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProAlaLeuLeuGluGlyLeu	700
Qy	2246	AGTTACTTGGAAATCGTTTATACCATGATGGACAGAAAGGAATAATTCAGATATCTCTGAA	2305
Db	701	SerTyrLeuGluSerPheTyrHisMetMetAspArgAsnIleSerAspIleSerGlu	720
Qy	2306	AACCTCAAGCGTTACCTTCTTCAGTATTTTAAGCCAGTGATTCACAGGCAAACTGGAGT	2365

Db 721 AsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSerTrpSer 740
 QY 2366 GACAAAGGCTCAGTCTGGACAGGATGCTCCGCTCTCTTGAAGCTGGCTGTGAC 2425
 Db 741 AspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAlaCysAsp 760
 QY 2426 CTGAACCATGCTCCTTGGATCCAGAAAGTGTGAACTCTTCCAGTGGATGAATCC 2485
 Db 761 LeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMetGluSer 780
 QY 2486 AGTGAAATTAATAATACCAACAGATGTTTTAAAGATTGTCTATTCTGTGGTCTCAG 2545
 Db 781 SerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrSerValGlyAlaGln 800
 QY 2546 ACAACAGCAGGATGAATTAACCTTTTAGACCAATATGAACCTCAATGTCAAGTCTGAA 2605
 Db 801 ThrThrAlaGlyTrpAsnTyrLeuLeuGluGlnTyrGluLeuSerMetSerSerAlaGlu 820
 QY 2606 CAAACAAAATCTGTATGCTTTGTCAACGACCAAGCATCAGGAAAAGTTACTGAAGTTA 2665
 Db 821 GlnAsnLysIleLeuTyrAlaLeuSerThrSerLysHisGlnGluLysLeuLysLeu 840
 QY 2666 ATTGAACCTAGGAATGGAAGAGGTATATCAAGACACAGAACTTGCAGCTCTCCTTCAT 2725
 Db 841 IleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaLeuLeuHis 860
 QY 2726 GCGATTGCCAGACGCTCAAGGGGAGCAACTAGCATGGATTTTGTAAAGAGAAATGG 2785
 Db 861 AlaIleAlaArgArgProLysGlyGlnGlnLeuAlaTrpAspPheValArgGluAsnTrp 880
 QY 2786 ACCCATCTCTGAAAAATTTGACTGGCTGATGGCTCATATGACATAGGATCATCTCTGGC 2845
 Db 881 ThrHisLeuLeuLysLysPheAspLeuGlySerTyrAspIleArgMetIleIleSerGly 900
 QY 2846 ACAACAGCTCAGTTTCTTCCAAAGATGAAGTTGCAAGAGTGAACTATTTTGAATCT 2905
 Db 901 ThrThrAlaHisPheSerSerLysAspLysLeuGlnGluValLysLeuPhePheGluSer 920
 QY 2906 CTTGAGGCTCAAGGATCAGATCTGGATATTTTCAAACTGTTCTGGAAACGATACCAAA 2965
 Db 921 LeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIleThrLys 940
 QY 2966 AATATAAATGGCTGGAGAAATCTTCGACTCTGAGACTTGAGCTTAATGTTAATCT 3025
 Db 941 AsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeuMetValAsnThr 960
 RESULT 4
 ID ABP63022 standard; protein; 785 AA.
 AC ABP63022;
 DT 14-OCT-2002 (first entry)
 XX Human polypeptide SEQ ID NO 459.
 DE Human; vulnery; dermatological; neuroprotective; nootropic; cancer;
 KW antiparkinsonian; immunostimulant; cytostatic; immunosuppressive;
 KW antidiabetic; antiallergic; gene therapy; wound healing; tissue repair;
 KW burn; central nervous system disorder; Alzheimer's disease;
 KW Parkinson's disease; Huntington's disease; immune disorder;
 KW autoimmune disorder; multiple sclerosis; diabetes; allergy.
 OS Homo sapiens.
 XX
 XX WO200218424-A2.
 XX
 XX 07-MAR-2002.
 XX
 XX 31-AUG-2001; 2001WO-US027093.
 XX
 XX 01-SEP-2000; 2000US-00654935.
 XX

(HYSE-) HYSEQ INC.
 Tang YT, Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;
 Zhao Qa, Wang D, Liu C, Drmanac RT, Wehrman T;
 WPT, 2002-583321/62.
 N-PSDB; ABQ93501.
 New polynucleotide and polypeptides, useful for treatment and diagnosis of Alzheimer's, Parkinson's, Huntington's, amyotrophic lateral sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies.
 Claim 20; SEQ ID NO 459; 284pp + Sequence Listing; English.
 The invention relates to an isolated polynucleotide (I) comprising one of 245 sequences (ABQ93288-ABQ93532). Treating a condition comprising administering to a mammalian subject a composition comprising the protein (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II). (I), (II) and (III) are useful for diagnosis and (II) can be used for therapeutic treatment. Diseases that may be treated include wound healing and tissue repair, burns, central nervous system disorders (e.g. Alzheimer's, Parkinson's, Huntington's and amyotrophic lateral sclerosis), immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 Sequence 785 AA;
 Alignment Scores:
 Pred. No.: 0 Length: 785
 Score: 4141.00 Matches: 782
 Percent Similarity: 99.74% Conservativeness: 0
 Best Local Similarity: 99.74% Mismatches: 2
 Query Match: 70.04% Indels: 0
 DB: 5 Gaps: 0
 US-10-039-073-2 (1-3366) x ABP63022 (1-785)
 QY 146 ATGTTCCATTCTTCTGCAATGGTTAATTCACAGAAAACCAATGTTTAACTTCACAGA 205
 Db 1 MetPheHisSerSerAlaMetValAsnSerHisArgLysProMetPheAsnIleHisArg 20
 QY 206 GGATTTTACTGCTTAACAGCCATCTGCCCAATATGCAATTTCTCTCAGTCTCAGTG 265
 Db 21 GlyPheTyrCysLeuThrAlaIleLeuProGlnIleCysIleCysSerGlnPheSerVal 40
 QY 266 CCATCTAGTTATCACTTCACTGAGGATCTGGGGCTTTCCAGTAGCCACTTAATGGGAA 325
 Db 41 ProSerSerTyrHisPheThrGluAspProGlyAlaPheProValAlaThrAsnGlyGlu 60
 QY 326 CGATTTCTTGGCAGGAGCTTAAGCTCCCAAGTGTGTCATCTCTCCATATGACCTC 385
 Db 61 ArgPheProTrpGlnGluLeuArgLeuProSerValValIleProLeuHisTyrAspLeu 80
 QY 386 TTTGTCACCCCAATCTCACTCTCTGACTTTGTCATCTGAGAGATCGAAGTCTTG 445
 Db 81 PheValHisProAsnLeuThrSerLeuAspPheValAlaSerGluLysIleGluValLeu 100
 QY 446 GTACGAATGCTACCCAGTTTATCATCTTGACAGCAAAAGATCTTGAATCAGCAATGCC 505
 Db 101 ValSerAsnAlaThrGlnPheIleLeuHisSerLysAspLeuGluIleThrAsnAla 120
 QY 506 ACCCTTCAGTCAGGAGGATTCAGATACATGAACACAGAAAAGAACTGAAAGTTTGT 565
 Db 121 ThrLeuGlnSerGluGluAspSerArgTyrMetLysProGlyLysGluLeuLysValLeu 140
 QY 566 AGTTACCTCTCATGAACAAATGCACTGCTGTTCCAGAGAACTTAGCCCTCAGCTG 625
 Db 141 SerTyrProAlaHisGluGlnIleAlaLeuLeuValProGluLysLeuThrProHisLeu 160


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QY 626 AAATACTATGTGGCTATGGAATCTCAAGCCCAAGTTAGTGATGGCTTTGAAGGGCTTTTAT 685
Db 161 LysTyrTyrValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTyr 180
QY 686 AAAAGCACAATCAGAACTCTTGGTGGTGAACAAGAAATCTTGGCAGTAACAGATTTTGAG 745
Db 181 LysSerThrTyrArgThrLeuGlyGlyGluThrArgIleLeuAlaValThrAspPheGlu 200
QY 746 CCACCCAGGCACCATGGCTTCCCTTGCCTTGTGATGNAACCGTTTTCAAAGCCCAACTTT 805
Db 201 ProThrGlnAlaArgMetAlaPheProCysPheAspGluProLeuPheLysAlaAsnPhe 220
QY 806 TCAATCAAGATACGAAGAGACAGCAGGCATATTGCACATATCAACATGCCCAAGAGTTAAG 865
Db 221 SerIleLysIleArgArgGluSerArgHisIleAlaLeuSerAsnMetProLysValLys 240
QY 866 ACAATTGAACCTGAAGAGGCTCTTTTGAAGATCACCTTTGAAACTACTGTAAAAATGAGT 925
Db 241 ThrIleGluLeuGluGlyGlyLeuLeuGluAspHisPheGluThrThrValLysMetSer 260
QY 926 ACATACCTGTAGCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACTTCATCA 985
Db 261 ThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThrSerSer 280
QY 986 GGGGTCAAGGTGTCATCTATGCATCCCGACACAAACGGAATCAAAACACATTATGCTTTG 1045
Db 281 GlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyrAlaLeu 300
QY 1046 CAGGCATCACTGAAGCTACTGATTTTATGAAAGTACTTTGTATATCTACTATCCACTC 1105
Db 301 GlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyrProLeu 320
QY 1106 TCCAAACTGGATTTAAATTTGCTATTCCCTGACTTTCACCTGGCAGCATGGAAAAATGGGGC 1165
Db 321 SerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsnTrpGly 340
QY 1166 CTCATTACATATAGGAGACGCTCACTGCTTTTGTGACCCCAAGACCTCTCTCTGCTCCGAT 1225
Db 341 LeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAlaSerAsp 360
QY 1226 AAATGTGGGTCAACAGAGTCATAGCCCATGAAGTGGCGCACCGAGTGTGGCAACTG 1285
Db 361 LysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeu 380
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KW Human; gene therapy; neural disorder; immune system disorder;
KW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; cardiovascular disorder; renal disorder;
XX proliferative disorder; inflammation.
OS Homo sapiens.
XX
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XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
PI

XX WPI; 2001-476161/51.
DR N-PSDB; ABA06560.
XX Isolated nucleic acid molecule encoding an inflammation-associated
PT polypeptide is used in preventing, treating or ameliorating a medical
PT condition.
XX
XX Claim 11; SEQ ID NO 646; 859pp + Sequence Listing; English.
XX
CC The present invention provides human cDNAs, proteins and related genomic
CC DNAs. These can be used in the treatment of neural, immune system,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal and proliferative disorders and inflammation. The present sequence
CC is a protein of the invention
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SQ Sequence 728 AA;

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Pred. No.: 0 Length: 728
Score: 3799.00 Matches: 722
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Best Local Similarity: 100.00% Mismatches: 0
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DT 18-DEC-2001 (first entry)
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KW Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
KW ligase; hyperproliferative disorder; immunodeficiency disorder;
KW autoimmune disorder; neurological disorder; metabolic disorder;
KW inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW blood-related disorder; infectious disorder; cytostatic; anti arthritic;
KW nephrotropic; anticoagulant.
XX
OS Homo sapiens.
PN
XX WO200155301-A2.
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KW      pulmonary disorder; cardiovascular disorder; renal disorder;
KW      proliferative disorder; inflammation.
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XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-476161/51.
DR N-PSDB; ABA06733.
XX
XX Isolated nucleic acid molecule encoding an inflammation-associated
PT polypeptide is used in preventing, treating or ameliorating a medical
PT condition.
XX
XX Claim 11; SEQ ID NO 819; 859pp + Sequence Listing; English.
PS
XX The present invention provides human cDNAs, proteins and related genomic
CC DNAs. These can be used in the treatment of neural, immune system,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal and proliferative disorders and inflammation. The present sequence
CC is a protein of the invention
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Score: 3770.00 Matches: 717
Percent Similarity: 99.31% Conservative: 0
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XX 09-DEC-2002 (first entry)
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KW antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine.
XX OS Homo sapiens.
XX US2002090672-A1.
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 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 13-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239935P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 XX (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 PI Rosen CA, Ruben SM, Barash SC;
 XX WPI; 2002-681727/73.
 DR N-PSDB; ABV84070.
 XX Novel polypeptide useful for diagnosis, prognosis, prevention, and
 PT treatment of immune, hyperproliferative, renal, respiratory,
 PT cardiovascular, reproductive, endocrine, gastrointestinal and
 PT neurological disorders.
 XX Claim 11; SEQ ID NO 819; 369pp + Sequence Listing; English.
 XX The invention relates to novel genes (ABV83682-ABV84101) and proteins
 CC (ABP66710-ABP67129) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune

CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
 CC infectious diseases such as viral, bacterial, fungal and parasitic
 CC infections. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pt_sequences
 XX
 SQ Sequence 722 AA;

Alignment Scores:
 Pred. No.: 0 Length: 722
 Score: 3770.00 Matches: 717
 Percent Similarity: 99.31% Conservative: 0
 Best Local Similarity: 99.31% Mismatches: 5
 Query Match: 63.77% Indels: 0
 DB: 5 Gaps: 0

US-10-039-073-2 (1-3366) x ABP67098 (1-722)

QY 860 GTTAAGACAATTGAACCTTGGAAGAGGTCTTTTGGAAAGATCACCTTGAAACTACTGTAAAA 919
 DB 1 ValLysThrIleGluLeuGluGlyGlyLeuLeuGluAspHisPheGluThrThrValLys 20
 QY 920 ATGAGTACATACCTTGTTAGCCTACATAGTTTGTGATTTCACACTCTCTGAGTGGCTTCACT 979
 DB 21 MetSerThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThr 40
 QY 980 TCATCAGGGTCAAGGTGTCCATCTATGCATCCCGACAGCAAAACGGAATCAAAACACATTAT 1039
 DB 41 SerSerGlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyr 60
 QY 1040 GCTTTCGAGCATCACCTGAAGCTACTTGATTTTATGAAAAGTACTTTGTATCTACTAT 1099
 DB 61 AlaLeuGlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyr 80
 QY 1100 CCACTCTCCAAACTGGGATTAAATTGCTATTCTGACTTTTGCACCTGGAGCATGGAAAAT 1159
 DB 81 ProLeuSerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsn 100
 QY 1160 TGGGGCTCATTAATAGGGAGACGTCACTCTTTTGCACCCCAAGACCTCTTCTGCT 1219
 DB 101 TrpGlyLeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAla 120
 QY 1220 TCCGATAAACTGTGGGTCCACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1279
 DB 121 SerAspLysLeuTrpValThrArgValIleAlaIleGluLeuAlaHisGlnTrpPheGly 140
 QY 1280 AACCTGGTCAATGGAATGGTGAATGATATTGCTTAAGGAGGGTTTTGCAAAATAC 1339
 DB 141 AsnLeuValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyr 160
 QY 1340 ATCGAACTTATCGCTGTTAATGCTATATCCAGAGCTGCAATTTGATGATGATGATGATGAT 1399
 DB 161 MetGluLeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeu 180
 QY 1400 AATGTGTGTTTGAAGTAATTACAAAGATTTCATTGAAATTCATCCGCCCTATCTCCAAA 1459
 DB 181 AsnValCysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLys 200
 QY 1460 CCAGCGGAAACCCGACTCAAATACAGGAAATGTTTGTGATGAAGTTCCTTAACAAGGGA 1519
 DB 201 ProAlaGluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGly 220
 QY 1520 GCTTGATTTTGAATATGCTCAAGGATTTTCTGGGTGAGGAGAAATTCAGAAAGGAATA 1579
 DB 221 AlaCysIleLeuAsnMetLeuLysAspPheLeuGlyGluGluLysPhe***LysGlyIle 240
 QY 1580 ATTCACTACTTAAGAGTTTCAGCTATAGAAATGCTAAGAAATGATGATGATGATGATGATGAT 1639
 DB 241 IleGlnTyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspAspLeuTrpSerSer 260

QY 1640 CTGTCMAATAGTCTTTTAAAGATGATTTTATCATCTGGTGGAGTTTGTGATTCGGATCCC 1699
DB 261 LeuSerAsnSerCysLeuGluSerAspPheThrSerGlyGlyValCysHisSerAspPro 280
QY 1700 AAGATTGACAAGTAACATGCTCCCTCTTCTGGGGGAAATGCAGAGGTCAAGAGATGATG 1759
DB 281 LysMetThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGlu***LysGluMetMet 300
QY 1760 ACTACATGGACTCTCCAGAAAGGAATCCCCCTGGCTGGTGTAAACAAGACGGGTGTCA 1819
DB 301 ThrThrTrpThrLeuGlnLysGlyLeuProLeuLeuValValLysGlnAspGlyCysSer 320
QY 1820 CTCGACCTGCAACAGAGCGCTTCTCCAGGGGGTTTTCCAGGAAGACCCGAAATGGAGG 1879
DB 321 LeuArgLeuGlnGlnGluArgPheLeuGlnGlyValPheGlnGlnuAspProGluTrpArg 340
QY 1880 GCCCTGCGAGGAGGTACCTGGGATATCCCATTTGACCTACTCCACGAGTCTCTCTAAT 1939
DB 341 AlaLeuGlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerThrSerSerSerAsn 360
QY 1940 GTGATCCACAGACACATTTAAATCAAAAGACAGATCTCTGGATCTACCTGAAAGACC 1999
DB 361 ValIleHisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThr 380
QY 2000 AGTTGGGTGAATTTAATGTGACTCAAAATGTTACTACATCGTTTCACTATGAGGTGAT 2059
DB 381 SerTrpValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHis 400
QY 2060 GGATGGGACCACTCATATACAGCTGAATCAGAACCCACACACTTCTCAGACCTAAGGAC 2119
DB 401 GlyTrpAspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAsp 420
QY 2120 AGAGTAGGTCTGATTCATGATGTGTTTTCAGCTAGTTGGTGCAGGAGACTGACCCCTAGAC 2179
DB 421 ArgValGlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAsp 440
QY 2180 AAGCTCTTGACATGACTTACTCTCCAAACATGAACAGCAGCCCGCACTTCTCGAA 2239
DB 441 LysAlaLeuAspMetThrTyrTyrLeuGlnHisLeuThrSerSerProAlaLeuLeuGlu 460
QY 2240 GCTCTGACTTACTTCCGAATCGTTTACCATGATGGACAGAGCAATATTCAGATATC 2299
DB 461 GlyLeuSerTyrLeuGluSerPheTyrHisMetMetAspArgArgAsnIleSerAspIle 480
QY 2300 TCTGAAACCTCAAGCGTTTACCTTCTCAGTATTTTAAAGCCAGTCAATGACAGGCAAGC 2359
DB 481 SerGluAsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSer 500
QY 2360 TGGAGTGAACAGGCTCAGTGGGACAGGATGCTCCGCTCGGCTCTCTTGAAGCTGCC 2419
DB 501 TrpSerAspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAla 520
QY 2420 TGTGACCTGCAACATGCTCTTGCATCCAGAAAGTGTGTAACCTTCTCCAGTGGATG 2479
DB 521 CysAspLeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMet 540
QY 2480 GAATCCAGTGGAAAAATTAATATACCAACAGATGTTTTAAAGATTGTGTATTCTGGGT 2539
DB 541 GluSerSerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrSerValGly 560
QY 2540 GCTCAGACAACAGCGAGTGAATTTACCTTTTAGAGCAATATGAATGTCAATGTCAAGT 2599
DB 561 AlaGlnThrThrAlaGlyTrpAsnTyrLeuLeuGluGlnTyrGluLeuSerMetSerSer 580
QY 2600 GCTGACAAAAAANAATCTGTATCTGTTGTCAAGCGACGACATCAGGAAGTACTG 2659
DB 581 AlaGluGlnAsnLysIleLeuTyrAlaLeuSerThrSerLysHisGlnGlnLysLeuLeu 600
QY 2660 AAGTTAATTGAATAGGAATGAAGAGGTTATCAAGACACAGAACTTGGCAGCTCTC 2719
DB 601 LysLeuIleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaLeu 620

QY 2720 CTTTCATGGATTGCCAGACGTCCTCAAGGGGCGAGCAACTAGCATGGATTTTGTAAAGAA 2779
DB 621 LeuHisAlaIleAlaArgArgProLysGlyGlnGlnLeuAlaTrpAspPheValArgGlu 640
QY 2780 AATTGGACCCATCTTCTGAAAAATTTGACTTGGGCTCATATGACATAGGATGATCATC 2839
DB 641 AsnTrpThrHisLeuLeuLysLysPheAspLeuGlySerTyrAspIleArgMetIleIle 660
QY 2840 TCTGCGCAACAGCTCACTTTTCTTCCAGGATAGTTGCAAGGTGAAACTATTTTTT 2899
DB 661 SerGlyThrThrAlaHisPheSerSerLysAspLysLeuGlnGluValLysLeuPhePhe 680
QY 2900 GAATCTCTTGGGCTCAAGGATCAGATCTGATATTTTCAACTGTTCTGGAACGATA 2959
DB 681 GluSerLeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIle 700
QY 2960 ACCAAAAATAAATAATGGCTGGAGAAGATCTTCCGACTCTGAGGACTTGGCTAATGGTT 3019
DB 701 ThrLysAsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeu***** 720
QY 3020 AATACT 3025
DB 721 ***Thr 722
RESULT 10
ADR41453
ID ADR41453 standard; protein; 722 AA.
XX AC ADR41453;
XX DT 07-OCT-2004 (first entry)
XX DE Human CD-like molecule HAIDK30, SEQ ID NO:252.
XX KW Human; CD-like molecule; cluster of differentiation; diagnosis;
KW prevention; immune disorder; immunodeficiency; autoimmune disorder;
KW blood-related disorder; haematological disorder; haemostatic disorder;
KW thrombolytic disorder; hyperproliferative disorder; cancer; tumour;
KW apoptotic disorder; cardiovascular disorder; respiratory disorder;
KW angiogenic disorder; neovascularisation; neurological disorder;
KW endocrine disorder; reproductive system disorder; infectious disease;
KW gastrointestinal disorder; drug screening; tissue regeneration;
KW chemotaxis; gene therapy; antibody therapy; drug targeting;
KW chromosome mapping; forensic analysis; immunophenotyping; cytostatic;
KW haemostatic; tranquiliser; vulnery; antiinflammatory; nephrotropic;
KW cardiant; antiallergic; anti-HIV; antirheumatic; antiarthritic;
KW antipruritic; immunosuppressive; vasotropic; nootropic; neuroprotective;
KW antithyroid; thyromimetic; gynaecological; virucide; hepatotropic;
KW antibacterial; dermatological; chromosome 16.
XX OS Homo sapiens.
XX PN WO200226930-A2.
XX PD 04-APR-2002.
XX PF 25-SEP-2001; 2001WO-US029838.
XX PP 26-SEP-2000; 2000US-0235484P.
XX PR (HUMA-) HUMAN GENOME SCI INC.
XX PA Rosen CA, Birse CE;
XX PI WPI; 2002-405050/43.
XX PS N-PSDB; ADR41277.
DR Novel polynucleotides and polypeptides useful for treating, preventing or
XX ameliorating cardiovascular, renal, neurovascular, and autoimmune
XX disorders.
XX Claim 11; SEQ ID NO 252; 1243pp; English.

CC The invention relates to 167 novel human CD (cluster of differentiation) -
CC like molecules (ADR41388-ADR41563) and to cDNAs encoding them (seqid:11)-
XX
SQ Sequence 722 AA;

Alignment Scores:

Pred. No.: 0 Length: 722
Score: 3763.00 Matches: 717
Percent Similarity: 99.31% Conservative: 0
Best Local Similarity: 99.31% Mismatches: 5
Query Match: 63.65% Indels: 0
DB: 5 Gaps: 0

US-10-039-073-2 (1-3366) x ADR41453 (1-722)

QY	860	GTTAAGCAATGAACCTGAAGGAGGCTCTTTTGGAGATCACTTTGAAACTGCTGTAATAA	919
DB	1	VallysThrIleGluLeuGluGlyGlyLeuLeuGluAspHisPheGluThrThrVallys	20
QY	920	ATGAGTACATACCTTGTAAGCCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACT	979
DB	21	MetSerThrTyrLeuValAlaTyrIleValCysaspPheHisSerLeuSerGlyPheThr	40
QY	980	TCATCAGGGGCAAGGTCCTCATCTATGTCATCCCGAGCAAAACGGAATCAAAACACATTAT	1039
DB	41	SerSerGlyValysValSerIleTyrAlaSerProaspLysArgAsnGlnThrHisTyr	60
QY	1040	GCTTTGCAAGGCATCACTGAAGCTACTTGATTTTATGAAAGTACTTTGATATCTACTAT	1099
DB	61	AlaLeuGlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyr	80
QY	1100	CCACTCTCCAACTGGATTAAATGCTATTCTCCTGACTTTGCACTGGAGCCATCGAAAT	1159
DB	81	ProLeuSerLysLeuAspLeuIleAlaIleProaspPheAlaProGlyAlaIleMetGluAsn	100
QY	1160	TGGGCGCTCATATACATATAGGAGACGTCCTGCTTTTGGACCCCAAGACCTCTCTGCT	1219
DB	101	TrpGlyLeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAla	120
QY	1220	TCCGATAAAGCTGGGTCAACAGAGTCATACCCATGACCTGGCGCCACGAGTGGTGGC	1279
DB	121	SerAspLysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGly	140
QY	1280	AACCTGGTCACAAATGGAGTGTGAATGATATTTGGCTTAAGAGGGTTTTGCAAAATAC	1339
DB	141	AsnLeuValThrMetGluTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyr	160
QY	1340	ATGGAACCTTATCGCTGTTAAATGCTACATATCCAGAGCTGCATTTGATGACTATTTTGT	1399
DB	161	MetGluLeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspTyrPheLeu	180
QY	1400	AATGCTGTTTGAAGTAATTAACAAAGATTCATTGAATTCATCCCGCCCTATCCCAA	1459
DB	181	AsnValCysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLys	200
QY	1460	CCAGCGAAACCCGACCTCAAAATCAGAAATGTTTGAATGAAGTTTCTATAACAAGGA	1519
DB	201	ProAlaGluThrProThrGlnIleGlnGluMet***aspGluValSerTyrAsnLysGly	220
QY	1520	GCTTGATTTTGAATATGCTCAAGATTTTCTGGTGAGGAGAAATTCAGAAAGGAATA	1579
DB	221	AlaCysIleLeuAsnMetLeuLysAspPheLeuGlyGluGluLysPheGlnLysGlyIle	240
QY	1580	ATTGAGTACTTAACAGAGTTCAGCTATAGAATCTGAAGATGATGACTTGTGAGCAGT	1639
DB	241	IleGlnTyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspLeuTrpSerSer	260
QY	1640	CTGTCAAAATAGTTGTTAGAAAGTGAATTTACATCTGGTGGAGTTTGTCAATTCGGATCCC	1699
DB	261	LeuSerAsnSer***LeuGluSerAspPheThrSerGlyValCysHisSerAspPro	280
QY	1700	AAGATGACAAATACATGCTCGCTTTCTGGGGGAAATATGACAGAGGTCAAGAGATGATG	1759

DB	281	LysMetThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGluValLysGluMetMet	300
QY	1760	ACTACATGGACTCTCCAGAAAGGAATCCCTCTGCTGGTGTAAACAAGCGGTGTCA	1819
DB	301	ThrThrTrpThrLeuGlnLysGlyIleProLeuLeuValLysGlnAspGlyCysSer	320
QY	1820	CTCGACTGCAACAGGAGCGCTTCTCCAGGGGTTTTCCAGGAAGACCTCGAATGAGG	1879
DB	321	LeuArgLeuGlnGlnGluArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArg	340
QY	1880	GCCTTCAGGAGAGGTACCTGTGGCATATCCCATTTGACCTACTCCACGAGTCTTCTAAT	1939
DB	341	AlaLeuGlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerThrSerSerAsn	360
QY	1940	GTGATCCACAGACACATCTTAAATCAAGACAGATACTCTGGATCTACCTGAAAGACC	1999
DB	361	ValIleHisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThr	380
QY	2000	AGTTGGGTGAAATTTAATGTGGACTCAAATGGTTTACTACATCGTTCACTATGAGGGTCAT	2059
DB	381	SerTrpValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHis	400
QY	2060	GGATGGGACCAACTCACTTACAGCTGAATCAGAACACACACTTCTCAGACCTTAAGAC	2119
DB	401	GlyTrpAspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAsp	420
QY	2120	AGAGTAGGCTGATTCATGATGTGTTTACAGTAGTTGGTCAGGGAGACTGACCTAGAC	2179
DB	421	ArgValGlyLeuIleHisaspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAsp	440
QY	2180	AAAGCTCTTGACATGACTTACTACTCCCAACATGAAACAGCAGCCCCGACTTCTCGAA	2239
DB	441	LysAlaLeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProAlaLeuLeuGlu	460
QY	2240	GGTCTGAGTTACTTGAATCGTTTTTACCACATGATGACAGAGGAATATTTGAGATATC	2299
DB	461	GlyLeuSerTyrLeuGluSerPheTyrHisMetMetAspArgArgAsnIleSerAspIle	480
QY	2300	TCTGAAACCTCAAGCGTTACCTTCTCAGTATTTTAAAGCCAGTGATGACAGGCAAGC	2359
DB	481	SerGluAsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSer	500
QY	2360	TGGAGTGACAAAGGCGCTCAGTCTGGGACAGGATGCTCGCTCGGCTCTCTTTGAAAGCTGCC	2419
DB	501	TrpSerAspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAla	520
QY	2420	TGTGACTGAAACCATGCTCTTGCATCCAGAAAGCTGCTGAACTCTTCTCCAGTGTGATG	2479
DB	521	CysAspLeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMet	540
QY	2480	GAATCCAGTGGAAATTAATATATACCAACAGATGTTTTTAAAGATTTGTGTTCTGTGGGT	2539
DB	541	GluSerSerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrSerValGly	560
QY	2540	GCTCAGACACACAGAGATGGAATTAACCTTTTATAGCAATATGAACCTGTCAATGTCAAGT	2599
DB	561	AlaGlnThrThrAlaGlyTrpAsnTyrLeuLeuGluGlnTyrGluLeuSerMetSerSer	580
QY	2600	GCTGAACAAACAAATTTCTGTATGCTTGTCTCAACGAGCAAGCATCAGGAAAAGTACTG	2659
DB	581	AlaGluGlnAsnLysIleLeuTyrAlaLeuSerThrSerLysHisGlnGluLysLeuLeu	600
QY	2660	AAGTTAATTCGAATAGGAAGGAAAGGTTTATCAAGACACAGAACTTGGGAGCTCTC	2719
DB	601	LysLeuIleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaLeu	620
QY	2720	CTTCATCGGATTCAGACGCTCCAAAGGGCAGCAACTAGCATGGGATTTTGTAAAGAGAA	2779
DB	621	LeuHisAlaIleAlaArgArgProLysGlyGlnGlnLeuAlaTrpAspPheValArgGlu	640
QY	2780	AATTGACCCCATCTTCTGAAAAAATTTGACTTGGGCTCATATGACATAAAGGATGATCATC	2839
DB	641	AsnTrpThrHisLeuLeuLysLysPheAspLeuGlySerTyrAspIleArgMetIleIle	660

QY 2840 TCTGGCACAACAGCTCCTCTTCTTCCCAAGGATAAGTTCCAAAGAGGTGAAACTATTTT 2899
Db 661 SerGlyThrAlaHisPheSerSerLysAspLysLeuGlnGluValLysLeuPhePhe 680
QY 2900 GAATCTCTTGGGCTCAAGGATCACATCTGGATATTTTCAAACTGTTCTGGAACGATA 2959
Db 681 GluSerLeuGlnAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIle 700
QY 2960 ACCAAAATATATAATGGCTGGAGAGAAATCTTCCGACTCTCAGGACTTGGCTAATGGTT 3019
Db 701 ThrLysAsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeu***** 720
QY 3020 AATACT 3025
Db 721 ***Thr 722
RESULT 11
AAU07829
ID AAU07829 standard; protein; 941 AA.
XX
AC AAU07829;
XX
DT 04-DEC-2001 (first entry)
XX
DE Human ARTS-1 polypeptide.
XX
KW Human; aminopeptidase regulator of type I; cytokine signalling; ARTS-1;
KW tumour necrosis factor receptor ectodomain shedding; interleukin-1;
KW interleukin-6; immune disorder; TNF-mediated immune disease;
KW inflammatory disorder; anti arthritic; vasotropic; immunomodulator;
KW immunosuppressive; antibacterial; gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 350..361 /label= Zinc_binding_domain
FT Domain 353..376 /label= Zinc_binding_domain
FT Domain 372..379 /label= Zinc_binding_catalytic_site
FT Domain 372..379 /label= Zinc_binding_catalytic_site
XX
PN WO200164856-A2.
XX
XX
PD 07-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US006464.
XX
PR 28-FEB-2000; 2000US-0185586P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Levine S;
XX
DR WPI; 2001-550175/61.
DR N-PSDB; AAS09227.
XX
XX Novel polypeptide useful for the regulation of ectodomain shedding of
PT type I, tumor necrosis factor receptor and other cytokine receptors and
PT for treating disorders and diseases of the immune system.
XX
PS Claim 2; Fig 1; 139pp; English.
XX
CC The present invention relates to the isolation of a novel human
CC polypeptide, defined as aminopeptidase regulator of type I, 55 kDa tumour
CC necrosis factor (TNF) receptor ectodomain shedding (ARTS-1), and the
CC polynucleotide sequence encoding for ARTS-1. The invention describes
CC compositions and methods for the regulation of cytokine signalling
CC through the TNF pathway. The ARTS-1 polypeptide and antibodies that bind
CC ARTS-1 are useful for regulating the shedding of the extracellular domain
CC of a cytokine receptor such as type-I tumour necrosis factor receptor,
CC type I or II interleukin-1 cytokine receptor and interleukin-6 cytokine

CC receptor alpha-chain gp80, by delivering the molecules to a tissue
CC comprising one or more cells expressing the cytokine receptor or their
CC plasma membrane extracellular surface. The ARTS-1 sequences are
CC useful for treating a subject, preferably human, displaying, suspected
CC of, or at risk of displaying a pathology resulting from abnormal cytokine
CC activity, such as tumour necrosis factor alpha, interleukin-alpha, beta
CC or interleukin-6. A vector comprising the polynucleotide encoding ARTS-1
CC is useful in gene therapy. The ARTS-1 sequences are useful in diagnosed
CC and therapeutic regimens in treating immune disorders (e.g. TNF-mediated
CC immune diseases) and inflammatory disorders (e.g. rheumatoid arthritis).
XX The present sequence represents human ARTS-1 polypeptide
SQ Sequence 941 AA;
Alignment Scores:
Pred. No.: 3.54e-245 Length: 941
Score: 2516.50 Matches: 478
Percent Similarity: 69.34% Conservative: 171
Best Local Similarity: 51.07% Mismatches: 268
Query Match: 42.57% Indels: 19
DB: 4 Gaps: 7
US-10-039-073-2 (1-3366) x AAU07829 (1-941)
QY 212 TACTGCTTAACAGGCATCTTCCCCCAATATGCATTTGTTCTCAGTTCAGTGCATCT 271
Db 15 PheLeuLeuSerSerLeuLeuAlaLeuLeuThrVal-----SerThrProSer 30
QY 272 AGTTATCATCTTCACTGAGGATCCTGGGGCTTTCCAGTAGCCACCTAATGGGGAACGATT 331
Db 31 TrpCysGlnSerThrGlu-----AlaSerProLysArgSerAspGlyThrProPhe 47
QY 332 CCTTGGCAGGAGCTAAGGCTCCCGAGTGTGTCTTCTCCATTTATGACCTCTTTGTC 391
Db 48 ProTrpAsnLysIleArgLeuProGluTyrrValIleProValHisTyrrAspLeuLeu 67
QY 392 CACCCCAATCTCCTCTCGGACTTTGTCATCTGAGAGATCGAAGTCTTGGTCAGC 451
Db 68 HisAlaAsnLeuThrThrLeuThrPheTrpGlyThrLysValGluIleThrAlaSer 87
QY 452 AATGCTACCCAGTTTATCATCTTCGACAGCAAGATCTTGAATCAGCAATGCCACCTT 511
Db 88 GlnProThrSerThrIleLeuHisHisLeuGlnIleSerArgAlaThrLeu 107
QY 512 CAGTCAGAGGAAGATTCAAGATACATGAAACACAGGAAAGAACTTGAAGTTTAC 571
Db 108 ArgLysGlyAlaGlyGluArgLeuSerGlu-----GluProLeuGlnValLeuGluHis 125
QY 572 CCTGCTCATGAACAAATTCGACTCTGCTGTTCCAGAGAACTTACGCTCAGTGAATAC 631
Db 126 ProArgGlnGluGlnIleAlaLeuLeuAlaProGluProLeuLeuValGlyLeuProTyr 145
QY 632 TATGTGGCTATGGACTTCCAGCCCAAGTTAGTGTGCTTTGAAGGTTTATAAAGC 691
Db 146 ThrValValIleHisTyrrAlaGlyAsnLeuSerGluThrPheHisGlyPheTyrrLysSer 165
QY 692 ACATACAGAACTCTTGTGTGTGAAACAAAGAAATCTTGCAGTAACAGATTTTTCAGCAACC 751
Db 166 ThrTyrrArgThrLysGluGlyGluLeuArgIleLeuAlaSerThrGlnPheGluProThr 185
QY 752 CAGCAGCATGGCTTCCCTTGTGTTGATGAACCGTTGTTCAAGGCCAACTTTCAATC 811
Db 186 AlaAlaArgMetAlaPheProCysPheAspGluProAlaPheLysAlaSerPheSerIle 205
QY 812 AAGATACAGAGAGAGACGACGATATTCACATCCCAACATGCCAAGGTTTAAACAAATT 871
Db 206 LysIleArgGluProArgHisLeuAlaIleSerAsnMetProLeuValLysSerVal 225
QY 872 GAACCTGAAGAGAGCTTTTGGAGATCCTTTGAAACTACTGTAAAAAGAGTACATAC 931
Db 226 ThrValAlaGluGlyLeuIleGluAspHisPheAspValThrValLysMetSerThrTyr 245
QY 932 CTTGTAGCCTACATAGTATTGTGATTTCCACTCTCTGAGTGGCTTCACTTCATCATAGGGGTC 991

Db LeuValAlaPheIleSerAspPheGluSerValSerLysIleThrLysSerGlyVal 265
QY AAGTGTCATCTATGCATCCCGACAAACGGGAATCAACACATTAATGCTTTCCAGGCA 1051
Db LysValSerValTyrAlaValProAspLysIleAsnGlnAlaAspTyrAlaLeuAspAla 285
QY TCACCTGAAGCTACTGATTTTATGAAAGTACTTTGATATCTACTACTCCTCCAAA 1111
Db AlaValThrLeuLeuGluPheTyrGluAspTyrPheSerIleProTyrProLeuProLys 305
QY CTGGAATTAAATGCTATCTGACATTTGACACTCGAGCCATGGAAAAATGGGGCTCAT 1171
Db GlnAspLeuAlaAlaIleProAspPheGlnSerGlyAlaMetGluAsnTrpGlyLeuThr 325
QY ACATATAGGGAGAGCTACTGCTTTTTCACCCCAAGACCTCTTCTGCTCCGATAAAGCTG 1231
Db ThrTyrArgGluSerAlaLeuLeuPheAspAlaGluLysSerSerAlaSerSerLysLeu 345
QY TGGGTCCACGAGTCATAGCCCATGAACTGCGCACAGCTGGTTTGGCAACCTGCTCACA 1291
Db GlyIleThrMetThrValAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeuValThr 365
QY ATGGAATGGTGAATGATATTGCTTAAGGAGGGTTTTCAAAATACATCGAACTTATC 1351
Db MetGluTrpTrpAsnAspLeuTrpLeuAsnGluGlyPheAlaLysPheMetGluPheVal 385
QY CTGTTAATGCTACATATCCAGAGTGCATTTGATGACTATTTTGAATGTGTGTTT 1411
Db SerValSerValThrHisProGluLeuLysValGlyAspTyrPhePheGlyLysCysPhe 405
QY GAAGTAATTACAAAGATTTCATTAATTCATCCCGCCCTATCTCCAAACGAGCGGAACC 1471
Db AspAlaMetGluValAspAlaLeuAsnSerSerHisProValSerThrProValGluAsn 425
QY CCGACTCAATPACAGGAATGTTTGATGAAGTTTCTTAACAAAGGAGCTGTGATTTTG 1531
Db ProAlaGlnIleArgGluMetPheAspAspValSerTyrAspLysGlyAlaCysIleLeu 445
QY AATATGCTCAGGATTTCCTGGTGAGGAGAAATCCAGAAAGGAATAATTCAGTACTTA 1591
Db AsnMetLeuArgGluTyrLeuSerAlaAspAlaPheLysSerGlyIleValGlnTyrLeu 465
QY AAGAAGTTCAGCTATAGAAATCTAAGAAATCATCATCTGTGGACAGCTGTCAATAGT 1651
Db GlnLysHisSerTyrLysAsnThrLysAsnGluAspLeuTrpAspSerMetAlaSerIle 485
QY TGTTTAGAAAGTATTTTACATCTGGT-----GGAGTTTGTCAATCCGATCCCAAGATG 1705
Db Cys---ProThrAspGlyValLysGlyMetAspGlyPheCys---SerArgSerGlnHis 503
QY ACAAGTAACATGCTCGCCTTTCTGGGGGAAATCGCAGAGTCAAGAGATGATGACTACA 1765
Db SerSerSerSerHisThrPheGlnGluGlyValAspValLysThrMetMetAsnThr 523
QY TGGACTCCCAAGGAATCCCTGCTGTGTGTAAACAAGACGGGTGTCACTCCGA 1825
Db TrpThrLeuGlnLysGlyPheProLeuIleThrIleThrValArgGlyArgAsnValHis 543
QY CTGCAACAGGAGCGCTTCCTCCAGGGGGTTTCCAGGAAGACCCCTGAATGAGGGCCCTG 1885
Db MetLysGlnGluHisTyrMetLysGly-----SerAspGlyAlaPro 557
QY CAGAGAGGTACCTGTGTCATATCCCATTTGACTTCCAGAGTCTTCTTAATGTGATC 1945
Db AspThrGlyTyrLeuTrpHisValProLeuThrPheIleThrSerLysSerAspMetVal 577
QY CACAGACATCTTAAATAACAAAGACAGACTCTGGATCTACCTGAAAGACCAAGTTGG 2005
Db HisArgPheLeuLeuLysThrLysThrAspValLeuLeuLeuProGluGluValGluTrp 597
QY GTGAAATTAATGGAATCAAAATGGTTTACTATGATCGTTTCACTATGAGGGTCATGGATGG 2065
:::|||||

Db IleLysPheAsnValGlyMetAsnGlyTyrTyrIleValHisTyrGluAspAspGlyTrp 617
QY GACCAACTCATTCACACAGCTGAATCAGAACCAACACACTTCTCAGACCTAAGGACAGATA 2125
Db AspSerLeuThrGlyLeuLeuLysGlyThrHisThrAlaValSerSerAsnAspArgAla 637
QY GGTCTGATTTCATGATGTTTTCAGCTAGTTGGTGCAGGGAGACTGACCCCTAGACAAAGCT 2185
Db SerLeuIleAsnAsnAlaPheGlnLeuValSerIleGlyLysLeuSerIleGluLysAla 657
QY CTTGACATGACTTACTACTCCCAACATGAAACAGACGCCCCGACACTTCTCGAAGGCTG 2245
Db LeuAspLeuSerLeuTyrLeuLysHisGluThrGluIleMetProValPheGlnGlyLeu 677
QY AGTTACTTGAATCGTTTACCATGATGACGACAGAGGAATATTTTCAGATATCTCTGAA 2305
Db AsnGluLeuIleProMetTyrLysLeuMetGluLysArgAspMetAsnGluValGluThr 697
QY AACCTCAAGCGTTTACCTTCTTCAGATTATTTAAAGCAGTGTATTCACAGGCCAAAGCTGAGT 2365
Db GlnPheLysAlaPheLeuIleArgLeuLeuArgAspLeuLeuAspLysGlnThrTrpThr 717
QY GACAAGGCTCAGTCTGGGACAGAGTCTCCGCTCGGCTCTCTTGAAGCTGGGCTGTGAC 2425
Db AspGluGlySerValSerGluArgMetLeuArgSerGlnLeuLeuLeuAlaCysVal 737
QY CTGACCATGCTCTTGCATCCAGAAAGCTGTGAACTCTTCTCCAGTCGATGGATCC 2485
Db HisAsnTyrGlnProCysValGlnArgAlaGluGlyTyrPheArgLysTrpLysGluSer 757
QY AGTGGAAAAATAATATACCAACAGATGTTTAAAGATTGTGTATTCTGTGGGTGCTCAG 2545
Db AsnGlyAsnLeuSerLeuProValAspValThrLeuAlaValPheAlaValGlyAlaGln 777
QY ACAACAGCAGATGGAATTAACCTTTTAGACAAATATGAATGTCAATGTCAAGTGTGAA 2605
Db SerThrGluGlyTrpAspPheLeuTyrSerLysTrpGlnPheSerLeuSerSerThrGlu 797
QY CAAAACAAAATTCGTATGCTTTGTCAACGACGACGATCAGGAAAGTTTACTGAACTTA 2665
Db LysSerGlnIleGluPheAlaLeuCysArgThrGlnAsnLysGluLysLeuGlnTrpLeu 817
QY ATTGAACCTAGGAATGGAAGAAAGTTTATCAAGACACAGAACTTGGCAGCTCTCTTCAT 2725
Db LeuAspGluSerPheLysGlyAspLysIleLysThrGlnGluPheProGlnIleLeuThr 837
QY GCATTTCCAGAGCTCAAAAGGGCGACAACTAGCATGGGATTTTGTAAAGAAAATGG 2785
Db LeuIleGlyArgAsnProValGlyTyrProLeuAlaTrpGlnPheLeuArgLysAsnTrp 857
QY ACCATCTTCTGAAAAATTTGACTTGGGCTCATATGACATAGGATGATCATCTCTGCG 2845
Db AsnLysLeuValGlnLysPheGluLeuGlySerSerIleAlaHisMetValMetGly 877
QY ACAACAGCTCACCTTTCTTCCAAAGATAAGTTTCAAGAGGTGAAACTATTTTGAATCT 2905
Db ThrThrAsnGlnPheSerThrArgThrArgLeuGluGluValLysGlyPhePheSerSer 897
QY CTTGAGGCTCAGAGTACATCTGGATATTTTCAACTCTTCTGGAAACGATAACAAA 2965
Db LeuLysGluAsnGlySerGlnLeuArgCysValGlnGlnThrIleGluThrIleGluGlu 917
QY AATATAAATGGCTGGAGAGAAATCTTCCGACTCTGAGGACTGGCTA 3013
Db AsnIleGlyTrpMetAspLysAsnPheAspLysIleArgValTrpLeu 933
RESULT 12
ABB90347
ID ABB90347 standard; protein; 941 AA.
XX ABB90347;
AC ABB90347;
XX
DT 24-MAY-2002 (first entry)

XX DE Human polypeptide SEQ ID NO 2723.

XX KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;

KW anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; anti-ulcer;

KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;

KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;

KW neurological disease; infection; human; secreted protein.

XX OS Homo sapiens.

XX PN WO200190304-A2.

XX PD 29-NOV-2001.

XX PF 18-MAY-2001; 2001WO-US016450.

XX PR 19-MAY-2000; 2000US-0205515P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Birce CE, Rosen CA;

XX DR WPI: 2002-122018/16.

XX DR N-PSDB; ABL90756.

XX PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders.

XX PS Claim 11; SEQ ID NO 2723; 2081pp + Sequence Listing; English.

XX CC The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemia; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 941 AA;

Alignment Scores:

Pred. No.:	4,47e-245	Length:	941
Score:	2515.50	Matches:	477
Percent Similarity:	69.34%	Conservative:	172
Best Local Similarity:	50.96%	Mismatches:	268
Query Match:	42.55%	Indels:	19
DB:	5	Gaps:	7

US-10-039-073-2 (1-3366) x ABB90347 (1-941)

QY 212 TACTGCTTAACGACCATCTTGCCCAAAATATGATTCATTGTTCTCAGTTCTCAGTGCCATCT 271

DB 15 PheLeuLeuSerSerLeuLeuAlaLeuLeuThrVal-----SerThrProSer 30

QY 272 AGTTATCACTTCACAGGATCCTGGGCTTTCCAGTAGCCACTAAATGGGGAAGATT 331

DB 31 TrpCysGlnSerThrGlu-----AlaSerProLysArgSerAspGlyThrProPhe 47

QY 332 CTTGGGAGGAGCTAAGGCTCCCGAGTGTCATCTCTCCCATATGACCTCTTGTGTC 391

DB 332 CTTGGGAGGAGCTAAGGCTCCCGAGTGTCATCTCTCCCATATGACCTCTTGTGTC 391

Db 48 ProTrpAsnLysIleArgLeuProGluTyrValIleProValHisTyrAspLeuLeuLeu 67

QY 392 CACCCCAATCTCACCTCTCTGACCTTTGTTGTCATCTGAGAAAGATCGAAGTCTTGTTCAGC 451

Db 68 HisAlaAsnLeuThrThrLeuThrPheTrpGlyThrThrLysValGluIleThrAlaSer 87

QY 452 AATGCTACCCAGTTTATCATCTTGCACAGCAAGATCTTGAATCACCAGTCCACCTT 511

Db 88 GlnProThrSerThrIleLeuHisSerHisLeuGlnLeuGlnIleSerArgAlaThrLeu 107

QY 512 CAGTCAGAGGAAGATTCAAGATACATGAACCCAGGAAAGAACTGAAAGTTTGTGATTAC 571

Db 108 ArgLysGlyAlaGlyGluArgLeuSerGlu-----GluProLeuGlnValLeuGluHis 125

QY 572 CTGCTCATGAACAAATGCACTGCTGTTCCAGAGAAACTTTACGCCCTCACCTGAATATAC 631

Db 126 ProProGlnGluGlnIleAlaLeuLeuAlaProGluProLeuLeuValGlyLeuProTyr 145

QY 632 TATGTGGCTATGGACTTCCAAAGCCAAAGTTAGTGATGCTTTGAAGGTTTATATAAAGC 691

Db 146 ThrValValIleHisTyrAlaGlyAsnLeuSerGluThrPheHisGlyPheTyrLysSer 165

QY 692 ACATACAGAACTCTTGGTGTGAAACAAAGAAATCTTGCAGTAACAGATTTTGAGCAACC 751

Db 166 ThrTyrArgThrLysGluGlyGluLeuArgIleLeuAlaSerThrGlnPheGluProThr 185

QY 752 CAGGCAGCATGGCTTTCCCTTGTGTTGATGAACCGTTGTTCAAGCCAACTTTTCAATC 811

Db 186 AlaAlaArgMetAlaPheProCysPheAspGluProAlaPheLysAlaSerPheSerile 205

QY 812 AAGTACGAAGAGAGAGCAGCATATTCACATATCCAAACATGCCAAAGGTTTAAGCAATT 871

Db 206 LysIleArgGluProArgHisLeuAlaIleSerAsnMetProLeuValLysSerVal 225

QY 872 GAATCTGAAGAGGCTTTTGGAGATCAGTCTTGAACACTGTAATAATGAGTACATAC 931

Db 226 ThrValAlaGluGlyLeuIleGluAspHisPheAspValThrValLysMetSerThrTyr 245

QY 932 CTTGTAGCTACATAGTTTGTGATTTCACATCTCTGAGTGGCTTCACATTCATCAGGGTCT 991

Db 246 LeuValAlaPheIleIleSerAspPheGluSerValSerLysIleThrLysSerGlyVal 265

QY 992 AAGTGTCCATCTATGATCCCGAGACAAACGGAATCAACACATATATGCTTTGAGGCA 1051

Db 266 LysValSerValTyrAlaValProAspLysMetAsnGlnAlaAspTyrAlaLeuAspAla 285

QY 1052 TCATCTGAAGTACTGATTTTATGAAAGTACTTTGATATCTACTACTCTCTCCACTCTCCAAA 1111

Db 286 AlaValThrLeuLeuGluPheTyrGluAspTyrPheSerIleProTyrProLeuProLys 305

QY 1112 CTGGATTTAATTTGCTATTCTCTGACTTTTGACCTCGAGCCATGGAAATTTGGGCGCTCAT 1171

Db 306 GlnAspLeuAlaAlaIleProAspPheGlnSerGlyAlaMetGluAsnTrpGlyLeuThr 325

QY 1172 ACATATAGGAGAGCGTCACTGCTTTTGGACCCCAAGACCTCTTCTGCTTCGATAACTG 1231

Db 326 ThrTyrArgGluSerAlaLeuLeuPheAspAlaGluLysSerSerAlaSerSerLysLeu 345

QY 1232 TGGGTCCACAGAGTCATAGCCCATGAACTGCGCACCATGCTGTTGGCAACTCGTGTACA 1291

Db 346 GlyIleThrMetThrValAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeuValThr 365

QY 1292 ATGGAATGGTGAATGATATTTGGCTTAAGAGAGGTTTTCGAAAATACATGGAACCTATC 1351

Db 366 MetGluTrpTrpAsnAspLeuTrpLeuAsnGluGlyPheAlaLysPheMetGluPheVal 385

QY 1352 GCTGTTAATGCTACATATCCAGAGCTGCAATTTGATGACTATATTTTGAATGTGTGTTT 1411

Db 386 SerValSerValThrHisProGluLeuLysValGlyAspTyrPhePheGlyLysCysPhe 405

QY 1412 GAAGTAATTACAAAGATTCATTAATTCATCCCGCCTATCTCCAAACAGCGGAACACC 1471

Db 406 AspAlaMetGluValAspAlaLeuAsnSerSerHisProValSerThrProValGluAsn 425

PT conditions, respiratory disorders, cancers, CNS disorders, or
PT neurodegenerative disorders.

XX Claim 13; SEQ ID NO 1010; 1754pp; English.

PS The invention relates to 592 new human secreted polypeptides useful for
XX diagnosing, treating or preventing e.g. immune disorders, inflammatory
CC conditions, respiratory disorders, cancers, CNS disorders, or
CC neurodegenerative disorders, or polypeptides comprising an amino acid
CC sequence at least 95% identical to the new sequences. The polypeptides,
CC antibodies or antibody fragments that bind to the polypeptides, nucleic
CC acids encoding the polypeptides, agonists or antagonists that binds to
CC the polypeptide, are useful in preparing diagnostic or pharmaceutical
CC compositions for diagnosing, treating or preventing an e.g. immune
CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,
CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
CC (e.g. multiple sclerosis or ischemic brain injury), neurodegenerative
CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and
CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
CC polynucleotides are useful for chromosome identification, chromosome
CC mapping, for controlling gene expression through triple helix formation
CC or antisense DNA or RNA, in gene therapy, for identifying individuals
CC from minute biological samples, in forensic biology, and as hybridization
CC probes. The polypeptides are useful for as molecular weight markers on
CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
CC gels, to raise antibodies, for testing biological activities, and for
CC treating or preventing neural disorders, immune system disorders,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal, proliferative and/or cancerous diseases. This sequence corresponds
CC to one of the polypeptide of the invention. Note: The sequence data for
CC this patent did form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 941 AA;

Alignment Scores:

Pred. No.:	4,476-245	Length:	941
Score:	2515.50	Matches:	477
Percent Similarity:	69.34%	Conservative:	172
Best Local Similarity:	50.96%	Mismatches:	268
Query Match:	42.55%	Indels:	19
DB:	6	Gaps:	7

US-10-039-073-2 (1-3366) x ADA56820 (1-941)

QY	212	TACTGCTTAACGCCATCTTGCCCAATATGCAATTTGTTCTCAGTTCTCAGTCCCATCT	271
DB	15	PhelLeuLeuSerSerLeuLeuAlaLeuLeuThrVal-----SerThrProSer	30
QY	272	AGTTATCACTTCACGTGAGGATCCTGGGCTTCCCGATGAGCAGTAAATGGGGAACGATTT	331
DB	31	TrpCysGlnSerThrGlu-----AlaSerProLysArgSerAspGlyThrProPhe	47
QY	332	CCTTGGCAGGAGCTAAGCTCCCGAGTGTGTCATCTCTCCATATGACCTCTTTGTC	391
DB	48	ProTrpAsnLeuValLeuProGluLeuValIleProValHisThrAspLeuLeu	67
QY	392	CACCCCAATCTACCTCTGACATCTTGTGATCTGAGAGATCGAAGTCTTGGTCAGC	451
DB	68	HisAlaAsnLeuThrLeuThrPheTrpGlyThrThrLysValGluIleThrAlaSer	87
QY	452	AATGCTACCCAGTTTATCATCTTGACAGCAAGATCTTGAATCACCAGATCCACCCCTT	511
DB	88	GlnProThrSerThrIleLeuLeuHisSerHisLeuLeuGlnIleSerArgAlaThrLeu	107
QY	512	CAGTCAGAGGAGATTCAAGATACATGAACACGAGAAAGAACTGAAAGTTTGTGATAC	571
DB	108	ArgLysGlyAlaGlyLeuArgLeuSerGlu-----GluProLeuGlnValLeuGluHis	125
QY	572	CCTGCTCATGAACAAATTTGCACTGCTGTTCCAGAGAAACCTTACGCCTCCTGAAATAC	631

Db	126	ProProGlnGluGlnIleAlaLeuLeuAlaProGluProLeuLeuValGlyLeuProTyr	145
QY	632	TATGTGCTATGGAGCTTTCAGCCAGTTAGGTGATGCTTTTGAAGGGTTTTATAAAGC	691
Db	146	ThrValValIleHisTyrAlaGlyAsnLeuSerGluThrPheHisGlyPheTyrLysSer	165
QY	692	ACATACAGAACTCTGGTGGTGAACAAGAAATCTTGCAGTAACAGATTTTGGAGCCAAC	751
Db	166	ThrTyrArgThrLysGluGlyLeuArgIleLeuAlaSerThrGlnPheGluProThr	185
QY	752	CAGCAGCATGGCTTCCCTTGTGATCAACCGTTGTTTCAAGGCCAACTTTTCAATC	811
Db	186	AlaAlaArgMetAlaPheProCysPheAspGluProAlaPheLysAlaSerPheSerIle	205
QY	812	AAGTACGAAGAGAGAGCAGCATATTGCATCTCCAAATCCCAAGAGTTTAAAGCAAT	871
Db	206	LysIleArgArgGluProArgHisLeuAlaIleSerAsnMetProLeuValLysSerVal	225
QY	872	GAACTTGAAGAGGCTCTTTGGAGATCAGCTTTGAACTACTGTAAATATGATACATAC	931
Db	226	ThrValAlaGluGlyLeuIleGluAspHisPheAspValThrValLysMetSerThrTyr	245
QY	932	CTTGTAGCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTTCACCTTCATCAGGGTC	991
Db	246	LeuValAlaPheIleIleSerAspPheGluSerValSerLysIleThrLysSerGlyVal	265
QY	992	AAGGTGTCATCTATGATCCCCAGACAAAGGAAATCAACACATATTGCTTTGCAGCA	1051
Db	266	LysValSerValTyrAlaValProAspLysMetAsnGlnAlaAspTyrAlaLeuAspAla	285
QY	1052	TCACTGAAGTACTGATTTTATGAAAGTACTTTGATATCTACTACTCTCCACTCTCCAA	1111
Db	286	AlaValThrLeuLeuGluPheTyrGluAspTyrPheSerIleProTyrProLeuProLys	305
QY	1112	CTGGATTTAATTTGCTATTCTGACTTTGCCTCGAGCCATGGAAATTTGGGGCTCATTT	1171
Db	306	GlnAspLeuAlaIleProAspPheGlnSerGlyAlaMetGluAsnTrpGlyLeuThr	325
QY	1172	ACATATAGGAGAGCGTCACCTGCTTTTGGACCCCAAGACCTCTTCTGCTCCGATAAATC	1231
Db	326	ThrTyrArgGluSerAlaLeuLeuPheAspAlaGluLysSerSerAlaSerSerLysLeu	345
QY	1232	TGGGTACACAGATCATAGCCCATGAACTGGCGCACACAGTGGTTTGGCAACTGGTCACA	1291
Db	346	GlyIleThrMetThrValAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeuValThr	365
QY	1292	ATGGAATGGTGGATGATATTGGCTTAAAGGAGGTTTTGCAAAATACATCGAATTCATC	1351
Db	366	MetGluTrpAsnAspLeuTrpLeuAsnGluGlyPheAlaLysPheMetGluPheVal	385
QY	1352	GCTGTTAATGCTACATATCCAGAGCTGCAATTTTGATGACTATTTTGAATGTGTGTTT	1411
Db	386	SerValSerValThrHisProGluLeuLysValGlyAspTyrPhePheGlyLysCysPhe	405
QY	1412	GAAGTAATACAAAGATTCATGAATTCATCCCGCCCTATCTCCAAACCGAGCGGAAC	1471
Db	406	AspAlaMetGluValAspAlaLeuAsnSerSerHisProValSerThrProValGluAsn	425
QY	1472	CCGACTCAATACAGGAAATGTTTGTGAAGTTTCTTATACAAAGGAGCTTGTATTGTTG	1531
Db	426	ProIleGlnIleArgGluMetPheAspAspValSerTyrAspLysGlyAlaCysIleLeu	445
QY	1532	AATATGCTCAAGGATTTTCTGGGTGAGAGAAATTCAGAGAAAGGAATTAATTCAGTACT	1591
Db	446	AsnMetLeuArgGluTyrLeuSerAlaAspAlaPheLysSerGlyIleValGlnTyrLeu	465
QY	1592	AAGAGTTTCAGCTATAGAAATGCTAAGAAATGATGACTTTGGAGCAGCTCTGTCAATAGT	1651
Db	466	GlnLysHisSerTyrLysAsnThrLysAsnGluAspLeuTrpAspSerMetAlaSerIle	485
QY	1652	TGTTTAGAAGTGAATTTTACATCTGGT-----GGAGTTTGTTCATTCGGATCCCAAGAT	1705
Db	486	Cys---ProThrAspGlyValLysGlyMetAspGlyPheCys---SerArgSerGlnHis	503

QY	1706	ACAAGTAA	CATGCTCG	CTCTTTCTGGGGG	AAATACGACAGGTCAAAGAGATGATGACTACA	1765
DB		::: :::	:::	:::	::: :::	
DB	504	SerSerSer	HisTyrHis	GlnGluGlyVal	AspValIysThrMetMetAsnThr	523
QY	1766	TGGNACTCT	CAGAAAGNA	TCCCCCTCTGGTGGT	TAAACAAGACGGGTGTTCACCTCCGA	1825
DB		:::	:::	:::	:::	
DB	524	TrpThrLeu	GlnArgGlyPhe	ProLeuIleThrIleThrVal	ArgGlyIysArgAsnValHis	543
QY	1826	CTGCAACAG	GAGCGCTTCTCC	TCCAGGGGGT	TTTCCAGGAAGACCCCTGAATCGAGGGCGCTG	1885
DB		::: :::	::: :::	::: :::	::: :::	
DB	544	MetIysGln	GluHisTyrMet	LysGly	-----SerAspGlyAlaPro	557
QY	1886	CAGGAGAGG	TACCTGTGGCATAT	CCCATGACTCTACCTAC	TCCACGAGTCTTCTTAATGTGATC	1945
DB		:::	:::	:::	:::	
DB	558	AspThrGly	TyrLeuTyrHis	ValProLeuThrPheIleThr	SerLysSerAspMetVal	577
QY	1946	CACAGACAC	ATTCTTAATCAAA	GACAGATACTCTGGATCT	TACCTGCTGCTGAAAGACCCAGTTGG	2005
DB		::: :::	::: :::	::: :::	::: :::	
DB	578	HisArgPhe	LeuLeuLysThrLys	ThrAspValLeuLeuLeu	ProGluGluValGluTyr	597
QY	2006	GTGAAATTT	TAATGTGGACTCA	AAATGGTTACTACATCGT	TCACTATGAGGTCTATGATGG	2065
DB		::: :::	::: :::	::: :::	::: :::	
DB	598	IleLysPhe	AsnValGlyMet	AsnGlyTyrTyrIleValHis	TyrGluAspAspGlyTyr	617
QY	2066	GACCAACT	CATTACACAGCTG	AATCAAGAACACACAC	ACTTCTCAGACCTAAGGACAGAGTA	2125
DB		:::	:::	:::	:::	
DB	618	AspSerLeu	ThrGlyLeuLeuLys	GlyThrHisThrAlaVal	SerSerAsnAspArgAla	637
QY	2126	GGTCTGATT	CATGATGTGTTT	TCAGTCTAGTGTGTCAG	GGAGACTGACCTTAGACAAAGCT	2185
DB		:::	:::	:::	:::	
DB	638	SerLeuIle	AsnAsnAlaPhe	GlnLeuValSerIleGly	LysLeuSerIleGluLysAla	657
QY	2186	CTTGACATG	ACTTACTCTCCAA	CATCAAGAAACAGCAG	CCCCGACCTTCTCGAAGTCTG	2245
DB		:::	:::	:::	:::	
DB	658	LeuAspLeu	SerLeuTyrLeuLys	HisGluThrGluIleMet	ProValPheGlnGlyLeu	677
QY	2246	AGTTACTTG	NAATCGTTTACC	ACCATGATGACAGAGAAG	AATATTTCCAGATATCTCTGAA	2305
DB		::: :::	::: :::	::: :::	::: :::	
DB	678	AsnGluLeu	IleProMetTyrLys	LeuMetGluLysArgAspMet	AsnGluValGluThr	697
QY	2306	AACCTCAAG	CGTTACCTTCTT	TCAGTATTTAAGCCAGT	GTGTTGACAGCGCAAGCTCGAGT	2365
DB		::: :::	::: :::	::: :::	::: :::	
DB	698	GlnPheLys	AlaPheLeuIleArg	LeuLeuArgAspLeuIleAsp	LysGlnThrTyrThr	717
QY	2366	GACAAGGG	CTCAGTCTGGGAC	AGATGCTCGCTCGCTCT	TTTGAAGCTGGCTGTGAC	2425
DB		:::	:::	:::	:::	
DB	718	AspGluGly	SerValSerGluArg	MetLeuArgSerGluLeuLeuLeu	LeuAlaCysVal	737
QY	2426	CTGNACCAT	GCTCCTTCATCC	AGAAAGCTGCTGAACT	CTTCTCCCAGTGGATGCC	2485
DB		:::	:::	:::	:::	
DB	738	HisAsnTyr	GlnProCysValGln	ArgAlaGluGlyTyrPhe	ArgLysTyrLysGluSer	757
QY	2486	AGTGGAAAA	TTAAATATACCA	ACAGATGTTTAAAGAT	TGTGTATTTCTGGGTGCTCAG	2545
DB		::: :::	::: :::	::: :::	::: :::	
DB	758	AsnGlyAsn	LeuSerLeuProVal	AspValThrLeuAlaVal	PheAlaValGlyAlaGln	777
QY	2546	ACAAACAG	CAGATGGAATTA	CTTTTAGACAATATGA	CTGTCATGTCAAGTGTGAA	2605
DB		:::	:::	:::	:::	
DB	778	SerThrGlu	GlyTyrAspPheLeu	TyrSerLysTyrGlnPhe	SerLeuSerThrGlu	797
QY	2606	CAAAACAAA	ATTCGTATGCTT	CTCAACAGCAAGCAT	CAGGAAAAGTTACTGAACTTA	2665
DB		::: :::	::: :::	::: :::	::: :::	
DB	798	LysSerGln	IleGluPheAlaLeu	CysArgThrGlnAsnLys	GluLysLeuGlnTyrLeu	817
QY	2666	ATTGAAC	TAGGAATGGA	AGGAAGTTATCAAG	ACACAGAACTTGGCAGCTCTCTTCAT	2725
DB		:::	:::	:::	:::	
DB	818	LeuAspGlu	SerPheLysGlyAsp	LysIleLysThrGln	LeuPheProGlnIleLeuThr	837
QY	2726	CGCATTC	CCAGACGCTCC	AAAGGGCCAGCA	ACTAGCTGGGATTTGTAAAGAAAATGG	2785
DB		:::	:::	:::	:::	
DB	838	LeuIleGly	ArgAsnProVal	IgLYTyrProLeuAla	TrpGlnPheLeuLysLysAsnTyr	857

Qy	2786	ACCCATCTTCTGAAAAAATTGTACTTGCGGCTCATATGACATAAGGATGATCATCTCTGGC	2845
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Qy	2846	ACAACAGCTCACITTTCTTCCAAGGATAAGTCGAAGAGGCTGAACTATTTTTTGAATCT	2905
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Qy	2906	CTTGAGGCTCAAGGATCACATCTGGATATTTTTCAAACCTCTTCTGGAACGATAACAAA	2965
Db	898	LeuLysGluAsnGlySerGlnLeuArgCysValGlnGlnThrIleGluThrIleGluGlu	917
Qy	2966	AATATAAAATGGCTGGAGAAGATCTTCCGACTCTGAGGACTTGGCTPA	3013
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RESULT 14			
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XX	ABR47686 standard; protein; 941 AA.		
AC	ABR47686;		
XX			
DT	12-JUN-2003 (first entry)		
XX			
DE	Human secreted protein, SEQ ID 577.		
XX			
KW	Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytosstatic;		
KW	vulnerary; antiinflammatory; nootropic; neuroprotective;		
KW	antiparkinsonian; gene therapy; human; cardiovascular disorder.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200295010-A2.		
XX			
PD	28-NOV-2002.		
XX			
PF	19-MAR-2002; 2002WO-US009785.		
XX			
PR	21-MAR-2001; 2001US-0277340P.		
PR	19-JUL-2001; 2001US-0306171P.		
PR	13-NOV-2001; 2001US-0331287P.		
XX	(HUMA-) HUMAN GENOME SCI INC.		
PA	Rosen CA, Ruben SM;		
PI	WPI; 2003-129429/12.		
DR			
XX			
PT	Novel human secreted proteins, useful for detecting, preventing,		
PT	diagnosing, prognosticating, treating and/or ameliorating cardiovascular		
PT	disorders such as arrhythmia.		
XX			
PS	Claim 13; SEQ ID NO 577; 1881pp; English.		
XX			
CC	The present invention relates to novel human secreted proteins (ABR47633-		
CC	ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins		
CC	and their coding sequences are useful for the preparation of a diagnostic		
CC	or pharmaceutical composition for diagnosing or treating a cardiovascular		
CC	disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary		
CC	arteriosclerosis and myocardial ischaemia), neural disorders, immune		
CC	system disorders, muscular disorders, reproductive disorders,		
CC	gastrointestinal disorders, pulmonary disorders, renal disorders,		
CC	proliferative disorders and/or cancerous diseases and conditions, for		
CC	wound healing and epithelial cell proliferation, to treat inflammation or		
CC	infection, for treating thrombosis and arteriosclerosis, for treating or		
CC	preventing neural damage which occurs in neuronal disorders or		
CC	neurodegenerative conditions such as Alzheimer's disease and Parkinson's		
CC	disease, to enhance bone and periodontal regeneration and aid in tissue		
CC	transplants or bone grafts, to prevent skin aging or hair loss, to		
CC	stimulate growth and differentiation of haematopoietic cells and bone		
CC	marrow cells when used in combination with other cytokines, to maintain		
CC	organs before transplantation or for supporting cell culture of primary		
CC	tissues, to increase or decrease differentiation or proliferation of		

CC embryonic stem cells, or to modulate mammalian characteristics or
 CC metabolism. Note: The sequence data for this patent was published in
 CC electronic format and is available from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 941 AA;

Alignment Scores:

Pred. No.: 4,476-245 Length: 941
 Score: 2515.50 Matches: 477
 Percent Similarity: 69.34% Conservative: 172
 Best Local Similarity: 50.96% Mismatches: 268
 Query Match: 42.55% Indels: 19
 Gaps: 7

US-10-039-073-2 (1-3366) x ABR47686 (1-941)

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 Db 15 PheLeuLeuSerSerLeuLeuAlaLeuLeuThrVal-----SerThrProSer 30
 QY 272 AGTTATCACTTCACTCAGGATCCTGGGGCTTTCCAGTAGCCACCTAAATGGGGAACGATTT 331
 Db 31 TrpCysGlnSerThrGlu-----AlaSerProLysArgSerAspGlyThrProPhe 47
 QY 332 CTTGGCAGGAGCTAAGGCTCCCGAGTGGTGCATCTCTCCATATGACCTCTTTGTC 391
 Db 48 ProTrpAsnLysIleArgLeuProGluTrpValIleProValHisThrAspLeuLeuIle 67
 QY 392 CACCCCAATCTCCTCTGACCTTTGTTGATCTCGAGAGATCGAAGTCTTGTGTGAC 451
 Db 68 HisAlaAsnLeuThrThrLeuThrPheTrpGlyThrThrLysValGluIleThrAlaSer 87
 QY 452 AATGCTACCCAGCTTTATCATCTTGACAGCAAGAGTCTTGAATCACCAGATGCCACCTT 511
 Db 88 GlnProThrSerThrIleIleLeuHisSerHisHisLeuGlnIleSerArgAlaThrLeu 107
 QY 512 CAGTCAGAGGAAGATTCAGATPACATGAACACGAGGAAGAACTGAAAGTTTGTGATTC 571
 Db 108 ArgLysGlyAlaGlyGluArgLeuSerGlu-----GluProLeuGlnValLeuGluHis 125
 QY 572 CTTGCTCATGACAAATGCACTGCTGGTTCAGAGAACTTACCCCTCAGCTGGAATAC 631
 Db 126 ProProGlnGluGlnIleAlaLeuLeuAlaProGluProLeuLeuValGlyLeuProTrp 145
 QY 632 TATGTGGCTATGAGCTTCCAGCCCAAGTTAGTGATGCTTTGAAGGGTTTATAAAGC 691
 Db 146 ThrValValIleHisThrAlaGlyAsnLeuSerGluThrPheHisGlyPheThrLysSer 165
 QY 692 ACATACAGAACTTTGGTGGTGAACAAAGAATCTTGCAAGTAAACAGATTTGAGCCAAC 751
 Db 166 ThrTyArgThrLysGluGlyGluLeuArgIleLeuAlaSerThrGlnPheGluProThr 185
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 Db 186 AlaAlaArgMetAlaPheProCysPheAspGluProAlaPheLysAlaSerPheSerIle 205
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 Db 206 LysIleArgGluProArgHisLeuAlaIleSerAsnMetProLeuValLysSerVal 225
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 QY 1352 GCTCTTAATGCTCATATCCAGAGCTGCAATTTGATGACTATTTTGAATGTGTGTTT 1411
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 QY 1412 GAAGTAATTAACAAGATTCATTCAATTCATCCCGCTTATCTCCAAACCCAGCGAACC 1471
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 QY 1472 CCGACTCAATACAGGAAATGTTTGTGAGTCTTCTATACAAAGGAGCTTGTGATTTG 1531
 Db 426 ProAlaGlnIleArgGluMetPheAspValSerTyArgLysGlyAlaCysIleLeu 445
 QY 1532 AATATGCTCAAGGATTTTCTGGGTGAGGAGAAATTCAGAAAGGAATAATTCAGTACTTA 1591
 Db 446 AsnMetLeuArgGluTyLeuSerAlaAspAlaPheLysSerGlyIleValGlnTyLeu 465
 QY 1592 AAGAAGTTCACTATAGAAATGCTAAGATGATGACTGTGAGGAGCTCTGCTCAATAGT 1651
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 QY 1652 TGTTTAGAAAGTGAATTTTACATCTGGT-----GGAGTTTCTCATTCGAGTCCCAAGATG 1705
 Db 486 Cys---ProThrAspGlyValLysGlyMetAspGlyPheCys---SerAspSerGlnHis 503
 QY 1706 ACAAGTAACTGCTCGCTTCTGGGGGAAATCGAGAGTCAAGAGATGATGACTACA 1765
 Db 504 SerSerSerSerHisTrpHisGlnGluGlyValAspValLysThrMetMetAsnThr 523
 QY 1766 TGGACTCTCCAGAAAGGAATCCCTCTGCTGTGTGTTAAACAAGCGGTGTCTACTCCGA 1825
 Db 524 TrpThrLeuGlnArgGlyPheProLeuIleThrIleThrValArgGlyArgAsnValHis 543
 QY 1826 CTGCAACAGGAGCGCTCTCCAGGGGTTTTCCAGGAAGACCCCTGAATGAGGGCCCTG 1885
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 QY 1886 CAGGAGAGGTACCTGTGGCATATCCCATGACCTACTCCACAGTTCTTCTTAATGTATC 1945
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 QY 2066 GACCAACTTATACAGCTGAATCAGAACACACACTTCTTCAGACCTTAAGCAGAGATA 2125
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Qy      2666 ATTGAACCTAGGAATGGAGAAAGTTATCAAGACACAGAACTTGGCAGCTCTCCTTCAT 2725
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Qy      2726 GCGATTGCCAGACGTCCAAAGGGGAGCACTAGCATGGGATTTTGTAAAGAGAAAATTGG 2785
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Qy      2906 CTTGAGGCTCAGGATCAGATCTGATATTTTCAAACCTGTCTGGAAACGATAACCAAA 2965
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Qy      2966 AATATAAATGGCTGGAGAGAAATCTTCCGACTCTGAGGACTTGGCTA 3013
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Search completed: September 26, 2005, 07:10:16
 Job time : 520.219 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model
Run on: September 26, 2005, 06:43:03 ; Search time 431.186 Seconds
(without alignments)
6354.782 Million cell updates/sec

Title: US-10-039-073-2
Perfect score: 5912
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Scoring table:
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1826554 seqs, 407025358 residues

Total number of hits satisfying chosen parameters: 3653108

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	5052	85.5	960	13	US-10-039-073-1	Sequence 1, Appli
2	5052	85.5	960	14	US-10-168-425-6	Sequence 6, Appli
3	4141	70.0	785	15	US-10-363-616-459	Sequence 459, App
4	3799	64.3	728	9	US-09-764-853-646	Sequence 646, App
5	3770	63.8	722	9	US-09-764-853-819	Sequence 819, App
6	2516.5	42.6	941	15	US-10-220-443-2	Sequence 2, Appli
7	2515.5	42.5	941	15	US-10-264-237-2723	Sequence 2723, App
8	2515.5	42.5	941	18	US-10-472-533-329	Sequence 329, App
9	2515.5	42.5	944	14	US-10-106-698-6381	Sequence 6381, Ap
10	2512.5	42.5	941	9	US-09-989-722-353	Sequence 353, App
11	2512.5	42.5	941	9	US-09-989-723-353	Sequence 353, App
12	2512.5	42.5	941	12	US-09-989-279-353	Sequence 353, App
13	2512.5	42.5	941	9	US-09-989-727-353	Sequence 353, App
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15	2512.5	42.5	941	9	US-09-989-732-353	Sequence 353, App
16	2512.5	42.5	941	9	US-09-991-073-353	Sequence 353, App
17	2512.5	42.5	941	9	US-09-990-442-353	Sequence 353, App
18	2512.5	42.5	941	18	US-09-991-163-353	Sequence 353, App
19	2512.5	42.5	941	9	US-09-993-604-353	Sequence 353, App
20	2512.5	42.5	941	9	US-09-990-456-353	Sequence 353, App
21	2512.5	42.5	941	9	US-09-989-721-353	Sequence 353, App
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26	2512.5	42.5	941	9	US-09-991-181-353	Sequence 353, App
27	2512.5	42.5	941	9	US-09-989-730-353	Sequence 353, App
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45	2512.5	42.5	941	10	US-09-997-514-353	Sequence 353, App

ALIGNMENTS

RESULT 1
US-10-039-073-1
; Sequence 1, Application US/10039073
; Publication No. US20020098177A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: 17867, A No. US20020098177A1el Human Amino peptidase
; FILE REFERENCE: 35800/240749(5800-36
; CURRENT APPLICATION NUMBER: US/10/039,073
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 09/345,650
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 960
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-073-1

Alignment Scores:

Pred. No.: 0 Length: 960
Score: 5052.00 Matches: 960
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.45% Indels: 0
DB: 13 Gaps: 0

US-10-039-073-2 (1-3366) x US-10-039-073-1 (1-960)

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DB 1 MetPheHisSerSerAlaMetValAsnSerHisArgLysProMetPheAsnIleHisArg 20
QY 206 GGATTTTACTGCTTAAACAGCATCTTGCCCAATAATGTCATTTGTTCTCAGTTCACAGT 265
DB 21 GlyPheTyrCysLeuThrAlaIleLeuProGlnIleCysIleCysSerGlnPheSerVal 40
QY 266 CCATCTAGTTATCACTTCACCTGAGGATCCTCGGGGCTTCCAGTAGCCACTAAATGGGGAA 325
DB 41 ProSerSerTyrHisPheThrGluAspProGlyAlaPheProValAlaThrAsnGlyGlu 60
QY 326 CGATTTCTTCGGCAGGAGCTAAGGCTCCCGAGTGTGTCATTCCTCTCCATTATGACCTC 385
DB 61 ArgPheProTyrGlnGluLeuArgLeuProSerValValIleProLeuHisTyrAspLeu 80
QY 386 TTTGTCACCCCAATCTCACCCTCTGACCTTGTGTCATCTGAGAGATCGAAGTCTTG 445
DB 81 PheValHisProAsnLeuThrSerLeuAspPheValAlaSerGluLysIleGluValLeu 100
QY 446 GTCAGCAATGCTACCCAGTTTATCATCTTGACACAGCAAAAGATCTTGAATCACCAATGCC 505
DB 101 ValSerAsnAlaThrGlnPheIleIleLeuHisSerLysAspLeuGluIleThrAsnAla 120
QY 506 ACCCTTCAGTCAGGAGAGATTCAAGATPACATGAATCAACAGGAAAAGAACTGAAAGTTTG 565
DB 121 ThrLeuGlnSerGluGluAspSerArgTyrMetLysProGlyLysGluLeuLysValLeu 140
QY 566 AGTTACCCCTGCATGAACAAATGTCACCTGCTGGTTCAGAGAAACTTACGCCCTCACCTG 625
DB 141 SerTyrProAlaHisGluGlnIleAlaLeuLeuValProGluLysLeuThrProHisLeu 160
QY 626 AAATACTATGTGGCTATGCACTTCCAGCCAAAGTTAGGTGATGGCTTTGAAGGGTTTAT 685
DB 161 LysTyrTyrValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTyr 180
QY 686 AAAAGCACATACAGAACTCTTTGGTGGTGAACAAGAATTCTTGCAAGTAAACAGATTTTGAG 745
DB 181 LysSerThrTyrArgThrLeuGlyGlyGluThrArgIleLeuAlaValThrAspPheGlu 200
QY 746 CCNACCCAGGCACGATGGCTTCCCTGCTTGTGATGACCGTGTTCNAGGCCAATCTT 805
DB 201 ProThrGlnAlaArgMetAlaPheProCysPheAspGluProLeuPheLysAlaAsnPhe 220
QY 806 TCAATCAAGATACGAAGAGACAGGAGCATATTGCACTATCAACATGCCAAAGGTTAAG 865
DB 221 SerIleLysIleArgArgGluSerArgHisIleAlaLeuSerAsnMetProLysValLys 240
QY 866 ACAATTGAACCTTGAGGAGGCTTTTGGAGAGATCACTTTGAAACTACTGTGTAATAATGAGT 925
DB 241 ThrIleGluLeuGluGlyGlyLeuLeuGluAspHisPheGluThrThrValLysMetSer 260
QY 926 ACATACCTTGAGCTACATAGTTGTGATTTCCACTCTGAGTGGCTTCACCTCATCA 985
DB 261 ThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThrSerSer 280
QY 986 GGGGTCAAGGTGCTCATCTATGATCCCGACAGCAAAACCGAATCAAAACATATTGCTTTG 1045
DB 281 GlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyrAlaLeu 300
QY 1046 CAGGCATCACTGAAGCTACTGATTTTATGAAAGATGATCTTGTGATATCTACTCCACTC 1105
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DB 301 GlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyrProLeu 320
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DB 321 SerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsnTrpGly 340
QY 1166 CTCAATTACATATAGGAGAGCGTCACTGCTTTTTCACCCCAAGACCTCTTCTGCTTCCGAT 1225
DB 341 LeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAlaSerAsp 360
QY 1226 AAATGTGGTCCACGAGTCATAGCCCATGAACTGGCGCACCAAGTGGTTGGTGGCAACCTG 1285
DB 361 LysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeu 380
QY 1286 GTCACATGAAGTGGTGAATGATATTGCTTAAGCAGGGTTTGCAAAATACATCGAA 1345
DB 381 ValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyrMetGlu 400
QY 1346 CTTATCGCTGTTAATGCTACATATCCAGAGCTGCAATTTTGATGACTATTATTTTGAATGTG 1405
DB 401 LeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeuAsnVal 420
QY 1406 TGTTTTGAAGTAAATCAAAAAGATTCAATGAAATTCATCCCGCCCTATCTCAAAACACGCG 1465
DB 421 CysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLysProAla 440
QY 1466 GAAACCCCGACTCAAATACAGGAAATGTTTGATGAAGTTTCTTATAACAAGGGAGCTTGT 1525
DB 441 GluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGlyAlaCys 460
QY 1526 ATTTTGAATATGCTCAAGGATTTTCTGGGTGAGGAGAAATTCAGAAAGGAATAATTTAG 1585
DB 461 IleLeuAsnMetLeuLysAspPheLeuGlyGluGluLysPheGlnLysGlyIleGln 480
QY 1586 TACTTAAAGAGTTCAGCTATAGAAATGCTAAGAATGATGACTTGTGGAGCAGTCTGTCA 1645
DB 481 TyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspLeuTrpSerSerLeuSer 500
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DB 521 ThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGluValLysGluMetMetThrThr 540
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DB 541 TrpThrLeuGlnLysGlyIleProLeuLeuValValLysGlnAspGlyCysSerLeuArg 560
QY 1826 CTGCAACAGGAGCGCTTCTCCAGGGGGTTTTCAGGAAGACCCCTGAATGAGGGCCCTG 1885
DB 561 LeuGlnGlnGluArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArgAlaLeu 580
QY 1886 CAGGAGAGTACCTGTGGCATATCCCATTCACCTACTCCACGAGTTCTTCTTAATGTGATC 1945
DB 581 GlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerThrSerSerSerAsnValIle 600
QY 1946 CACGACACATCTTAAATCAAAGACAGATACTCTGATCTACTGAAAGACCAAGCTGG 2005
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QY 2006 GTGAAATTTAATGTGGACTCAAATGGTTTACTACATCGTTTCACTATGAGGGTCACTGGATGG 2065
DB 621 ValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHisGlyTrp 640
QY 2066 GACCAACTCAATTACAGCTGAATCAGAACACACACTTCTCAGACCTTAAGGACAGAGTA 2125
DB 641 AspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAspArgVal 660
QY 2126 GGTCTGATTTCAATGTTGTTTTCAGCTAGTTGGTCAGGAGACTGACCTAGACAAAGCT 2185
DB 661 GlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAspLysAla 680
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QY 2186 CTTGACATGACTTACTTACCTCAACATGAACAGCAGCCCGCACTTCTCGAAGTCTG 2245
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QY 681 LeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProAlaLeuLeuGluGlyLeu 700
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QY 2246 AGTTACTTGGATCGTTTACCACATGATGGACAGAGGAAATATTCAGATATCTCTGAA 2305
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QY 701 SerTyrLeuGluSerPheTyrHisMetMetAspArgAsnIleSerAspIleSerGlu 720
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QY 2306 AACCTCAAGCGTTACTCTTTCAGTATTTTAAAGCCAGTATTGACAGGCAAGCTGGAGT 2365
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QY 2366 GACAGGGCTCAGTCTGGGACAGGATGCTCCGCTCGCTCTCTTGAAGCTGCGCTGTGAC 2425
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QY 2486 AGTGAAATTAATATATACCAACAGATGTTTAAAGATGTGTATTTCTGTGGTCTCAG 2545
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QY 781 SerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrSerValGlyAlaGln 800
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QY 2546 ACAACAGCAGGATGGAATTTACCTTTTAGAGCAATATGAACCTGCTCAATGTCAAGTCTGAA 2605
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QY 801 ThrThrAlaGlyTrpAsnTyrLeuLeuGluGlnTyrGluLeuSerMetSerSerAlaGlu 820
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QY 821 GlnAsnLysIleLeuTyrAlaLeuSerThrSerLysHisGlnGluLysLeuLeuLysLeu 840
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QY 2666 ATTGAACTAGGAATGGAAGAGTTATCAAGACACAGAACTCTGCGAGCTCTCCTTCAT 2725
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QY 841 IleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaLeuLeuHis 860
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QY 2726 GCGATTGCCAGACGTCCAAAGGGCAGCAACTAGCATGGATTTTGTGAAGAGAAATGG 2785
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QY 941 AsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeuMetValAsnThr 960
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RESULT 2

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US-10-168-425-6
; Sequence 6, Application US/10168425
; Publication NO. US20030124706A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YANG, Junming
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: BURFORD, Neil
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: REDDY, Roopa
; APPLICANT: YUE, Henry
; APPLICANT: NGUYEN, Dannel B.
; APPLICANT: TANG, Y. Tom
; APPLICANT: YAO, Monique G.
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; APPLICANT: LAL, Preeti
; TITLE OF INVENTION: PROTEASES
; FILE REFERENCE: PI-0003 PCT
; CURRENT APPLICATION NUMBER: US/10/168,425
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/172,055; 60/177,334; 60/178,884; 60/179,903
; PRIOR FILING DATE: 1999-12-23; 2000-01-21; 2000-01-28; 2000-02-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PERL Program
; SEQ ID NO 6
; LENGTH: 960
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030124706A1 60116897CD1
US-10-168-425-6

Alignment Scores:
Pred. No.: 0 Length: 960
Score: 5052.00 Matches: 960
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatch: 0
Query Match: 85.45% Indels: 0
DB: 14 Gaps: 0

US-10-039-073-2 (1-3366) x US-10-168-425-6 (1-960)
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QY 161 LysTyrTyrValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTyr 180
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QY 746 CCAACCCAGGACGATGCTTCCCTTTCCTTTGATGAACCGCTTGTTCAAAGCCCACTTT 805
Db |||||
QY 201 ProThrGlnAlaArgMetAlaPheProCysPheAspGluProLeuPheLysAlaAsnPhe 220
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QY 806 TCAATCAAGATACGAAGAGAGAGGAGGATATTGCACTATTCACATCCCAAGGTTAAG 865
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QY 1106 TCCAAACTGGATTTAAATGCTATTCTGACTTTTCACCTGGAGGCATGGAAAAATGGGGC 1165
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Db 341 LeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAlaSerAsp 360
QY 1226 AAACGTGGGTCACCGAGTCCATAGCCCATCACTGGCGCACCACTGGTTTGGCAACTG 1285
Db 361 LysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeu 380
QY 1286 GTCACAAATGGAAATGGTGAATGATATTTGGCTTAAGGAGGGTTTTGCAAAATACATGGAA 1345
Db 381 ValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyrMetGlu 400
QY 1346 CTTATCGCTGTTAATGCTACATATCCAGAGCTGCAATTTTGATGACTATTTTGAATGTG 1405
Db 401 LeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeuAsnVal 420
QY 1406 TGTTTGAAGTAATTACAAAGATTCATTGAAATTCATCCCGCCCTATCTCCAAACCCAGCG 1465
Db 421 CysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLysProAla 440
QY 1466 GAAACCCCGACTCAAAATACAGGAAATGTTTGATGAAGTTTCTTATAACAAGGGAGCTGT 1525
Db 441 GluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGlyAlaCys 460
QY 1526 ATTTTGAATATGCTCAAGGATTTCTGGTGAGGAGAAATTCAGAAAGGAATTAATTCAG 1585
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QY 1646 AATAGTCTTTAGAAAGTGAATTTTACATCTCGTGGAGTTTCTCATTCGGATCCCAAGATG 1705
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QY 1766 TGGACTCTCCAGAAGGAATCCCTGCTGCTGTTAAACAGACGGGTTCCTACTCCGA 1825
Db 541 TrpThrLeuGlnLysGlyIleProLeuLeuValValLysGlnAspGlyCysSerLeuArg 560
QY 1826 CTGCAACAGGAGCGCTTCCTCCAGGGGTTTTCCAGGAAGACCTGGAATGAGAGGCCCTG 1885
Db 561 LeuGlnGlnArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArgAlaLeu 580
QY 1886 CAGGAGGTTACCTGTGGCATATCCATTGACCTACTCCAGGATTTCTCTAATGTGATC 1945

Db 581 GlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerThrSerSerSerAsnValle 600
QY 1946 CACAGACACATCTTAAATCAAAAGACAGATACTCTGATCTACTCTGAAAAACAGATTGG 2005
Db 601 HisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThrSerTrp 620
QY 2006 GTGAAATTTAATGTGACTCAAAATGTTTACTACATCGTTCACATGATGAGGTCATGGATGG 2065
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QY 2066 GACCAACTCATTTACACAGCTGAATCAGAACACACACACTTCTCAGACCTAAGACAGAGTA 2125
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QY 2126 GGTCTGATTCATGATGTTTTCAGCTAGTTGGTCAGGGAGACTGACCCCTAGACAAAGCT 2185
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QY 2186 CTTGACATGACTTACTACCTCCAAACATGAAACAGCAGCCCCGACCTTCTCGAAGGCTG 2245
Db 681 LeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProAlaLeuLeuGluGlyLeu 700
QY 2246 AGTTACTTGGAAATCGTTTACACATGATGACAGAGGAATATTTTCAGATATCTCTGAA 2305
Db 701 SerTyrLeuGluSerPheTyrHisMetMetAspArgAsnIleSerAspIleSerGlu 720
QY 2306 AACCTCAAGGCTTACCTTCTTCACTATTTTAAAGCCAGTGTATGACAGGCCAAGCTGGAGT 2365
Db 721 AsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSerTrpSer 740
QY 2366 GACAAGGCTCAGTCTGGGACAGGATGCTCCGCTCGGCTCTCTGAAAGCTGGGCTGTGAC 2425
Db 741 AspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAlaCysAsp 760
QY 2426 CTGAACCATGCTCTCTGATCCAGAAAGCTGCTGAACCTTCTCCAGTGGATGGAATCC 2485
Db 761 LeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMetGluSer 780
QY 2486 AGTGGAAAAATTAATATACCAACAGATGTTTAAAGATTGTGATTCTGTGGGTGCTCAG 2545
Db 781 SerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrSerValGlyAlaGln 800
QY 2546 ACAACAGCAGGATGGAATTAACCTTTTAGACAAATATGAACCTGTCATGTCAAGTCTGAA 2605
Db 801 ThrThrAlaGlyTrpAsnTyrLeuLeuGluGlnTyrGluLeuSerMetSerSerAlaGlu 820
QY 2606 CAAAACAAATTCGTATGCTTTGTCAAACGACCAAGCATCAGAAAGTTACTGAACTTA 2665
Db 821 GlnAsnLysIleLeuTyrAlaLeuSerThrSerLysHisGlnGluLysLeuLeuLysLeu 840
QY 2666 ATTGAACCTAGGAATGGAAGGAAAGGTTTATCAAGACACAGAACTTGGCAGCTCTCCTTCAT 2725
Db 841 IleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaAlaLeuLeuHis 860
QY 2726 GCGATTGCCAGACGTCCAAAGGGGACGAACTAGCATGGGATTTTGTAGAGAAAAATTGG 2785
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QY 2786 ACCCATCTTCTGAAAAAATTTGACTTGGGCTCATATGACATAGGATGATCATCTCTGGC 2845
Db 881 ThrHisLeuLeuLysLysPheAspLeuGlySerTyrAspIleArgMetIleIleSerGly 900
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RESULT 3

US-10-363-616-459
; Sequence 459, Application US/10363616
; Publication No. US20040044181A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-113 (793)
; CURRENT APPLICATION NUMBER: US/10/363,616
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 09/654,935
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 490
; SEQ ID NO 459
; LENGTH: 785
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-616-459

Alignment Scores:

Pred. No.:	0	Length:	785
Score:	4141.00	Matches:	782
Percent Similarity:	99.74%	Conservative:	0
Best Local Similarity:	99.74%	Mismatches:	2
Query Match:	70.04%	Indels:	0
DB:	15	Gaps:	0

US-10-039-073-2 (1-3366) x US-10-363-616-459 (1-785)

QY	146	ATGTTCCATTCTTCGCAATGTTAATTCACACAGAAACCAATGTTTAACTTCACAGA	205
DB	1	MetPheHisSerSerAlaMetValAsnSerHisArgLysProMetPheAsnIleHisArg	20
QY	206	GGATTTTACTGCTTAACGCCATCTGCCCAAATATGCATTTGCTCAGTTCTCAGTG	265
DB	21	GlyPheTyrCysLeuThrAlaIleLeuProGlnIleCysIleCysSerGlnPheSerVal	40
QY	266	CCATCTAGTTATCACTTCACTGAGGATCCTGGGGCTTTCCAGTAGCCCAATGGGAA	325
DB	41	ProSerSerTyrHisPheThrGluAspProGlyAlaPheProValAlaThrAsnGlyGlu	60
QY	326	CAATTTCTTGGCAGAGCTAAGGCTCCCAAGTGGTTCATTCCTCTCCATTATGACCTC	385
DB	61	ArgPheProTyrGlnGluLeuArgLeuProSerValValIleProLeuHisTyrAspLeu	80
QY	386	TTTGTCCACCCCAATCTCACCTCTCTGGACTTTGTTGTCATCTGAGAAGTCGAAGTCTTG	445
DB	81	PheValHisProAsnLeuThrSerLeuAspPheValAlaSerGluLysIleGluValLeu	100
QY	446	GTCAGCAATGCTTACCCAGTTTATCATCTTGCAAGCAAGATCTTGAATCACGAATGCC	505
DB	101	ValSerAsnAlaThrGlnPheIleIleLeuHisSerLysAspLeuGluIleThrAsnAla	120
QY	506	ACCTTTCAGTCAGAGAAGATTCAAGATACATGAAACCCAGGAAAGAACTGAAAGTTTG	565
DB	121	ThrLeuGlnSerGluGluAspSerArgTyrMetLysProGlyLysGluLeuLysValLeu	140
QY	566	AGTTACCTGCTCATGACAAATTCACCTGCTGGTTCCAGAGAACTTACGCTCACCTG	625
DB	141	SerTyrProAlaHisGluGlnIleAlaLeuLeuValProGluLysLeuThrProHisLeu	160
QY	626	AAATACTATGTGGCTATGACTTCCAAAGCCAAAGTAGGTAGGTGGCTTTGAAGGGTTTAT	685
DB	161	LysTyrTyrValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTyr	180
QY	686	AAAAGCACATACAGAACTCTTGGTGTGAAACAAGAAATCTTTCAGTACAGATTTGAG	745
DB	181	LysSerThrTyrArgThrLeuGlyGlyGluThrArgIleLeuAlaValThrAspPheGlu	200
QY	746	CCAAACCCAGGACGATGGCTTCCCTTCTGTTGATGAACCGTTGTTCAAAGCCAACTTT	805
DB	201	ProThrGlnAlaArgMetAlaPheProCysPheAspGluProLeuPheLysAlaAsnPhe	220

QY	806	TCAATCAAGATACGAAGAGAGAGAGGAGGATATTGCACTATCCAACTATCCAAAGGTTAAG	865
DB	221	SerIleLysIleArgArgGluSerArgHisIleAlaLeuSerAsnMetProLysValLys	240
QY	866	ACAATTGAACCTGAAGGAGGCTTTTGAAGACTCACTTTGAAACTACTGTAAATAGT	925
DB	241	ThrIleGluLeuGluGlyLeuLeuGluAspHisPheGluThrThrValLysMetSer	260
QY	926	ACATACCTTGTAGCCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCATCTCATCA	985
DB	261	ThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThrSerSer	280
QY	986	GGGTCAAGGTGTCATCTATGCAATCCCGACAGAAACGGAATCAACACATATATCTTTG	1045
DB	281	GlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyrAlaLeu	300
QY	1046	CAGGCATCACCTGAAGCTACTTGTATTTATCAAAAGTACTTTGATATCTACTATCCACTC	1105
DB	301	GlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyrProLeu	320
QY	1106	TCCAAACTGGGATTTAAATGCTATTCTGACTTTTGCACTGGAGCCATCGAAAATTTGGGC	1165
DB	321	SerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsnTrpGly	340
QY	1166	CTCATTTACATATAGGAGACGCTCACTGCTTTTTCACCCCAAGACCTCTTCTGCTTCCGAT	1225
DB	341	LeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAlaSerAsp	360
QY	1226	AACTGTGGTCCACAGAGTCATAGCCCATCACTGGCGCACCCAGTGGTTGGCAACCTG	1285
DB	361	LysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeu	380
QY	1286	GTCAAAATGGAATGGTGAATGATATTGGCTTAAGGAGGGTTTTGCAAAATACATCGAA	1345
DB	381	ValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyrMetGlu	400
QY	1346	CTTATCGCTGTTAATGTACATATCCAGAGCTGCAATTTGATGACTATTTTTGAATGTG	1405
DB	401	LeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeuAsnVal	420
QY	1406	TGTTTGAAGTAATACAAAAGATTCATTGAATTCATCCCGCCCTATCTCCAAACACGG	1465
DB	421	CysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLysProAla	440
QY	1466	GAACCCCGACTCAAATACAGAAATGTTTCATGAAGTTTCTCTATAACAAGGAGCTTGT	1525
DB	441	GluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGlyAlaCys	460
QY	1526	ATTTTGAATATGCTCAAGGATTTTCTGGGTGAGGAGAAATTCAGAAAGGAATATTCAG	1585
DB	461	IleLeuAsnMetLeuLysAspPheLeuGlyGluGluLysPheGlnLysGlyIleIleGln	480
QY	1586	TACTTAAAGAAGTTCACTATAGAAATGCTTAAGAAATGATGATGCTTGTGAGCAGCTGTCA	1645
DB	481	TyrLeuLysLysPheSerTyrArgAsnAlaAsnAsnAspAspLeuTrpSerSerLeuSer	500
QY	1646	AATAGTTGTTTGAAGAGTATTTCATCTCGTGGAGTTTCTCATTCGGATCCCAAGATG	1705
DB	501	AsnSerCysLeuGluSerAspPheThrSerGlyGlyValCysHisSerAspProLysMet	520
QY	1706	ACAAAGTAACTGCTCGCTTTCTCGGGGAAATTCAGAGGTCAAAGAGATGATGACTACA	1765
DB	521	ThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGluValLysGluMetMetThrThr	540
QY	1766	TGGACTCTCCAGAAAGAAATCCCTCTGCTGGTGTAAACAAGACGGGTGTTCATCCGA	1825
DB	541	TrpThrLeuGlnLysGlyIleProLeuLeuValValLysGlnAspGlyCysSerLeuArg	560
QY	1826	CTGCAACAGGAGCCCTTCTCCAGGGGTTTTCCAGGAAGACCTGTAATGAGGGCCCTG	1885
DB	561	LeuGlnGlnAlaArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArgAlaLeu	580

Qy 1886 CAGGAGAGTACCTGTGGCATATCCCATGTGACCTACTCCAGAGTCTCTTAATGTGATC 1945
Db |||||
581 GlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerThrSerSerSerAsnValIle 600
Qy 1946 CACGACACATTCATAAATCAAGACAGATACTCTGGATCTACCTGAAAAGACAGATTGG 2005
Db |||||
601 HisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThrSerTrp 620
Qy 2006 GTGAAATTTAATGTGGACTCAAAATGGTTACTACATCGTTCACTATGAGGGTCATGGATGG 2065
Db |||||
621 ValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHisGlyTrp 640
Qy 2066 GACCAACTCATTACACAGCTCAATCAGAAACACACACTTCTCAGACCTTAAGGACAGAGTA 2125
Db |||||
641 AspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuAsgProLysAspArgVal 660
Qy 2126 GGTCTGATTCATGATGTTTTCAGCTAGTTGGTGAGGAGACTGACCCCTAGACAAAGCT 2185
Db |||||
661 GlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAspLysAla 680
Qy 2186 CTTGACATGACTTACTACTCTCAACATGAACAAGCAGCCCGCACTTCTCGAAGGCTG 2245
Db |||||
681 LeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProAlaLeuLeuGluGlyLeu 700
Qy 2246 AGTTACTTGGAAATCGTTTTACCACATGATGACAGAGAAGAAATATTTACAGATATCTCTGAA 2305
Db |||||
701 SerTyrLeuGluSerPheTyrHisMetMetAspArgArgAsnIleSerAspIleSerGlu 720
Qy 2306 AACCTCAAGCGTTACTCTTCAGTATTTTAAGCCAGTGATGACAGGCAAGCTGGAGT 2365
Db |||||
721 AsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSerTrpSer 740
Qy 2366 GACAAGGCTCAGTCTGGGACAGGATGCTCCGCTCGGCTCTTTGAAGCTGGCTGTGAC 2425
Db |||||
741 AspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAlaCysAsp 760
Qy 2426 CTGAACCATGCTCTTCGTGATCCAGAAAGCTGCTGAACCTCTTCTCCAGTGGATGGAATCC 2485
Db |||||
761 LeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheGlnTrpMetGluSer 780
Qy 2486 AGTGAAAATTA 2497
Db |||||
781 SerGlyLysLeu 784

RESULT 4
US-09-764-853-646
; Sequence 646, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ206
; CURRENT APPLICATION NUMBER: US/09/764,853
; PENDING FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 646
; LENGTH: 728
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-853-646

Alignment Scores:
Pred. No.: 0 Length: 728
Score: 3799.00 Matches: 722
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 64.26% Indels: 0
DB: 9 Gaps: 0

US-10-039-073-2 (1-3366) x US-09-764-853-646 (1-728)

Qy 860 GTTAAGACAAATTGAACCTTGAGGAGGTCTTTTGGAGATCACATTTGAAACACTACTGTAAAA 919
Db |||||
7 ValLysThrIleGluLeuGluGlyGlyLeuLeuGluAspHisPheGluThrThrValLys 26
Qy 920 ATGAGTACATACCTTGAGGCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACT 979
Db |||||
27 MetSerThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThr 46
Qy 980 TCATCAGGGGTCAAGGTGCTCCATCTATGCATCCCCACAGAAACCGAATCAAAACACATTAT 1039
Db |||||
47 SerSerGlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyr 66
Qy 1040 GCTTTGCAGGCATCACCTGAAAGTACTTTGATTTTTATGAAAAGTACTTTTGATATCTACTAT 1099
Db |||||
67 AlaLeuGlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyr 86
Qy 1100 CCACTCTCCAAACCTGGATTTAANTGCTATTTCCTGACTTTGCACCTTGAGCCATCGGAAAT 1159
Db |||||
87 ProLeuSerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsn 106
Qy 1160 TGGGGCTCATATTACATAGGGAGACGTCACTGCTTTTTCACCCCAAGACACTCTTCTGCT 1219
Db |||||
107 TrpGlyLeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAla 126
Qy 1220 TCCGATAAACTGTGGGTACCAGAGTCATAGCCCATGAACCTGGCGCACCAAGTGTTTGGC 1279
Db |||||
127 SerAspLysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGly 146
Qy 1280 AACCTGCTCAATGGAATGCTGGAATGATATTGGCTTAAGGAGGGTTTGGCAATATC 1339
Db |||||
147 AsnLeuValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyr 166
Qy 1340 ATGGAACCTTATCGCTGTTAATGTCTACATATCCAGAGCTGCAATTTGTATGACTATTTTGTG 1399
Db |||||
167 MetGluLeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeu 186
Qy 1400 AATGTGTGTTTGAAGTAATTACAAAAGATTCATTTGAATTCATCCGCCCTATCTCAAA 1459
Db |||||
187 AsnValCysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLys 206
Qy 1460 CCAGCGGAAACCCGACTCAAATACAGGAATGTTTGTATGATGAGTTTCTTATACAAAGGA 1519
Db |||||
207 ProAlaGluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGly 226
Qy 1520 GCTTGTATTTTGAATATGCTCAAGGATTTTCTGGTGAGGAGAAATTCAGAAAGGAATA 1579
Db |||||
227 AlaCysIleLeuAsnMetLeuLysAspPheLeuGlyGluGluLysPheGlnLysGlyLe 246
Qy 1580 ATTCAAGTACTTAAAGAAAGTTCAAGCTATAGAAATGCTAAGAAATGATGACTTGTGAGCAGT 1639
Db |||||
247 IleGlnTyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspAspLeuTrpSerSer 266
Qy 1640 CTGTCAAATAGTTGTTTAGAAAGTATTTACATCTGCTGGAGTTTCTCATCTCCGATCCC 1699
Db |||||
267 LeuSerAsnSerCysLeuGluSerAspPheThrSerGlyGlyValCysHisSerAspPro 286
Qy 1700 AAGATGACAAAGTAACTGCTCGCCTTTCTGGGGGAAAAATGCAGAGGTCAAAAGAGATGATG 1759
Db |||||
287 LysMetThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGluValLysGluMetMet 306
Qy 1760 ACTACATGGACTCTCCAGAAAGGAATCCCTGCTGCTGGTTTAAACAGACGGGTGTTC 1819
Db |||||
307 ThrThrTrpThrLeuGlnLysGlyIleProLeuLeuValLysGlnAspGlyCysSer 326
Qy 1820 CTCGACTGCAACAGGAGCGCTTCTCCAGGGGGTTTTCCAGGAAGACCTCGAATGAGG 1879
Db |||||
327 LeuArgLeuGlnGlnGluArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArg 346
Qy 1880 GCCCTGAGGAGAGGTATCCTGTGGCATATCCCATTTGACTTCCAGCAGGTCTTCTTAAT 1939
Db |||||
347 AlaLeuGlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerThrSerSerAsn 366
Qy 1940 GTGATCCACAGACACATTTCAAAATCAAGACAGATATCTCTGGATCTTACCTGAAAAGACC 1999

Db	367	ValIleHisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThr	386	Db	727	AsnThr	728
QY	2000	AGTTGGGTGAAATTAATGTGACCTCAATGCTTACTACATCGTTCACTATGAGGTCAT	2059	Db	728	AsnThr	729
Db	387	SerTrpValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHis	406	Db	729	AsnThr	730
QY	2060	GGATGGGCAACTCATATACAGCTGAATCAGAACCCACACTTCTCAGACCTAAGGAC	2119	Db	730	AsnThr	731
Db	407	GlyTrpAspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAsp	426	QY	2120	AGAGTAGGTCGATTCATGATGTTTTCAGCTAGTTGTCAGGCGAGACTGACCCCTAGAC	2179
QY	2120	AGAGTAGGTCGATTCATGATGTTTTCAGCTAGTTGTCAGGCGAGACTGACCCCTAGAC	2179	Db	427	ArgValGlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAsp	446
Db	427	ArgValGlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAsp	446	QY	2180	AAAGCTCTTGACATGACTTACTCTCAACATGAACAAGCAGCCCGCCTCTTCGAA	2239
QY	2180	AAAGCTCTTGACATGACTTACTCTCAACATGAACAAGCAGCCCGCCTCTTCGAA	2239	Db	447	LysAlaLeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProAlaLeuLeuGlu	466
Db	447	LysAlaLeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProAlaLeuLeuGlu	466	QY	2240	GGTCTGAGTTACTTGGAAATCGTTTTCACATGATGGACAGAAAGAAATATTCAGATATC	2299
QY	2240	GGTCTGAGTTACTTGGAAATCGTTTTCACATGATGGACAGAAAGAAATATTCAGATATC	2299	Db	467	GlyLeuSerTyrLeuGluSerPheTyrHisMetMetAspArgAsnIleSerAspIle	486
Db	467	GlyLeuSerTyrLeuGluSerPheTyrHisMetMetAspArgAsnIleSerAspIle	486	QY	2300	TCTGAAACCTCAAGCGTTACCTTCTCAGTATTTTAAGCCAGTATTCACAGGCAAGC	2359
QY	2300	TCTGAAACCTCAAGCGTTACCTTCTCAGTATTTTAAGCCAGTATTCACAGGCAAGC	2359	Db	487	SerGluAsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSer	506
Db	487	SerGluAsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSer	506	QY	2360	TGGAGTGACAAGGGCTCAGCTGGGACAGAGATGCTCCGCTCGCTCTTGAAGCTGGCC	2419
QY	2360	TGGAGTGACAAGGGCTCAGCTGGGACAGAGATGCTCCGCTCGCTCTTGAAGCTGGCC	2419	Db	507	TrpSerAspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAla	526
Db	507	TrpSerAspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAla	526	QY	2420	TGTGACCTGAACCATGCTCTTTCGATCCAGAAAGCTGTGAATCTTCTCCAGTGGATG	2479
QY	2420	TGTGACCTGAACCATGCTCTTTCGATCCAGAAAGCTGTGAATCTTCTCCAGTGGATG	2479	Db	527	CysAspLeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMet	546
Db	527	CysAspLeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMet	546	QY	2480	GAATCCAGTGGAAATTAATATACACAGATGTTTAAAGATTGCTGATCTCTGGGT	2539
QY	2480	GAATCCAGTGGAAATTAATATACACAGATGTTTAAAGATTGCTGATCTCTGGGT	2539	Db	547	GluSerSerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrSerValGly	566
Db	547	GluSerSerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrSerValGly	566	QY	2540	GCTCAGACAAACAGCAGATGGAATACCTTTTGAAGCAATATGAATGTCAATGTCAAGT	2599
QY	2540	GCTCAGACAAACAGCAGATGGAATACCTTTTGAAGCAATATGAATGTCAATGTCAAGT	2599	Db	567	AlaGlnThrThrAlaGlyTrpAsnTyrLeuLeuGluGlnTyrGluLeuSerMetSerSer	586
Db	567	AlaGlnThrThrAlaGlyTrpAsnTyrLeuLeuGluGlnTyrGluLeuSerMetSerSer	586	QY	2600	GCTGAACAAACAAATCTGTATGCTTTGTCAACAGCAAGCATCAGGAAAGTTACTG	2659
QY	2600	GCTGAACAAACAAATCTGTATGCTTTGTCAACAGCAAGCATCAGGAAAGTTACTG	2659	Db	587	AlaGluGlnAsnLysIleLeuTyrAlaLeuSerThrSerLysHisGlnGluLysLeuLeu	606
Db	587	AlaGluGlnAsnLysIleLeuTyrAlaLeuSerThrSerLysHisGlnGluLysLeuLeu	606	QY	2660	AGTTAATGAACTAGGATGCAAGCAAGGTTATCAACACAGCAACTTGGCAGCTCTC	2719
QY	2660	AGTTAATGAACTAGGATGCAAGCAAGGTTATCAACACAGCAACTTGGCAGCTCTC	2719	Db	607	LysLeuIleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaLeu	626
Db	607	LysLeuIleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaLeu	626	QY	2720	CTTCATGCGATTGCCAGAGCTCCAAAGGGGAGCAACTAGCATGGGATTTTGTAAAGAA	2779
QY	2720	CTTCATGCGATTGCCAGAGCTCCAAAGGGGAGCAACTAGCATGGGATTTTGTAAAGAA	2779	Db	627	LeuHisAlaIleAlaArgArgProLysGlyGlnGlnLeuAlaTrpAspPheValArgGlu	646
Db	627	LeuHisAlaIleAlaArgArgProLysGlyGlnGlnLeuAlaTrpAspPheValArgGlu	646	QY	2780	AAATGGACCCATCTTCTGAAAAATTTGACTTTGGGCTCATATGACATAGGATGATATC	2839
QY	2780	AAATGGACCCATCTTCTGAAAAATTTGACTTTGGGCTCATATGACATAGGATGATATC	2839	Db	647	AsnTrpThrHisLeuLeuLysLysPheAspLeuGlySerTyrAspIleArgMetIleIle	666
Db	647	AsnTrpThrHisLeuLeuLysLysPheAspLeuGlySerTyrAspIleArgMetIleIle	666	QY	2840	TCGGCACAACAGCTCATTCTTCCCAAGGATAAGTTCCAGAGTGAAGTAACTATTTT	2899
QY	2840	TCGGCACAACAGCTCATTCTTCCCAAGGATAAGTTCCAGAGTGAAGTAACTATTTT	2899	Db	667	SerGlyThrThrAlaHisPheSerSerLysAspLysLeuGlnGluValLysLeuPhePhe	686
Db	667	SerGlyThrThrAlaHisPheSerSerLysAspLysLeuGlnGluValLysLeuPhePhe	686	QY	2900	GAATCTCTTGAGCTCAAGGATCACATCTGGATATTTTCAAACTGTTCTCGAAACGATA	2959
QY	2900	GAATCTCTTGAGCTCAAGGATCACATCTGGATATTTTCAAACTGTTCTCGAAACGATA	2959	Db	687	GluSerLeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIle	706
Db	687	GluSerLeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIle	706	QY	2960	ACCAAAATATAAATGGCTGGAGAGAAATCTTCCGACTCTCAGGACTTGGCTTAATGGTT	3019
QY	2960	ACCAAAATATAAATGGCTGGAGAGAAATCTTCCGACTCTCAGGACTTGGCTTAATGGTT	3019	Db	707	ThrLysAsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeuMetVal	726
Db	707	ThrLysAsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeuMetVal	726	QY	3020	ATACT 3025	1279

RESULT 5

US-09-764-853-819

; Sequence 819, Application US/09764853

; Patent No. US20020090672A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: P206

; CURRENT APPLICATION NUMBER: US/09/764,853

; CURRENT FILING DATE: 2001-01-17

; Prior application data removed - consult PALM or file wrapper

; NUMBER OF SEQ ID NOS: 939

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 819

; LENGTH: 722

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (237)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (296)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (719)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (720)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (721)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-764-853-819

Alignment Scores:

Pred. No.: 0

Score: 3770.00

Length: 722

Matches: 717

Percent Similarity: 99.31%

Conservative: 0

Best Local Similarity: 99.31%

Mismatch: 5

Query Match: 63.77%

Indels: 0

Gaps: 9

DB:

US-10-039-073-2 (1-3366) x US-09-764-853-819 (1-722)

QY 860 GTTAAGCAATGAAGTGAAGGAGGCTTTTGAAGATCACTTTGAAACTACTCTATAA 919

Db 1 VallysthrIleGluLeuGluGlyGlyLeuLeuGluAspHisPheGluThrThrVallys 20

QY 920 ATGAGTACATACCTTTGTAGCCTACATAGTTTGTGATTTTCCACTCTCTGAGTGGCTTCACT 979

Db 21 MetSerThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThr 40

QY 980 TCATCAGGGTCAAGGTGTCCATCTATGCATCCCGACAGCAAAACGGAATCAACACATTAT 1039

Db 41 SerSerGlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyr 60

QY 1040 GCTTTGGAGGCTCACCTGAGCTACTTGTATTTTATGAAAAGTACTTTGATATCTACTAT 1099

Db 61 AlaLeuGlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyr 80

QY 1100 CCATCTCTCAAACTGGATTTAATTTGCTATTCTCTGCTTTTGCACCTGGAGCCATCGAAAT 1159

Db 81 ProLeuSerLysLeuAspLeuLeuAlaIleProAspPheAlaProGlyAlaMetGluAsn 100

QY 1160 TGGGGCTCTATTACATATAGGAGAGCTACTGCTGCTTTTGTACCCCAAGACCTCTTCTGCT 1219

Db 101 TrpGlyLeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAla 120

QY 1220 TCCGATAAAGTCTGGGTCAACAGATCATAGCCATGAGCTGGCGCAGCTGGTTTGGC 1279

Db 121 SerAspLysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGly 140
Qy 1280 AACCTGGTCACAAATCGAATGGTGAATGATATTTGGCTTAAGAGGGGTTTTGCAAAATAC 1339
Db 141 AsnLeuValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyr 160
Qy 1340 ATGGAACCTTATCGCTGTTAATGCTACATATCCAGAGCTGCAATTTTGATGACTATTTTGTG 1399
Db 161 MetGluLeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeu 180
Qy 1400 AATGTGTGTTTGAAGTAATTCACAAAGATTCATGAATTCATCCCGCCCTATCTCCAAA 1459
Db 181 AsnValCysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLys 200
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Db 221 AlaCysIleLeuAsnMetLeuLysAspPheLeuGlyGluGluLysPhe**LysGlyIle 240
Qy 1580 ATTCACTACTTTAAAGNAGTTCACTATAGAATCTTAAGATGATGACTTGTGAGCAGT 1639
Db 241 IleGlnTyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspLeuTrpSerSer 260
Qy 1640 CTGTCAAAATAGTTGTTAGAAGTGATTTTACATCTGGTGGAGTTTGTTCATTTCGATCCC 1699
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Qy 1700 AAGATGACAAATACATGCTCGCTCCCTTTCTGGGGGAAATGCAGAGGTCAAAGAGATGATG 1759
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Qy 1760 ACTACATGGACTCCAGAAAGGAATCCCCCTGCTGGTTAAACAAGACGGGTGTTC 1819
Db 301 ThrThrTrpThrLeuGlnLysGlyIleProLeuLeuValLysGlnAspGlyCysSer 320
Qy 1820 CTCCGACTGCAACAGGAGCGCTTCCTCCAGGGGGTTTTCCAGGAAGACCCCTGAATGGAGG 1879
Db 321 LeuArgLeuGlnGlnGluArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArg 340
Qy 1880 GCCTTGCAAGAGAGGTACCTGTGGCATATCCATGACCTACTCCACGAGTTCCTTAAT 1939
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Qy 2000 AGTTGGGTGAAATTTAATGTGGACTCAAAATGGTTACTACATCGTTCACTATGAGGGTCAT 2059
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Qy 2060 GGATGGGACCAACTCATTACACAGCTGAATCAGAACCCACACACTTCTCAGACCTTAAGGAC 2119
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Qy 2120 AGAGTAGTCTGATTCATGATGTGTTTCAGTAGTTGGTGGAGGAGACTGACCTAGAC 2179
Db 421 ArgValGlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAsp 440
Qy 2180 AAAGCTCTTGACATGACTTACTCTCCAAATCAAAACAGCAGCCCGCACTTCTCGAA 2239
Db 441 LysAlaLeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProAlaLeuLeuGlu 460
Qy 2240 GGTCGTGATTTACTTGGAAATCGTTTTTACCACATGATGCAGAGAAATATTTTCAGATATC 2299
Db 461 GlyLeuSerTyrLeuGluSerPheTyrHisMetMetAspArgArgAsnIleSerAspIle 480
Qy 2300 TCTGAAAACCTCAAGCGTTACTCTTTCAGTATTTTAAAGCAGTATGATGACAGCAAGC 2359
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Qy 2360 TGGAGTGACAAAGGCTCAGTCTGGGACAGGATGCTCGCTCGGCTCTCTTTCAAAGCTGGCC 2419
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Qy 2420 TGTGACCTGAACCATGCTCCTTGCATCCAGAAAGCTGCTGAACTCTTCTCCAGTGATG 2479
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Qy 2480 GAATCCAGTGGAAATTAATATATACCAACAGATGTTTAAAGATGTGTATCTTGTGCGGT 2539
Db 541 GluSerSerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrSerValGly 560
Qy 2540 GCTCAGACAAACAGCAGGATGGAATTTACCTTTTATAGACAAATATGAATGTCAATGTCAAGT 2599
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Qy 2600 GCTGAACAAACAAATCTCTGTATGCTTGTCAACGAGCAAGCATCAGGAAAAGTTACTG 2659
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Qy 2660 AAGTTAATTGAATAGGAATGGAAGGAAAGGTTATCAAGACACAGAACTTGGCAGCTCTC 2719
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Qy 2720 CTTTCATCGCATTCGCCAGACGTCCTCAAAAGGGCAGCAACTAGCATGGGATTTTGTAAAGAAA 2779
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Qy 2780 AATTGACCCATCTCTGAAAAATTTGACTTGGGCTCATATGACATAGAAGATGATCATC 2839
Db 641 AsnTrpThrHisLeuLeuLysLysPheAspLeuGlySerTyrAspIleArgMetIleIle 660
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Db 681 GluSerLeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIle 700
Qy 2960 ACCAAAAATATAAATGGCTGGAGAGAAATCTTCCGACTCTGAGGACTTGGCTTAATGGTT 3019
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Qy 3020 AATACT 3025
Db 721 ***Thr 722
RESULT 6
US-10-220-443-2
; Sequence 2, Application US/10220443
; Publication No. US20030215820A1
; GENERAL INFORMATION:
; APPLICANT: Levine, Stewart
; TITLE OF INVENTION: REGULATORS OF TYPE-1 TUMOR NECROSIS FACTOR RECEPTOR AND OTHER CYT
; FILE OF INVENTION: RECEPTOR SHEDDING
; FILE REFERENCE: 218732
; CURRENT APPLICATION NUMBER: US/10/220,443
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06464
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/185,586
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 941
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-220-443-2
Alignment Scores:

Pred. No.:	7,628-224	Length:	941
Score:	2516.50	Matches:	478
Percent Similarity:	69.34%	Conservative:	171
Best Local Similarity:	51.07%	Mismatches:	268
Query Match:	42.57%	Indels:	19
DB:	15	Gaps:	7
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DB	15	PhelLeuLeuSerSerLeuLeuAlaLeuLeuThrVal	30
QY	272	AGTTATCACTTCCAGAGATCCTGGGCTTCCAGTAGCACTAATGGGGAACGATT	331
DB	31	TrpCysGlnSerThrGlu	47
QY	332	CCTGGCAGGAGCTAAGCTCCAGTGTGGTCTCTCCATATGATGATCTCTTGTCT	391
DB	48	ProTrpAenLysIleArgLeuProGluTyValIleProValHisTyAspLeuLeuIle	67
QY	392	CACCCCAATCTCACCTCTGACCTTGTGTCATCTGAGAGATCGAAGTCTTGTGTACG	451
DB	68	HisAlaAenLeuThrLeuThrPheTrpGlyThrThrLysValGluIleThrAlaSer	87
QY	452	AATGCTACCCAGTTTATCATCTTGACAGCAAGACTTGTGAATCAGCAATGCCACCTT	511
DB	88	GlnProThrSerThrIleLeuHisSerHisLeuGlnIleSerArgAlaThrLeu	107
QY	512	CAGTCAGAGGAGATTCAAGATACATGAACCCAGGAAAGAACTGAAAGTTTGTGTTAC	571
DB	108	ArgLysGlyAlaGlyGluArgLeuSerGlu	125
QY	572	CCTGCTCATGAACAAATGCACTGTGTTCCAGAGAACTTACGCCCTCACCTGAAATAC	631
DB	126	ProArgGlnGluGlnIleAlaLeuLeuAlaProGluProLeuLeuValGlyLeuProTy	145
QY	632	TATGCGCTATGACCTCCAGCCAAAGTTAGTGATGGCTTTGAAGGGTTTATAAAGC	691
DB	146	ThrValValIleHisTyAlaGlyAenLeuSerGluThrPheHisGlyPheTyLysSer	165
QY	692	ACATACAGACTCTTGGTGGTGAACACAGAAATCTTGCAAGTACAGATTTGAGCCACC	751
DB	166	ThrTyArgThrLysGluGlyLeuArgIleLeuAlaSerThrGlnPheGluProThr	185
QY	752	CAGGCACGATCGCTTCCCTTGTGATGAACCGTTGTTCAAGCCAACTTTCAATC	811
DB	186	AlaAlaArgMetAlaPheProCysPheAspGluProAlaPheLysAlaSerPheSerIle	205
QY	812	AAGATACGAAGAGAGCAGGCATATTCATCCATCAACATGCCAAAGGTTAAGACAAT	871
DB	206	LysIleArgArgGluProArgHisLeuAlaIleSerAenMetProLeuValLysSerVal	225
QY	872	GAACCTGAAGGAGCTTTTGGAGATCACCTTTGAACTACTGTAAAATAGATCATAC	931
DB	226	ThrValAlaGluGlyLeuIleGluAspHisPheAspValThrValLysMetSerThrTy	245
QY	932	CTTGTAGCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCCATTTCACTCAGGGTC	991
DB	246	LeuValAlaPheIleIleSerAspPheGluSerValSerLysIleThrLysSerGlyVal	265
QY	992	AAGGTGTCCATCTATGCATCCCGACAAACCGAAATCAACACATATGCTTTTGAGCCA	1051
DB	266	LysValSerValTyAlaValProAspLysIleAenGlnAlaAspTyAlaLeuAspAla	285
QY	1052	TCATGAGCTACTGATTTTATGAAGTACTTTGATATCTACTATCCACTCTCCAAA	1111
DB	286	AlaValThrLeuLeuGluPheTyGluAspTyPheSerIleProTyProLeuProLys	305
QY	1112	CTGGATTAAATGCTATCTCCTGACCTTGCACCTGAGCAGCATGGAAATGGGGCTCAT	1171
DB	306	GlnAspLeuAlaAlaIleProAspPheGlnSerGlyAlaMetGluAenTrpGlyLeuThr	325
QY	1172	ACATATAGGAGAGCGTCACTGCTTTTGTGACCCCAAGACCTCTTCTGCTTCGATAAACTG	1231
DB	326	ThrTyArgGluSerAlaLeuLeuPheAspAlaGluLysSerSerAlaSerSerLysLeu	345
QY	1232	TGGGTCAACAGAGTCATAGCCCATGCGCAGCAGTGGTGTGGCAACTGTGTACACA	1291
DB	346	GlyIleThrMetThrValAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeuValThr	365
QY	1292	ATGGAATGGTGAATGATATTTGGCTTAAGAGGGTTTGCAAAATACATGAACTTATC	1351
DB	366	MetGluTrpTrpAenAspLeuTrpLeuAenGluGlyPheAlaLysPheMetGluPheVal	385
QY	1352	GCTGTTAATGCTACATATCCAGAGCTGCAATTTGATGACTATTTTTCGAATGTGTGTTT	1411
DB	386	SerValSerValThrHisProGluLeuLysValGlyAspTyPhePheGlyLysCysPhe	405
QY	1412	GAAGTAATTAACAAAGATTTCATCAATTCATCCCGCTTATCTCCAAACACGAGCGAAACC	1471
DB	406	AspAlaMetGluValAlaAspAlaLeuAenSerSerHisProValSerThrProValGluAen	425
QY	1472	CCGACTCAAAATACAGGAAATGTTTGTGAAAGTTCCTATAACAAGGGAGCTGTGATTTG	1531
DB	426	ProAlaGlnIleArgGluMetPheAspAspValSerTyAspLysGlyAlaCysIleLeu	445
QY	1532	AATATGCTCAAGGATTTTCTGGGTGAGGAGAAATTCGAAAGAGGAATTAATTCAGTACTTA	1591
DB	446	AsnMetLeuArgGluTyLeuSerAlaAspAlaPheLysSerGlyIleValGlnTyLeu	465
QY	1592	AAGAAGTTTCAGTATAGAAATGCTAAGAAATCATGACTTGTGAGCAGTCTGCAATAGT	1651
DB	466	GlnLysHisSerTyLysAenThrLysAenGluAspLeuTrpAspSerMetAlaSerIle	485
QY	1652	TGTTTAGAAAGTGAATTTTACATCTGGT-----GGAGTTTGTCTCATTCGGATCCCAAGATG	1705
DB	486	Cys---ProThrAspGlyValLysGlyMetAspGlyPheCys---SerArgSerGlnHis	503
QY	1706	ACAAGTAACTGCTCGCCTTCTCGGGGAAATCGCAGGTCAAGAGATGATGACTACA	1765
DB	504	SerSerSerSerHisTrpHisGlnGluGlyValAspValLysThrMetMetAsnThr	523
QY	1766	TGGACTCTCCAGAAAGNAATCCCTGCTGTGTTAAACAAGCGGTGTCTACTCCGA	1825
DB	524	TrpThrLeuGlnLysGlyPheProLeuIleThrIleThrValArgGlyArgAsnValHis	543
QY	1826	CTGCAACAGGAGCGCTTCTCCAGGGGTTTTCCAGGAAGACCTGAAATGAGGCGCCTG	1885
DB	544	MetLysGlnGluHisTyMetLysGly-----SerAspGlyAlaPro	557
QY	1886	CAGGAGAGGTACCTGTGGCATATCCCATTTGACTTCCACGAGTCTTCTAATGTGATC	1945
DB	558	AspThrGlyTyLeuTrpHisValProLeuThrPheIleThrSerLysSerAspMetVal	577
QY	1946	CACAGACACATCTTAAATCAACACAGATACTCTGGATCTTACCTGAAAGACCACTGGG	2005
DB	578	HisArgPheLeuLeuLysThrLysThrAspValLeuLeuLeuProGluLysValGluTrp	597
QY	2006	GTGAAATTTAATGTGGAGCTCAAATGGTTACTTACATCGTTTCACTATGAGGGTCTGATGG	2065
DB	598	IleLysPheAenValGlyMetAsnGlyTyTyIleValHisTyGluAspAspGlyTrp	617
QY	2066	GACCACTCATTCACAGCTGAATCAGAACACACACTTCTCAGACCTTAAGCAGCAGTA	2125
DB	618	AspSerLeuThrGlyLeuLeuLysGlyThrHisThrAlaValSerSerAsnAspArgAla	637
QY	2126	GGTCTGATTCATGATGTTTTCAGTAGTGGTGCAGGAGACTGACCTAGACAAAGCT	2185
DB	638	SerLeuIleAenAenAlaPheGlnLeuValSerIleGlyLysLeuSerIleGluLysAla	657
QY	2186	CTTGACACTTACTTACCTCCAAACATCAACAGCAGCCCGCAGCTTCTCGAAGGCTG	2245
DB	658	LeuAspLeuSerLeuTyLeuLysHisGluThrGluIleMetProValPheGlnGlyLeu	677
QY	2246	AGTTACTTGGAAATCGTTTTTACCACATGATGACAGAGGAATATTTTCAGATATCTCTGAA	2305


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678 AsnGluLeuIleProMetTyrLysLeuMetGluLysArgAspMetAsnGluValGluThr 697
QY 2306 AACCTCAGCGCTACCTCTTCAGTATTTTAAGCCAGTGATGACAGCAAGCTGGAGT 2365
Db 698 GlnPheLysAlaPheLeuIleArgLeuLeuArgAspLeuIleAspLysGlnThrTrpThr 717
QY 2366 GACAAGGCGCTCAGTCTGGGACAGAGATGCTCGGCTCGGCTCTCTTGAAGCTGGCTGTGAC 2425
Db 718 AspGluGlySerValSerGluArgMetLeuArgSerGlnLeuLeuLeuLeuAlaCysVal 737
QY 2426 CTGAACCAATGCTCTTGTCATCCAGAAAGCTGCTGAACCTCTTCTCCAGTGATGGAATCC 2485
Db 738 HisAsnTyrGlnProCysValGlnArgAlaGluGlyTyrPheArgLysTrpLysGluSer 757
QY 2486 AGTGAAATTAATATACCAACAGATGCTTTTAAGATGTGTATTCTGTGGTGCTCAG 2545
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QY 2606 CAAACAAATTCGTATGCTTTGTCATCCAGCAAGCATCAGCAAGAAAGTACTGAAAGTTA 2665
Db 798 LysSerGlnIleGluPheAlaLeuCysArgThrGlnAsnLysGluLysLeuGlnTrpLeu 817
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Db 818 LeuAspGluSerPheLysGlyAspLysIleLysThrGlnGluPheProGlnIleLeuThr 837
QY 2726 GCGATTGCGCAGCTGCCAAGGGGCGAGCAACTAGCATGGGATTTTGTAAAGAGAAATGG 2785
Db 838 LeuIleGlyArgAsnProValGlyTyrProLeuAlaTrpGlnPheLeuArgLysAsnTrp 857
QY 2786 ACCCATCTTCGAAAAATTTGACTTGGGCTCATATGACATAGATGATCATCTCTGGC 2845
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QY 2846 ACACAGCTCAGCTTTCTCCAGAGTAAGTTGCAAGAGGTGAAACTATTTTGAATCT 2905
Db 878 ThrThrAsnGlnPheSerThrArgThrArgLeuGluGluValLysGlyPhePheSerSer 897
QY 2906 CTTCAGGCTCAAGATCATCTCGATATATTTTCAAACCTGTTCTCGAAACGATTAACCAA 2965
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RESULT 7

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US-10-264-237-2723
; Sequence 2723, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P313P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2723
; LENGTH: 941
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-237-2723
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Alignment Scores:
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Score: 2515.50 Matches: 477
Percent Similarity: 69.34% Conservative: 172
Best Local Similarity: 50.96% Mismatches: 268
Query Match: 42.55% Indels: 19
DB: 15 Gaps: 7

US-10-039-073-2 (1-3366) x US-10-264-237-2723 (1-941)
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QY 272 AGTTATCATTCACTGAGGATCCTGGGCGTTTCCAGTAGCCACTAATGGGAAACGATTT 331
Db 31 TrpCysGlnSerThrGlu-----AlaSerProLysArgSerAspGlyThrProPhe 47
QY 332 CTTTGGCAGGAGTAAGGCTCCCGAGTGTGTCATTCTCTCCATTATGACCTTTTGTGTC 391
Db 48 ProTrpAsnLysIleArgLeuProGluTyrValIleProValHisTyrAspLeuLeuIle 67
QY 392 CACCCCAATCTCAGCTCTCGGACTTTGTCATCTCAGAGATCGAAGTCTTGGTCAGC 451
Db 68 HisAlaLeuLeuThrThrLeuThrPheTrpGlyThrThrLysValGluIleThrAlaSer 87
QY 452 AATGCTACCCAGTTTATCATCTTGCACAGCAAAAGATCTTGAAATCAGAAATGCCACCCTT 511
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Db 166 ThrTyrArgThrLysGluGlyGluLeuArgIleLeuAlaSerThrGlnPheGluProThr 185
QY 752 CAGCAGCGACTGCTTCCCTGCTTGTGATGACCGTTGTTCAAAGCCAACTTTTCAATC 811
Db 186 AlaAlaArgMetAlaPheProCysPheAspGluProAlaPheLysAlaSerPheSerIle 205
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QY 872 GAACTTGAAGAGAGTCTTTTGGAAAGATCAGCTTTGAAACTACTGTGAAAAATGAGTACATAC 931
Db 226 ThrValAlaGluGlyLeuIleGluAspHisPheAspValThrValLysMetSerThrTyr 245
QY 932 CTTGTAGCCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACCTCATCAGGCGTC 991
Db 246 LeuValAlaPheIleIleSerAspPheGluSerValSerLysIleThrLysSerGlyVal 265
QY 992 AAGGTGTCCCATCTATGCATCCCGACAGCAAAACGGAATCAAAACACATATTATGCTTTTCAGGCA 1051
Db 266 LysValSerValTyrAlaValProAspLysMetAsnGlnAlaAspTyrAlaLeuAspAla 285
QY 1052 TCACTGAAGCTACTTGATTTTTATGAAAAGTACTTTTGATATCTACTATCTCCTCCAAA 1111
Db 286 AlaValThrLeuLeuGluPheTyrGluAspTyrPheSerIleProTyrProLeuProLys 305
QY 1112 CTGGATTTAATGCTATTCTGCTTTGCACCTTGAGCCATGGAATTTGGGGCTCATTT 1171
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Qy	1172	ACATATAGGGAGACGTCACTGCTTTTTTGAACCCCAAGACCTCTTCTGCTCCGATAAACTG	1231
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Qy	1292	ATGGAATGGTGAATGATATTGGCTTTAAGGAGAGGTTTTGCAAAATACATGGAACTTATC	1351
Db	366	MetGluTrpTrpAsnAspLeuTrpLeuAsnGluGlyPheAlaLysPheMetGluPheVal	395
Qy	1352	GCTGTTAATGCTACATATCCAGAGCTGCAATTGATGACTATTTTTTGAATGTGTGTTTT	1411
Db	386	SerValSerValThrHisProGluLeuLysValGlyAspTyrPhePheGlyLysCysPhe	405
Qy	1412	GAAGTAATTACAAAAGATTCAATCAAAATTCATCCCGCCCTATCTCCAAACACGACGGAAACC	1471
Db	406	AspAlaMetGluValAspAlaLeuAsnSerSerHisProValSerThrProValGluAsn	425
Qy	1472	CCGACTCAAATACAGGAAATGTTTGATGAAGTTTCTTATAACAAGGAGCTTGTATTGTTG	1531
Db	426	ProAlaGlnIleArgGluMetPheAspAspValSerTyrAspLysGlyAlaCysIleLeu	445
Qy	1532	AATATGCTCAAGGATTTTCTGGGTGAGGAGAGAAATCCAGAAAGGAATAATTTCAGTACTTA	1591
Db	446	AsnMetLeuArgGluTyrLeuSerAlaAspAlaPheLysSerGlyIleValGlnTyrLeu	465
Qy	1592	AAGAAGTTACGCTATAGAAATGCTAAGAATGATGACTGTGGAGCACTGTCGTAATAGT	1651
Db	466	GlnLysHisSerTyrLysAsnThrLysAsnGluAspLeuTrpAspSerMetAlaSerIle	485
Qy	1652	TGTTTGAAGAACTGATTTTACATCTGCTG-----GGAGTTTGTCAATCCGGATCCCAAGATG	1705
Db	486	Cys---ProThrAspGlyValLysGlyMetAspGlyPheCys---SerArgSerGlnHis	503
Qy	1706	ACAAGTAACATGCTCGCGCTTCTCGGGGGAATAATCCAGAGGTCAAAGAGATGACTGACTACA	1765
Db	504	SerSerSerSerSerHisTrpHisGlnGluGlyValAspValLysThrMetMetAsnThr	523
Qy	1766	TGGACTCTCCAGAAAGGAATCCCTCTGCTGGTGGTTAAACAAGACGGGTGTTCACTCCGA	1825
Db	524	TrpThrLeuGlnArgGlyPheProLeuIleThrIleThrValArgGlyArgAsnValHis	543
Qy	1826	CTGCAACAGGAGCGCTTCTCCAGGGGGTTTTCCAGGAAGACCTGTAATGGAGGGGCCCTG	1885
Db	544	MetLysGlnGluHisTrpMetLysGly-----SerAspGlyAlaPro	557
Qy	1886	CAGGAGAGGTACCTGTGGCATATCCCATGACCTTACCAGAGTCTTCTTAATGTGATC	1945
Db	558	AspThrGlyTyrLeuTrpHisValProLeuThrPheIleThrSerLysSerAspMetVal	577
Qy	1946	CACAGACACATTTCAAATCAAGACAGATACTCTGGATCTACCTGAAAGACACAGTTGG	2005
Db	578	HisArgPheLeuLeuLysThrLysThrAspValLeuIleLeuProGluGluValGluTrp	597
Qy	2006	GTGNAATTTAATGTGGACTCAATGGTTACTACATCGTTCACTATGAGGGTCATGATGG	2065
Db	598	IleLysPheAsnValGlyMetAsnGlyTyrTyrIleValHisTyrGluAspAspGlyTrp	617
Qy	2066	GACCAACTCATTTACACAGCTGMAATCAGAACACACACACTTCTCAGACCTAAGGACAGATG	2125
Db	618	AspSerLeuThrGlyLeuLeuLysGlyThrHisThrAlaValSerSerAsnAspArgAla	637
Qy	2126	GGTCTGATTCAATGATGTTTTCAGCTAGTTGGTGGCAGGAGACTGACCCCTAGACAAAGCT	2185
Db	638	SerLeuIleAsnAsnAlaPheGlnLeuValSerIleGlyLysLeuSerIleGluLysAla	657
Qy	2186	CTTGACATGACTTACTACCTCCAAACATGAACAGACGCCCGGCACTTCTCGAAGGTCTG	2245
Db	658	LeuAspLeuSerLeuTyrLeuLysHisGluThrGluIleMetProValPheGlnGlyLeu	677

QY 2346 AGTTACTTGGAAATCGTTTTHACCAATCATGATGGACAGAGAAGNATAATTTCAGATATCTCTGTGA 2305
Asn Glu Leu Ile Pro Met Tyr Lys Val Glu Met Glu Lys Arg Asp Met Asn Glu Val Glu Thr 697
Db

QY 2306 AACCTCAAGCGTTTACCTTCTTCAGTATTTTTAAGCCAGTGATTCACAGGCCAACGCTCGAGT 2365
Gln Phe Lys Ala Phe Ile Leu Arg Leu Val Arg Ser Glu Leu Leu Leu Ala Cys Val 737
Db

QY 2366 GACAAGGGCTCAGTCTGGGCAGACGATGCTCCGCTCGGCTCTCTTTGAAGCTGGCGCTGTGAC 2425
Asp Glu Gly Ser Val Ser Glu Arg Met Leu Arg Ser Glu Leu Leu Leu Ala Cys Val 737
Db

QY 2426 CTGAACCATCTCTCTTCATCCAGAAAGCTGCTGAACTCTTCTCCAGTGGATGGAAATCC 2485
His Asn Tyr Gln Pro Cys Val Gln Arg Ala Glu Gly Tyr Phe Arg Lys Trp Lys Glu Ser 757
Db

QY 2486 AGTGGAAAAATTAATATACCACACAGATGTTTTAAAGATTGCTGTATTCTGTGGGTGCTCAG 2545
Asn Gln Asn Leu Ser Leu Pro Val Asp Val Thr Leu Ala Val Phe Ala Val Gln Val 777
Db

QY 2546 ACAACAGCAGGATGGAATTACCTTTTAGACCAATATGAACTGTCAAATGTCAAAGTGTGTGA 2605
Ser Thr Glu Gly Trp Asp Phe Leu Tyr Ser Lys Tyr Gln Phe Ser Leu Ser Thr Glu 797
Db

QY 2606 CAATAACAAAATTCGTATGCTTTGTCAACAGCACGATCAGAGAAAGTACTTGAAGTTA 2665
Lys Ser Gln Ile Glu Phe Ala Leu Cys Arg Thr Gln Asn Lys Glu Lys Leu Gln Trp Leu 817
Db

QY 2666 ATTGAAC TAGGAATGGAAGGAAGGTTATCNAGACACAGNACTTTGGCAGCTCTCCCTTCAT 2725
Leu Asp Glu Ser Phe Lys Gly Asp Lys Ile Lys Thr Gln Glu Phe Pro Gln Ile Leu Thr 837
Db

QY 2726 GCGATTGCCAGCAGCTCCAAAGGGGCGACCACTAGCATGGATTTCTTAAGAGAAAAATTGG 2785
Leu Ile Gly Arg Asn Pro Val Gly Tyr Pro Leu Ala Trp Gln Phe Leu Arg Lys Asn Trp 857
Db

QY 2786 ACCCATCTTCTGAAAAAATTTGACTTTGGGCTCATATGACATAAGGATGATCATCTCTGGC 2845
Asn Lys Leu Val Gln Lys Phe Glu Leu Lys Ser Ser Ile Ala His Met Val Met Gly 877
Db

QY 2846 ACAACAGCTCAGTTTCTTCCAAGGATAAGTTCCAGAGGTGNAATATTTTTTGAATCT 2905
Thr Thr Asn Gln Phe Ser Thr Arg Thr Arg Leu Glu Glu Val Lys Gly Phe Phe Ser Ser 897
Db

QY 2906 CTTGAGCTCAACGATCATCATCTGGATATTTTTTCAAACCTGTTCTCGAAAACGATAACCAA 2965
Leu Lys Glu Asn Gly Ser Gln Leu Arg Cys Val Gln Gln Thr Ile Glu Thr Ile Glu Glu 917
Db

QY 2966 AATATAAATGGCTGGAGAGATCTTCCGACTCTCAGGACTTTGGCTA 3013
Asn Ile Gly Trp Met Asp Lys Asn Phe Asp Lys Ile Arg Val Trp Leu 933
Db

RESULT 8
US-10-472-533-329
; Sequence 329, Application US/10472533
; Publication No. US20050197285A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS906PCT
; CURRENT APPLICATION NUMBER: US/10/472,533
; CURRENT FILING DATE: 2003-09-20
; PRIOR APPLICATION NUMBER: US 60/331,287
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/306,171
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/277,340
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 650
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 329
; LENGTH: 941
; TYPE: PRP

; ORGANISM: Homo sapiens									
US-10-472-533-329									
Alignment Scores:									
Pred. No.:	9.44e-224	Length:	941						
Score:	2515.50	Matches:	477						
Percent Similarity:	69.34%	Conservative:	172						
Best Local Similarity:	50.96%	Mismatches:	268						
Query Match:	42.55%	Indels:	19						
DB:	18	Gaps:	7						
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Qy	212	TACTGCTTAACAGGCATCTTCCCCCAATATGCAATTTGTTCTCGATGTTCTCAGTGCCCATCT	271						
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Qy	272	AGTTATCATCTCACTGAGGATCCTGGGGCTTTCCTCCAGTAGCCATCAATAGGGAAACGATTT	331						
Db	31	TrpCysGlnSerThrGlu-----AlaSerProLysArgSerAspGlyThrProPhe	47						
Qy	332	CTTTGGCAGGAGTAAGCTCCCGAGTGTGGTCAATCTCTCCATTTATGACCTCTTTGTC	391						
Db	48	ProTrpAsnLysIleArgLeuProGluTyrValIleProValHisTyrAspLeuLeuIle	67						
Qy	392	CACCCCAATCTCAGCTCTCGAGCTTTGTCATCTGAGAGATCGAAGTCTTGGTCAGC	451						
Db	68	HisAlaAsnLeuThrLeuThrPheTrpGlyThrThrLysValGluIleThrAlaSer	87						
Qy	452	AATGCTACCCAGTTTATCATCTTGACAGCAAAAGATCTTGAATACGAATGCCCCTT	511						
Db	88	GlnProThrSerThrIleIleLeuHisSerHisLeuGlnIleSerArgAlaThrLeu	107						
Qy	512	CAGTCAGAGGAGATTCAGATACATGAACACCGAAGAAAGCAATGAAAGTTTCAGTTAC	571						
Db	108	ArgLysGlyAlaGlyGluArgLeuSerGlu-----GluProLeuGlnValLeuGluHis	125						
Qy	572	CCTGCTCATGAACAAATGCACTGCTGGTCCAGAGAAACTTACGCCCTCCTCAAAATAC	631						
Db	126	ProProGlnGluGlnIleAlaLeuLeuAlaProGluProLeuLeuValGlyLeuProTyr	145						
Qy	632	TATGTGCTATGGACTTCCAAACCAAGTATAGTATGGCTTTGAAGGTTTATAAAGC	691						
Db	146	ThrValValIleHisTyrAlaGlyAsnLeuSerGlnThrPheHisGlyPheTyrLysSer	165						
Qy	692	ACATACAGAACTCTGGTGGTGAACAGAAATCTTCGAGTAACAGATTTTGAGCCCAACC	751						
Db	166	ThrTyrArgThrLysGluGlyGluLeuArgIleLeuAlaSerThrGlnPheGluProThr	185						
Qy	752	CAGGCACGCATGGCTTCCCTTGTCTTGTATGAACCGTGTGTTCAAAGCCAACTTTCAATC	811						
Db	186	AlaAlaArgMetAlaPheProCysPheAspGluProAlaPheLysAlaSerPheSerIle	205						
Qy	812	AAGTACGAAGAGAGAGCATATTCATATCCCAATGCCAAAGGTTTAAGACAATT	871						
Db	206	LysIleArgGluProArgHisLeuAlaIleSerAsnMetProLeuValLysSerVal	225						
Qy	872	GAACTTGAAGAGGCTTTTGGAGATCACATTTGAAACTACTGTAAATAAGTACATAC	931						
Db	226	ThrValAlaGluGlyLeuIleGluAspHisPheAspValThrValLysMetSerThrTyr	245						
Qy	932	CTTGTAGCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACTTCAATCAGGGGTC	991						
Db	246	LeuValAlaPheIleIleSerAspPheGluSerValSerLysIleThrLysSerGlyVal	265						
Qy	992	AAGGTGTCCATCTATGCAATCCCGACAGCAAAACGGAAATCAAAACATATGCTTTGCAGCA	1051						
Db	266	LysValSerValTyrAlaValProAspLysMetAsnGlnAlaAspTyrAlaLeuAspAla	285						
Qy	1052	TCACGTGAAGCTACTGATTTTATGAAAGTACTTTGATATCTACTATCTCCACTCTCCAAA	1111						
Db	286	AlaValThrLeuLeuGluPheTyrGluAspTyrPheSerIleProTyrProLeuProLys	305						
Qy	1112	CTGGATTAAATGCTATTCTGATTTTGCACCTGGAGCCATGGAAAATTTGGGGCTCATTT	1171						
Db	306	GlnAspLeuAlaIleIleProAspPheGlnSerGlyAlaMetGluAsnTrpGlyLeuThr	325						
Qy	1172	ACATATAGGAGAGAGCTGCTGCTTTTGGACCCCAAGACCTCTTCTGCTTCGATAAATCTG	1231						
Db	326	ThrTyrArgGluSerAlaLeuLeuPheAspAlaGluLysSerSerAlaSerSerLysLeu	345						
Qy	1232	TGGGTCAACAGAGTCATAGCCCATGACTGCGCCAGCAGTGGTTTGGCAACCTGGTCACA	1291						
Db	346	GlyIleThrMetThrValAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeuValThr	365						
Qy	1292	ATGGAATGGTGGAAATGATATTTGGCTTAAGAGAGGGTTTTGCAAAATACATGGAATCTATC	1351						
Db	366	MetGluTrpTrpAsnAspLeuTrpLeuAsnGluGlyPheAlaLysPheMetGluPheVal	385						
Qy	1352	GCTGTTAATCTCATATCCAGAGCTGCAATTTGATGACTATTTTGAATGTGTGTTTT	1411						
Db	386	SerValSerValThrHisProGluLeuLysValGlyAspTyrPhePheGlyLysCysPhe	405						
Qy	1412	GAAAGTAATTAACAAAGATTCATTGAATTCATCCGCCCTATCTCCAAACACAGCGGAAACC	1471						
Db	406	AspAlaMetGluValAspAlaLeuAsnSerSerHisProValSerThrProValGluAsn	425						
Qy	1472	CCGACTCAAAATACAGGAAATGTTTGATGAAGTTTCTTATAAACAGGGAGCTTGTATTTTG	1531						
Db	426	ProAlaGlnIleArgGluMetPheAspAspValSerTyrAspLysGlyAlaCysIleLeu	445						
Qy	1532	AATATGCTCAAGATTTTCTGGGTGAGGAGAAATTCAGAAAGGAATAATTCAGTACTTA	1591						
Db	446	AsnMetLeuArgGluTyrLeuSerAlaAspAlaPheLysSerGlyIleValGlnTyrLeu	465						
Qy	1592	AAGAAGTTACGATATGAAATGCTAAGAATGATGACTTGTGGAGCAGCTGTCAAAATAGT	1651						
Db	466	GlnLysHisSerTyrLysAsnThrLysAsnGluAspLeuTrpAspSerMetAlaSerIle	485						
Qy	1652	TGTTTGAAGAGTGAATTTACATCTGGT-----GGAGTTTGTTCATTCGGATCCCAAGATG	1705						
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Qy	1706	ACAAGTAACATGCTCGCTTCTGGGGGAAATTCGACAGGTCAAAGAGATGATCAGTACA	1765						
Db	504	SerSerSerSerSerHisTyrHisGlnGluGlyValAspValLysThrMetMetAsnThr	523						
Qy	1766	TGACTCTCCAGAAAGGAATCCCTCTGCTGCTGTAAACAAGACGGGTGTTCTCCGCA	1825						
Db	524	TrpThrLeuGlnArgGlyPheProLeuIleThrIleThrValArgGlyArgAsnValHis	543						
Qy	1826	CTGCAACAGAGCGCTTCTCCAGGGGGTTTTCCAGGAAGACCTGAAATGGAGGGCCCTG	1885						
Db	544	MetLysGlnGluHisTyrMetLysGly-----SerAspGlyAlaPro	557						
Qy	1886	CAGGAGAGGTACCTGTGGCATATCCCATTCACCTACTCCACGAGTCTTCTTAATGTGATC	1945						
Db	558	AspThrGlyTyrLeuTrpHisValProLeuThrPheIleThrSerLysSerAspMetVal	577						
Qy	1946	CACAGACACATCTCAAATCAAAGACAGATACTCTGATCTACCTGAAAAACAGTGG	2005						
Db	578	HisArgPheLeuLeuLysThrLysThrAspValLeuLeuProGluGluValGluTrp	597						
Qy	2006	GTGAAATTTAATGTGGACTCAAATGGTTACTACATGCTTCACTATGAGGGTCAATGG	2065						
Db	598	IleLysPheAsnValGlyMetAsnGlyTyrTyrIleValHisTyrGluAspAspGlyTyr	617						
Qy	2066	GACCAACTATTACACAGCTGAATCAGAACACACACTTCTCAGACCTTAAGGACAGATA	2125						
Db	618	AspSerLeuThrGlyLeuLeuLysGlyThrHisThrAlaValSerSerAsnAspArgAla	637						
Qy	2126	GGTCTGATTCATGATGTTTTCAGTAGTTGGTGCAGGAGACTGACCTTAGACAAAGCT	2185						
Db	638	SerLeuIleAsnAsnAlaPheGlnLeuValSerIleGlyLysLeuSerIleGluLysAla	657						
Qy	2186	CTTGACATGACTTACTACTCCAAACATGAACACAGACGCCCGGCACCTTCTCGAAGGCTG	2245						

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Db 658 LeuAspLeuSerLeuTyrLeuIleuYshsGluThrGluLeuMetProValPheGlnGlyLeu 677
Qy 2246 AGTTACTTGGAAATCGTTTACACATGATGAGCAGAGGAATATTTTCAGATCTCTCGAA 2305
Db 678 AsnGluLeuIleProMetTyrLysLeuMetGluLysArgAspMetAsnGluValGluThr 697
Qy 2306 AACCTCAAGCGTTACTCTTCAGTATTTTAAAGCAGATGATGACAGGAAAGCTGGAGT 2365
Db 698 GlnPheLysAlaPheLeuIleArgLeuLeuArgAspLeuLeuAspLysGlnThrTrpThr 717
Qy 2366 GACAAGGCTCAGTCGGACAGGATGCTCGCTCGCTCTCTTCAAGCTGGCCCTGTCAC 2425
Db 718 AspGluGlySerValSerGluArgMetLeuArgSerGluLeuLeuLeuLeuAlaCysVal 737
Qy 2426 CTGAACCATGCTCTTGGCATCCAGAAAGCTGCTGAACCTCTTCTCCAGTGGATGGAATCC 2485
Db 738 HisAsnTyrGlnProCysValGlnArgAlaGluGlyTyrPheArgLysTrpLysGluSer 757
Qy 2486 AGTGAATAATTAATATACCAACAGATGTTTAAAGATTTGTATTTCTGTGGTCTCAG 2545
Db 758 AsnGlyAsnLeuSerLeuProValAspValThrLeuAlaValPheAlaValGlyAlaGln 777
Qy 2546 ACAACAGCAGGATGCAATTTACCTTTTACAGCAATATGAACCTCAATGTCAGTCTGAA 2605
Db 778 SerThrGluGlyTrpAspPheLeuTyrSerLysTyrGlnPheSerLeuSerSerThrGlu 797
Qy 2606 CAAACAAATTTCTATGCTTTGTCACAGCAAGCATCAGGAAAGTTACTGAAGTTA 2665
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Qy 2666 ATTGAATAGGAATGGAAGAAAGTTATCAAGACACAGCAAGCTTGGCAGCTCTCTCAT 2725
Db 818 LeuAspGluSerPheLysGlyAspLysIleLysThrGlnGluPheProGlnIleLeuThr 837
Qy 2726 GCGATTCGACAGCTCCAAAGGGCAGCAACTAGCATGGATTTTGTAAAGAGAAATGG 2785
Db 838 LeuIleGlyArgAsnProValGlyTyrProLeuAlaTrpGlnPheLeuArgLysAsnTrp 857
Qy 2786 ACCCATCTCTGAAAAATTTGACTTGGCTCATATGACATAAGATGATCATCTCTCGC 2845
Db 858 AsnLysLeuValGlnLysPheGluLeuGlySerSerSerIleAlaHisMetValMetGly 877
Qy 2846 ACAACAGCTCACTTTTCTTCCAGGATAAGTTGCAAGGAGTGAACACTATTTTGAATCT 2905
Db 878 ThrThrAsnGlnPheSerThrArgThrArgLeuGluGluValLysGlyPhePheSerSer 897
Qy 2906 CTTGAGGCTCAAGGATCATCTCGATATTTTCAAACTGTTCTCGAAACGATACCAAA 2965
Db 898 LeuLysGluAsnGlySerGlnLeuArgCysValGlnGlnThrIleGluThrIleGluGlu 917
Qy 2966 AATATAAATGGCTGGAGAAGATCTCCGACTCTGAGGACTTGGCTA 3013
Db 918 AsnIleGlyTrpMetAspLysAsnPheAspLysIleArgValTrpLeu 933

RESULT 9
US-10-106-698-6381
; Sequence 6381, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
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; SEQ ID NO 6381
; LENGTH: 944
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-106-698-6381

Alignment Scores:
Pred. No.: 9,45e-224 Length: 944
Score: 2515.50 Matches: 477
Percent Similarity: 69.34% Conservative: 172
Best Local Similarity: 50.96% Mismatches: 268
Query Match: 42.55% Indels: 19
DB: 14 Gaps: 7

US-10-039-073-2 (1-3366) x US-10-106-698-6381 (1-944)
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Qy 272 AGTTATCACTTTCATCAGGATCTCTGGGCTTTCCAGTAGCCACTTAATGGGGAACGATTT 331
Db 34 TrpCysGlnSerThrGlu-----AlaSerProLysArgSerAspGlyThrProPhe 50
Qy 332 CTTGGCAGGAGCTTAAGCTCCCGAGTGTGCTCCTCTCCATTATGATGACCTCTTTGTC 391
Db 51 ProTrpAsnLysIleArgLeuProGluTyrValIleProValHisTyrAspLeuLeuIle 70
Qy 392 CACCCCAATCTCCTCTGACTTTGTCATCTGAGAAGATCGAAGTCTTGGTCAGC 451
Db 71 HisAlaLeuLeuThrThrLeuThrPheTrpGlyThrThrLysValGluIleThrAlaSer 90
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Db 91 GlnProThrSerThrIleLeuHisSerHisLeuGlnIleSerArgAlaThrLeu 110
Qy 512 CAGTCAGAGGAGATTCAGATACATGAAACAGGAAAGAACTGAAAGTTTGTGATTAC 571
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Qy 572 CTTGCTCATGAACAAATTTGCATCTGCTTCCAGAGAACTTTAGCCCTCCTCAGTGAATAC 631
Db 129 ProProGlnGlnIleAlaLeuLeuAlaProGluProLeuLeuValGlyLeuProTyr 148
Qy 632 TATGTGCTATAGACTTCCAAAGCCAAGTTAGGTAGGTCTTGAAGGGTTTATATAAGC 691
Db 149 ThrValValIleHisTyrAlaGlyAsnLeuSerGluThrPheHisGlyPheTyrLysSer 168
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Qy 752 CAGCAGCGATGGCTTTCCCTTGTGTTGATCAACCGTTGTTCAAAGCCAACTTTTCAATC 811
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Qy 872 GAACCTTGAGGAGTCTTTGGAGAGATCCTTTGAAACTACTGTAAAATAGTACATACATAC 931
Db 229 ThrValAlaGluGlyLeuIleGluAspHisPheAspValThrValLysMetSerThrTyr 248
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Db 249 LeuValAlaPheIleIleSerAspPheGluSerValSerLysIleThrLysSerGlyVal 268
Qy 992 AAGGTGTCATCTATGATCCCCAGACAAAGCGGATCAAAACACACATATATGCTTTGCAGCA 1051
Db 269 LysValSerValTyrAlaValProAspLysMetAsnGlnAlaAspTyrAlaLeuAspAla 288
Qy 1052 TCACCTGAAGTACTTGTGATTTTATGAAAGTAGTACTTTGATATCTACTATCCACTCTCCAAA 1111
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APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Pao, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC63
CURRENT APPLICATION NUMBER: US/09/989,722
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deanovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C62
; CURRENT APPLICATION NUMBER: US/09/989,723
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Qy	1946	CACAGACACATCTAAATCAAAAGACAGATACTCTCGATCTACTCTGAAAAGACCATGTGG	2005
Db	578	HisArgPheLeuLeuLysThrLysThrAspValLeuIleLeuProGluGluValGluTrp	597
Qy	2006	GTGAAATTTAATGTGGACTCAAAATGGTTACTACATCGTTTCACCTATCAGGTCATGATGG	2065
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Qy	2066	GACCAACTATTACAGAGCTGAATCAGAACCAACACACTTCTCAGACCTTAAGCAGACAGTA	2125
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Qy	2126	GGTCTGATTCAATGTGTTTACGTAGTTGTGGTGCAGGAGACTGACCTTAGACAAAGCT	2185
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;	APPLICANT:	Grimaldi, J. Christopher
;	APPLICANT:	Gurney, Austin L.
;	APPLICANT:	Kljasin, Ivar J.
;	APPLICANT:	Napier, Mary A.
;	APPLICANT:	Pan, James
;	APPLICANT:	Paoni, Nicholas F.
;	APPLICANT:	Roy, Margaret Ann
;	APPLICANT:	Stewart, Timothy A.
;	APPLICANT:	Tumas, Daniel
;	APPLICANT:	Watanabe, Colin K.
;	APPLICANT:	Williams, P. Mickey
;	APPLICANT:	Wood, William I.
;	APPLICANT:	Zhang, Zemin
;	TITLE OF INVENTION:	Secreted and Transmembrane Polypeptides and Nucleic
;	TITLE OF INVENTION:	Acids Encoding the Same
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; PRIOR FILING DATE: 1998-07-09

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Score: 2512.50 Matches: 477
Percent Similarity: 69.34% Conservative: 172
Best Local Similarity: 50.96% Mismatches: 268
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RESULT 13
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; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC65
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; PRIOR FILING DATE: 1998-07-07

; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.: 1.79e-223 Length: 941
Score: 2512.50 Matches: 477
Percent Similarity: 69.34% Conservative: 172
Best Local Similarity: 50.96% Mismatches: 268
Query Match: 42.50% Indels: 19
DB: 9 Gaps: 7

US-10-039-073-2 (1-3366) x US-09-989-727-353 (1-941)
Qy 212 TACTGCTTAACAGCCATCTTGGCCCAATATGATTTGTTCTCAGTTCCTCAGTGCCATCT 271
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
15 PheLeuLeuSerSerLeuLeuAlaLeuLeuThrVal-----SerThrProSer 30
Qy 272 AGTTATCATTCTAGAGGATCCTGGGGCTTTCCAGTAGCCACTAATGGGGAACGATTT 331
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
31 TrpCysGlnSerThrGlu-----AlaSerProLysArgSerAspGlyThrProPhe 47
Qy 332 CCTTGGCAGGAGCTAAGGCTCCCGAGTGGTGCATTCCTCTCCATTATGACCTTTTGTG 391
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
48 ProTrpAsnLysIleArgLeuProGluTyrValIleProValHisTyrAspLeuLeuIle 67
Qy 392 CACCCCAATCTCACCTCTCTGGACTTTTGTTCATCTCAGAGATCGAAGTCTTGGTCAGC 451
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
68 HisAlaAsnLeuThrThrLeuThrPheTrpGlyThrLysValGluIleThrAlaSer 87
Qy 452 AATGCTACCCAGTTTATCATCTTTGCACAGCAAAAGATCTTGAAATCAGCAATGCCACCCT 511
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
88 GlnProThrSerThrIleIleLeuHisSerHisLeuGlnIleSerArgAlaThrLeu 107
Qy 512 CAGTCAGAGGAAGATTCAAGATACATGAACACGAGAAAGAACTGAAAGTTTTCAGTTAC 571
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
108 ArgLysGlyAlaGlyGluArgLeuSerGlu-----GluProLeuGlnValLeuGluHis 125
Qy 572 CCTGCTCATGAACAAATTGCACTGCTGTTCCAGAGAAACTTACGCCTCACCTGAAATAC 631
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
126 ProProGlnGluGlnIleAlaLeuLeuAlaProGluProLeuLeuValGlyLeuProTyr 145
Qy 632 TATGTGGCTATGGACTTCCAAAGCCCAAGTTAGGTGATGGCTTTGAAGGTTTATAAAGC 691
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
146 ThrValValIleHisTyrAlaGlyAsnLeuSerGluThrPheHisGlyPheTyrLysSer 165
Qy 692 ACATACAGAACTCTTGGTGGTGAACAAGAAATCTTCAGTAACAGATTTTGACCCCAACC 751
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
166 ThrTyrArgThrLysGluGlyGluLeuAlaSerThrGlnPheGluProThr 185
Qy 752 CAGGCAGCATGGCTTTCCCTTGTCTTGTGATGAACCGTTGTTCAAAGCCAACCTTTTCAATC 811
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
186 AlaAlaArgMetAlaPheProCysPheAspGluProAlaPheLysAlaSerPheSerIle 205
Qy 812 AAGATACGAAGAGAGACGCGCATATTGCACTATCCAAACATGCCAAAGTTTAAGACAATT 871
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
206 LysIleArgArgGluProArgHisLeuAlaIleSerAsnMetProLeuValLysSerVal 225
Qy 872 GAACCTGAAGAGGCTTTTGGAGATACACTTTGAAACTACTGTAAAAAGAGTACATAC 931
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
226 ThrValAlaGluGlyLeuIleGluAspHisPheAspValThrValLysMetSerThrTyr 245
Qy 932 CTTGTAGCCTACATAGTTTGTGATTTTCCACTCTCTGAGTGGCTTCACTTTCATCAGGGTC 991
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
246 LeuValAlaPheIleIleSerAspPheGluSerValSerLysIleThrLysSerGlyVal 265
Qy 992 AAGGTGTCCATCTATGCATCCCCAGACAAACGGAATCAAAACACATTATGCTTTTCAGGCA 1051
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
266 LysValSerValTyrAlaValProAspLysIleAsnGlnAlaAspTyrAlaLeuAspAla 285
Qy 1052 TCACCTGAGCTACTTGTATTTTATGAAAAGTACTTCTGATCTACTATCCACTCTCCAAA 1111
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
286 AlaValThrLeuLeuGluPheTyrGluAspTyrPheSerIleProTyrProLeuProLys 305
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QY 1112 CTGGATTAAATGCTATTCCTGACCTTTGCACTTGAGCGCATCGAAAAATGGGGCCCTCAT 1171
DB 306 GlnAspLeuAlaAlaileProAspPheGlnSerGlyAlaMetGluAsnTrpGlyLeuThr 325
QY 1172 ACATATAGGGAGACGCTCACTGCTTTTTCACCCCAAGACCTCTTCCTCGATAAACATG 1231
DB 326 ThrTyArgGluSerAlaLeuLeuPheAspAlaGluLysSerAlaSerSerLysLeu 345
QY 1232 TGGGTCCACAGAGTCATACCCCATGAACCTGGCGCACCACTGTTTGGCAACCTGCTCACA 1291
DB 346 GlyIleThrValThrValAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeuValThr 365
QY 1292 ATGGAATGGTGAATGATATTTGGCTTAAGAGGGTTTTGCAAAATACATGAACTTATC 1351
DB 366 MetGluTrpTrpAsnAspLeuTrpLeuAsnGluGlyPheAlaLysPheMetGluPheVal 385
QY 1352 GCTGTTAATGCTACATATCCAGAGCTGCNAATTTGATGACTATTTTGAATGCTGTTT 1411
DB 386 SerValSerValThrHisProGluLeuLysValGlyAspTyPhePheGlyLysCysPhe 405
QY 1412 GAAGTAATTCACAAAAGATTCATTGAATTCATCCCGCCCTATCTCCAAACCCAGCGGAAACC 1471
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QY 1532 AATATGCTCAAGGATTTTCTGGTCAGGAGAAATTCAGAAAGGAATTAATTCAGTACTTA 1591
DB 446 AsnMetLeuArgGluTySerAlaAspAlaPheLysSerGlyIleValGlnTyLeu 465
QY 1592 AAGAGTTTCAGCTATAGAAATCTAAGAAATGATGACTTGTGAGCAGCTCTGCAAAATAGT 1651
DB 466 GlnLysHisSerTyLysAsnThrLysAsnGluAspLeuTrpAspSerMetAlaSerIle 485
QY 1652 TGTTTAGAAAGTAAATTTACATCTCGT-----GGAGTTTGTTCATTCGGATCCCAAGATG 1705
DB 486 Cys-----ProThrAspGlyValLysGlyMetAspGlyPheCys---SerArgSerGlnHis 503
QY 1706 ACAAGTACATGCTCGCTTCTGGGGGAAATGCAAGAGTCAAGAGATGATGACTACA 1765
DB 504 SerSerSerSerHisThrHisGlnGluGlyValAspValLysThrMetMetAsnThr 523
QY 1766 TGGACTCCAGAAAGGAATCCCTGCTGCTGGTGTAAACAAGACGGGTTCCTACCCGA 1825
DB 524 TrpThrLeuGlnArgGlyPheProLeuIleThrIleThrValArgGlyArgAsnValHis 543
QY 1826 CTGCAACAGGAGCGCTTCTCCAGGGGTTTTCCAGGAAGACCCCTGAATGGAGGGCCCTG 1885
DB 544 MetLysGlnGluHisTyMetLysGly-----SerAspGlyAlaPro 557
QY 1886 CAGGAGAGTACCTTGCGCATATCCATGACCTACTCCAGAGTCTCTTAATGTCATC 1945
DB 558 AspThrGlyTyLeuTrpHisValProLeuThrPheIleThrSerLysSerAsnMetVal 577
QY 1946 CACAGACATTTCTAAATCAAAGACAGATCTCTGGATCTACCTCGAAAGAACACCATGGG 2005
DB 578 HisArgPheLeuLeuLysThrLysThrAspValLeuIleLeuProGluGluValGluTrp 597
QY 2006 GTGAAATTAATGTCGATCAAAATGTTTACATCGTTTCACTATGAGGGGTGATGATGG 2065
DB 598 IleLysPheAsnValGlyMetAsnGlyTyTyIleValHisTyLeuAspAspGlyTrp 617
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DB 618 AspSerLeuThrGlyLeuLysGlyThrHisThrAlaValSerSerAsnAspArgAla 637
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DB 678 AsnGluLeuIleProMetTyLysLeuMetGluLysArgAspMetAsnGluValGluThr 697
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RESULT 14
US-09-989-731-353
; Sequence 353, Application US/09989731
; Patent No. US20020103125A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deanovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaudi, J. Christopher

; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PlC70
; CURRENT APPLICATION NUMBER: US/09/989,731
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.: 1,798-223 Length: 941
Score: 2512.50 Matches: 477
Percent Similarity: 69.34% Conservative: 172
Best Local Similarity: 50.96% Mismatches: 268
Query Match: 42.50% Indels: 19
Db: 9 Gaps: 7

US-10-039-073-2 (1-3366) x US-09-989-731-353 (1-941)
QY 212 TACTGCTTAACAGCCATCTTGCCCAAAATATGCAATTTGCTCAGTTCCTCAGTGCCATCT 271
Db 15 PheLeuLeuSerSerLeuLeuAlaLeuLeuThrVal-----SerThrProSer 30
QY 272 AGTTATCACTTCAGTCAGATCCTGGGCTTCCAGTAGGCCACTAAATGGGGAAGATT 331
Db 31 TrpCysGlnSerThrGlu-----AlaSerProLysArgSerAspGlyThrProPhe 47
QY 332 CTTGGCAGGAGCTAAGCTCCAGTGTGGTTCCTCTCCATTATGACTCTTTGTC 391
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QY 392 CACCCCAATCTCACCTCTCTGACCTTTGTCATCTGAGAAGATCGAAGTCTTGTCAGC 451
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QY 452 AATGCTACCCAGTTTATCATCTTGACAGCAAGATCTTGAATCAGCAATGCCACCTT 511
Db 88 GlnProThrSerThrIleLeuHisSerHisLeuGlnIleSerArgAlaThrLeu 107
QY 512 CAGTCAGAGGAGATTCAAGATACATGAACCCAGGAAAAGAACTGAAAGTTTTCAGTTAC 571
Db 108 ArgLysGlyAlaGlyGluArgLeuSerGlu-----GluProLeuGlnValLeuGluHis 125

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QY 692 ACATACAGAACTCTTGGTGTGAACAAGAAATTTTCAGTAACACAGATTTTGAGCAACCC 751
Db 166 ThrTyrArgThrLysGluGlyLeuArgIleLeuAlaSerThrGlnPheGluProThr 185
QY 752 CAGCAGCATGGCTTTCCCTTGTGTTGATGAACCGTGTTCACAAAGCCAACTTTCAATC 811
Db 186 AlaAlaArgMetAlaPheProCysPheAspGluProAlaPheLysAlaSerPheSerIle 205
QY 812 AAGATACGACAGAGAGCAGGCATATTGCACATATCCACATGCCCAAGGTTTAAGCAATT 871
Db 206 LysIleArgArgGluProArgHisLeuAlaIleSerAsnMetProLeuValLysSerVal 225
QY 872 GAACCTTGAAGGAGCTTTTGGAAAGATCACATTTGAAACTACTGTAAAAATGAGTACATAC 931
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QY 932 CTTGTAGCCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACATTCATCAGGGTC 991
Db 246 LeuValAlaPheIleIleSerAspPheGluSerValSerLysIleThrLysSerGlyVal 265
QY 992 AAGGTGTCATCTATGATCCCGACAGCAACGGAATCAACACATATTGCTTTGCAGGCA 1051
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Db 346 GlyIleThrValThrValAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeuValThr 365
QY 1292 ATGGAATGGTGAATGATATTGCTTTAAGAGGGGTTTTGCAAAATACATGGAATTCATC 1351
Db 366 MetGluTrpTrpAsnAspLeuTrpLeuAsnGluGlyPheAlaLysPheMetGluPheVal 385
QY 1352 GCTGTTAATGTCATATCCAGAGCTGCAATTTGATGACTATTTTTTGAATGTGTGTTTT 1411
Db 386 SerValSerValThrHisProGluLeuLysValGlyAspTyrPhePheGlyLysCysPhe 405
QY 1412 GAAGTAATTACAAAGATTCATGAATTCATCCCGCCTATCTCCAAACACAGCGGAAACC 1471
Db 406 AspAlaMetGluValAspAlaLeuAsnSerHisProValSerThrProValGluAsn 425
QY 1472 CCGACTCAATACAGGAAATGTTTGTGAAGTTCCTATACCAAGGGAGCTGTGATTTTG 1531
Db 426 ProAlaGlnIleArgGluMetPheAspValSerTyrAspLysGlyAlaCysIleLeu 445
QY 1532 AATATGCTCAAGGATTTTGGGTGAGGAGAAATTCAGAAAGGAATTAATTCAGTACTTA 1591
Db 446 AsnMetLeuArgGluTyrLeuSerAlaAspAlaPheLysSerGlyIleValGlnTyrLeu 465
QY 1592 AAGAAGTTCACTATGAAATGCTAAGATGTCAGCTTGTGGAGCAGTCTGTCAATAGT 1651
Db 466 GlnLysHisSerTyrLysAsnThrLysAsnGluAspLeuTrpAspSerMetAlaSerIle 485

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71	PRIOR FILING DATE: 1998-07-07
72	PRIOR APPLICATION NUMBER: 60/091982
73	PRIOR FILING DATE: 1998-07-07

; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

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US-10-039-073-2 (1-3366) x US-09-989-732-353 (1-941)

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512	QY	CAGTCNAGGAGAGATTCAGATACATGAAACCAGGAAGAAAGACTGAAGTTTGTAGTTAC	571
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752	QY	CAGGCACGATCGCTTCCCTTGCTTTGATGAACCCGTTGTTCAAAGCCAACTTTTCAATC	811
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206	Db	LysIleArgArgGluProArgHisLeuAlaIleSerAsnMetProLeuValLysSerVal	225
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226	Db	ThrValAlaGluGlyLeuIleGluAspHisPheAspValThrValLysMetSerThrTyr	245
932	QY	CTTGTAGCCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCATCTCATCAGGGGTC	991
246	Db	LeuValAlaPheIleIleSerAspPheGluSerValSerLysIleThrLysSerGlyVal	265
992	QY	AAAGTGTCTCATCTATGTCATCCCGACAAACGGGAATCAAAACATATGCTTTTGCAGGCA	1051
266	Db	LysValSerValTyrAlaValProAspLysIleAsnGlnAlaAspTyrAlaLeuAspAla	285
1052	QY	TCACGTGAAGCTACTTGATTTTTATGAAAGPACTTTTGATATCTACTATCATCTCTCCAA	1111
286	Db	AlaValThrLeuLeuGluPheTyrGluAspTyrPheSerIleProTyrProLeuProLys	305

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QY	1172	ACATATAGGAGAGCTCAGCTGCTTTTTCAGCCCAAGACCTCTCTGCTTCGGATAAACTG	1231
DB	326	ThrTyrArgGluSerAlaLeuLeuPheAspAlaGluLysSerAlaSerSerLysLeu	345
QY	1232	TGGGCTCACCAGAGTCATAGCCCATGAATCCGCGCACCAAGTGGTTTGGCAACCTGGTCACA	1291
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QY	1412	GAAGTAATACAAAAGATTCATTGAATTCATCCGCGCTATCTCCAAACCCAGCGGAAACC	1471
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DB	466	GlnLysHisSerTyrLysAsnThrLysAsnGluAspLeuTrpAspSerMetAlaSerIle	485
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DB	504	SerSerSerSerHisIstTrpHisGlnGluGlyValAspValLysThrMetMetAsnThr	523
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QY	1886	CAGGAGAGGTACCTGTGGCATATCCCATTTGACTCTCCAGAGTCTTCTTAATGTGATC	1945
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QY	1946	CACAGACACATTCTAAATCAAAGACAGATCTCTGATCTACTCTGAAAGACCAAGTGTGG	2005
DB	578	HisArgPheLeuLeuLysThrLysThrAspValLeuLeuLeuProGluGluValGluTrp	597
QY	2006	GTGAAATTTAATGTGGACTCAAAATGGTTTACTACATCGTTCACTATGAGGTCATGATGG	2065
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QY	2066	GACCAACTCATATACAGCTGAATTCAGAACACACACTTCTCAGACTTAAGGACAGAGTA	2125
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DB	638	SerLeuIleAsnAlaPheGlnLeuValSerIleGlyLysLeuSerIleGluLysAla	657
QY	2186	CTTGACATGACTACTACCTCCCAACTGAAACCAAGCAGCCGCCACCTTCTCGAAGGTCTG	2245

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QY      2306 AACCTCAAGCGTTACTCTTTCAGTATTTTAAAGCCAGTATTGACAGGCAAGCTGGAGT 2365
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QY      2366 GACAAGGCTCAGTCTGGACAGGATGCTCCGCTCTCTGAACTGCTGAACTGGCTGTGAC 2425
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QY      2426 CTGAACACCTCTCTTGCATCCAGAAAGCTGCTGAACCTCTCTCCAGTGGATGGAATCC 2485
Db      738 HisAsnTyrGlnProCysValGlnArgAlaGluGlyTyrPheArgLysTrpLysGluSer 757
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QY      2666 ATTGAACCTAGGAATGGAAGAAAGTTATCAAGACACAGAACTTGGCAGCTCTCCTCAT 2725
Db      818 LeuAspGluSerPheLysGlyAspLysIleLysThrGlnGluPheProGlnIleLeuThr 837
QY      2726 GCGATTGCCAGCTCCAAAGGGCAGCACTAGCATGGATTTTGTAAAGAGAAATTTGG 2785
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Db      878 ThrThrAsnGlnPheSerThrArgThrArgLeuGluGluValLysGlyPhePheSerSer 897
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QY      2966 AATATAAATGGCTGGAGAGAAATCTTCGACTCTGAGGACTTGGCTA 3013
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GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2016.5	34.1	1026	2	US-08-530-792D-22
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6	1440	24.4	964	4	US-09-949-016-7431
7	1264.5	21.4	967	3	US-09-139-802-701
8	1264.5	21.4	967	4	US-09-659-786-201
9	1225	20.7	919	4	US-09-919-039-222
10	1165	19.7	977	3	US-08-335-844A-22
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13	1117	18.9	972	4	US-09-129-366-24	Sequence 24, Appl
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16	1083	18.3	699	4	US-09-270-767-45507	Sequence 45507, A
17	986	16.7	593	4	US-08-637-670-38	Sequence 38, Appl
18	908	15.4	608	4	US-08-637-670-36	Sequence 36, Appl
19	884	15.0	850	4	US-09-902-540-10199	Sequence 10199, A
20	868.5	14.7	990	4	US-09-657-931A-11	Sequence 11, Appl
21	867	14.7	848	4	US-09-583-110-2738	Sequence 2738, Ap
22	863	14.6	995	4	US-09-657-931A-1	Sequence 1, Appl
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24	841.5	14.2	946	4	US-09-657-931A-10	Sequence 10, Appl
25	820.5	13.9	1009	4	US-09-657-931A-13	Sequence 13, Appl
26	818.5	13.8	986	4	US-09-657-931A-12	Sequence 12, Appl
27	785.5	13.3	942	4	US-09-657-931A-9	Sequence 9, Appl
28	711.5	12.0	616	4	US-08-637-670-26	Sequence 26, Appl
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33	659	11.1	528	4	US-08-637-670-27	Sequence 27, Appl
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37	477.5	8.1	346	4	US-08-637-670-24	Sequence 24, Appl
38	466	7.9	362	4	US-08-637-670-35	Sequence 35, Appl
39	460.5	7.8	359	4	US-08-637-670-37	Sequence 37, Appl
40	459	7.8	350	4	US-08-637-670-39	Sequence 39, Appl
41	458	7.7	350	4	US-08-637-670-25	Sequence 25, Appl
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43	392.5	6.6	867	4	US-09-602-777A-104	Sequence 104, App
44	379.5	6.4	242	4	US-09-248-796A-18160	Sequence 18160, A
45	364.5	6.2	380	4	US-09-270-767-44186	Sequence 44186, A

ALIGNMENTS

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; Sequence 1, Application US/09345650
; Patent No. 6362324
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: 17867, A No. 6362324el Human Aminopeptidase
; FILE REFERENCE: 5800-36
; CURRENT APPLICATION NUMBER: US/09/345.650
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 960
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-345-650-1

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Best Local Similarity: 100.00% Mismatches: 0
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DB: 3 Gaps: 0

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QY 446 GTCAGCAATGTCTACCCAGCTTATCATCTTGCACAGCAAGATCTTGAATCACCAGTCCC 505
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QY 506 ACCCTTCAGTCAGAGGAAGATCAAGATACATGAATCAACAGGAAAAGAACTGAAGTTTG 565
DB 121 ThrLeuGlnSerGluGluAspSerArgTyrMetLysProGlyLysGluLeuLysValLeu 140
QY 566 AGTTACCTGCTCATGAACAATTCACCTGCTGCTGCTCCAGAGAACTTACGCTCACCTG 625
DB 141 SerTyrProAlaHisGluGlnIleAlaLeuLeuValProGluLysLeuThrProHisLeu 160
QY 626 AAATACTATGTGGCTATGCACTTCCAGCCCAAGTTAGGTGATGGCTTTGAAGGGTTTAT 685
DB 161 LysTyrTyrValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTyr 180
QY 686 AAAAGCACAATCAGAACTCTTGGTGGTGAACAAGAAATCTTGCAGTAACAGATTTTGAG 745
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DB 201 ProThrGlnAlaArgMetAlaPheProCysPheAspGluProLeuPheLysAlaAsnPhe 220
QY 806 TCAATCAAGATACGAAGAGAGAGAGCATATTGCATCTCAACATGCCCAAGGTTAAG 865
DB 221 SerIleLysIleArgArgGluSerArgHisIleAlaLeuSerAsnMetProLysValLys 240
QY 866 ACAATTGAACCTGAAGAGGCTTTTGGAGATCACTTTGAACTACTGTAAAAATGAGT 925
DB 241 ThrIleGluLeuGluGlyGlyLeuLeuGluAspHisPheGluThrThrValLysMetSer 260
QY 926 ACATACCTGTGAGCTACATAGTTGTGATTTCCACTCTCTGAGTGGCTTCATCTCA 985
DB 261 ThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThrSerSer 280
QY 986 GGGGTCAAGGTGTCATCTATGTCATCCCGACACAAACGGAATCAACACATATTGCTTTG 1045
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QY 1046 CAGGCATCACTGAAGCTACTGATTTTATGAAAGTACTTTGTATCTACTATCCACTC 1105
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DB 461 IleLeuAsnMetLeuLysAspPheLeuGlyGluLysPheGlnLysGlyIleIleGln 480
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QY 1886 CAGGAGAGGTACCTGTGGCATATCCCATTCACCTACTCCACGAGTTCCTCTAATGTGATC 1945
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DB 721 AsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSerTrpSer 740
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DB 741 AspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAlaCysAsp 760
QY 2426 CTGAACCATGCTCTCTTGCATCCAGAAAGCTGTGCTGAACTCTTCTCCCGAGTGGATGCC 2485

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Db 306 GlnAspLeuAlaIleProAspPheGlnSerGlyAlaMetGluAsnTrpGlyLeuThr 325
QY 1172 ACATATAGGGAGAGCTCAGCTCTCTTTTACCCCAAGACCTCTCTCGCTCCGATAAACTG 1231
Db 326 ThrTyrArgGluSerAlaLeuLeuPheAspAlaGluLysSerSerAlaSerLysLeu 345
QY 1232 TGGGTCCACGAGTCATAGCCCATGAATGCGGCACAGTGGTTGGCAACCTGGTCACA 1291
Db 346 GlyIleThrValThrValAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeuValThr 365
QY 1292 ATGGAATGGTGAATGATATTTGCTTAAGAGAGGTTTCCAAATACATGGAACCTTATC 1351
Db 366 MetGluTrpTrpAsnAspLeuTrpLeuAsnGluGlyPheAlaLysPheMetGluPheVal 385
QY 1352 GCTGTTAATGCTACATATCCAGAGCTGCAATTTTGATGACTATTTTGAATGTGTGTTT 1411
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QY 1592 AAGAAGTTCAGCTATAGAAATGCTAAGATGATGACTTGTGAGCAGCTGCTCAATAGT 1651
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QY 1946 CACAGACACATTTCAAAATCAAGACAGATACTCTGGATCTACTGAAAGACACCGATTGG 2005
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QY 2006 GTGAAATTTAATGGAGCTCAAAATGGTTTACTACATCGTTTCACTATGAGGGTCATGGATGG 2065
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QY 2126 GGTCTGATCATGATGTGTTACACTAGTTGGTCCAGGAGACTGACCCCTAGACAAAGCT 2185
Db 638 SerLeuIleAsnAlaPheGlnLeuValSerIleGlyLysLeuSerIleGluLysAla 657

QY 2186 CTTGACATGACTTTACTACCTCCCAACATGAACAAGCAGCCCCGCACTTCTCGAAGCTG 2245
Db 658 LeuAspLeuLeuTyrLeuLysHisGluThrGluIleMetProValPheGlnGlyLeu 677
QY 2246 AGTTACTTGGAAATCGTTTTTACCACATGATGACGACAGGAATATTTTCAGATATCTCTGAA 2305
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QY 2666 ATTGAAGTAGGATGGAAGAAAGTTTATCAACAGACAGACTTGGCAGCTCTCTTCAT 2725
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QY 2726 GCATTTGCCAGCAGCTCCAAAGGGGAGCAACTAGCATGGGATTTTGTAAAGAAATTTGG 2785
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QY 2966 AATATAAATGGCTGGAGAGAATCTTCGAGCTCTCGAGGACTTGGCTA 3013
Db 918 AsnIleGlyTrpMetAspLysAsnPheAspLysIleArgValTrpLeu 933

RESULT 3

US-08-530-792D-23
; Sequence 23, Application US/08530792D
; Patent No. 5972680

GENERAL INFORMATION:

; APPLICANT: Knowles, W. J.; Guralski, D.; Haigh, W.; Letsinger, J. T.;
; APPLICANT: Clairmont, K.; and Hart, J.
; TITLE OF INVENTION: Glucose Transporter Vesicle Amino peptidase
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bayer Corporation
; CITY: West Haven
; STATE: Connecticut
; COUNTRY: U.S.A.
; ZIP: 06516

249	GlusSerLeuLeuThrGlyHisAsnTyrThrLeuLysIleGluTyrSerAlaAsnIleSer	268
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725	CTTGGCAGTAACAGATTTTGGAGCCAAACCCAGCAGCATGGCTTTCCCTTGGCTTTGATGAA	784
289	PheAlaAlaThrGlnPheGluProLeuAlaAlaArgSerAlaPheProCysPheAspGlu	308
785	CCGTGTGTTCAAGCCCACTTTTCAATCAAGATACGAAGAGAGAGAGCGGCATATTGGCACTA	844
309	ProAlaPheLysAlaThrPheIleIleLysIleThrArgAspGluHisHisThrAlaLeu	328
845	TCCAACATGTCCTGAAGGTTTAAGACAATTTGAAGAGAGGTCCTTTTGGAGATCACTTT	904
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349	SerGluSerValLysMetSerThrTyrLeuValAlaPheIleValGlyGluMetArgAsn	368
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369	LeuSerGln---AspValAsnGlyThrLeuValSerValIleThrAlaValProGluLysIle	387
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1085	TTTGGATATCATCATCACTCTCCAACTCGGATTTTAATTCGTATCTCTGACTTTTGCACTT	1144
408	PheGluIleGlnTyrProLeuLysLysLeuAspLeuValAlaIleProAspPheGluAla	427
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1385	GATGACTATTTTGAATGTGTGTTTGAAGTAATTTACAAAGATTCATTGAAATTCATCC	1444
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1445	CGCCCTATCTCCAAACCCAGCGGAACCCCGACTCAAAATACAGGAATTTGTTGATGAAGTT	1504
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1565	TTCCAGAAAGGAATAATTCAGTACTTAAAGAGTTCAGCTATAGAAATGCTAAGAATGAT	1624
568	PheGlnHisAlaIleIleLeuTyrLeuHisAsnHisSerTyrAlaAlaIleGlnSerAsp	587
1625	GACTTGTGGAGCAGCTCTGTCAAAATAGTTGTTTGAAGAAGTGATTTTACATCTGGTGGAGTT	1684
588	AspLeuTrpAspSerPheAsnGlu-----	595
1685	TGTCATTCGGATCCCAAGATGACAGTAACATGCTCGCCTTTCTGGGGGAAAATGCAGAG	1744
596	-----ValThrGlyLysThrLeuAsp	602

Alignment Scores:

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Pred. No.: 3,79e-198 Length: 1026
Score: 2016.50 Matches: 402
Percent Similarity: 61.74% Conservative: 158
Best Local Similarity: 44.32% Mismatches: 310
Query Match: 34.11% Indels: 37
DB: 2 Gaps: 6

US-10-039-073-2 (1-3366) x US-08-530-792D-22 (1-1026)

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QY 365 ATTCTCTCCATATGACCTTTTGTCCACCCCAATCTCACCTCTCTGGACTTTGTGCA 424
DB 173 IleProGlnArgTyrGluLeuSerLeuHisProAsnLeuThrSerMetThrPheArgGly 192
QY 425 TCTGAGAGATCGAAGTCTTGTGTCAGCAATGCTACCCAGTTTATCATCTTGCACAGCAA 484
DB 193 SerValThrIleSerLeuGlnAlaLeuGlnAspThrArgAspIleIleLeuHisSerThr 212
QY 485 GATCTTGAATCAGCAATCCACCTTCAGTCAGAGGAAGATTCAAGATACATGAACCA 544
DB 213 GlyHisAsnIleSerValThrPheMetSerAlaValSerSerGln----- 228
QY 545 GGAAAGAACTGAAAGTTTGTAGTTTACCTGCTCATGAACAAATGCACTGCTGTTCCA 604
DB 229 GluLysGlnValGluLeuLeuGluTyrProTyrHisGluGlnIleAlaValAlaPro 248
QY 605 GAGAACTTACGCTCACCTGAAATACTATGTGGTGTGGACTTCAAGCCAAAGTTAGT 664
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QY 785 CCGTGTTCAAAGCCACTTTTCAATCAAGATACGAAAGAGAGAGAGGATATTCGACTA 844
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DB 388 AspGlnValTyrHisAlaLeuAspThrThrValLysLeuLeuGluPheTyrGlnAsnTyr 407
QY 1085 TTTGATATCTACTATCTCACTCCAACTGGATTTAATTTGCTATTCTCTGACTTTGCACCT 1144
DB 408 PheGluIleGlnTyrProLeuLysLysLeuAspLeuValAlaIleProAspPheGluAla 427
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DB 488 GlyPheAlaThrPheMetGluTyrPheSerValGluLysIlePheLysGluLeuAsnSer 507
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QY 1922 TCCACGAGTCTTCTTAATGTATCCACAGACAC-----ATTCTAAAATCAAAGACA 1972
DB 660 ValThrAspGlyArgAsnTyrSerGluTyrArgSerValSerLeuLeuAspLysLysSer 679
QY 1973 GATCTCTGGATCTACCTGAAAGACACAGTTGGGTGAAATTTTAAATGTGCGACTCAATGGT 2032
DB 680 AspValIleAsnLeuThrGluGlnValGlnTyrValLysValAsnThrAsnMetThrGly 699
QY 2033 TACTACATCGTTCATGAGGGTCATGCGGTCATGGAGGACCAACTCATACACAGCTGAATCAG 2092
DB 700 TyrTyrIleValHisTyrAlaHisAspGlyTrpAlaAlaLeuIleAsnGlnLeuLysArg 719
QY 2093 AACACACACATCTCTCAGACCTTAAGGACAGAGTAGTCTGTGATTCATGATGTGTTCCAGCTA 2152
DB 720 AsnProTyrValLeuSerAspLysAspArgAlaAsnLeuIleAsnAsnIlePheGluLeu 739
QY 2153 GTTGGTGGAGGAGACTGACCTTACAGAAAGCTCTTGTGACGACTTACTACTCCACAT 2212
DB 740 AlaGlyLeuGlyLysValProLeuGlnMetAlaPheAspLeuIleAspTyrLeuArgAsn 759
QY 2213 GAAACAGACCCCGCAGCTTCTCGAAGGTCTGAGTTACTTGGAACTCGTTTACCACATG 2272
DB 760 GluThrHisThrAlaProIleThrGluAlaLeuPheGlnThrAspLeuIleTyrAsnLeu 779
QY 2273 ATGACAGAAAGGAATATTTTCAGATATCTCTCAAAACCTCAAGCGTTACTCTTTCAGTAT 2332
DB 780 LeuGluLysLeuGlyHisMetAspLeuSerSerArgLeuValThrArgValHisLysLeu 799
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QY 2333 TTTAAGCCAGTGATTGACAGCAAGAGCTGGAGTGACAAAGGCTCAGTCTGGGACAGGATG 2392
Db 800 LeuGlnAsnGlnGlnGlnThrPrpThrAspGluGlyThrProSerMetArgGlu 819
QY 2393 CTCGGCTCGGCTCTCTTGAAGCTGCTGGTGAACCTGACCTGAACCACTGCTCTTGTGATCCAGAAA 2452
Db 820 LeuArgSerAlaLeuLeuGluPheAlaCysAlaHisSerLeuGluAsnCysThrThrMet 839
QY 2453 GCTGCTGAACCTCTCCAGTGGATGAATCCAGTGGAAAAATTAATATACCAACAGAT 2512
Db 840 AlaThrLysLeuPheAspGlyTrpMetAlaSerAsnGlyThrGlnSerLeuProThrAsp 859
QY 2513 GTTTTAAAGATGTGTATCTGTGGTGTCTCAGACAAACAGCAGGATGAATTAACCTTTTA 2572
Db 860 ValMetThrThrValPheLysValGlyAlaArgThrGluLysGlyTrpLeuPheLysPhe 879
QY 2573 GAGCAATATGAACCTGTCNAATCTCAAGTCTGAGCAACAAACAAAATCTGTATGCTTTGTCA 2632
Db 880 SerMetTyrSerSerMetGlySerGluAlaGluLysAspLysIleLeuGluAlaLeuAla 899
QY 2633 ACGAGCAGCATCAGGAAAGTTACTGAAGTTAATTGAACCTAGGAATGGAAGGAAGGTT 2692
Db 900 SerSerAlaAspAlaHisLysLeuTyrTrpLeuMetLysSerSerLeuAspGlyAspIle 919
QY 2693 ATCAAGACACAGAACTTGGCAGCTCTCTTCATCGCATTTGCCAGACGTCCTCAAGGGGCAG 2752
Db 920 IleArgThrGlnLysLeuSerLeuIleIleArgThrValGlyArgGlnPheProGlyHis 939
QY 2753 CAACTAGCATGGATTTTGAAGAGAAATTTGGACCCCATCTTCTGAAAAATTTGACTTG 2812
Db 940 LeuLeuAlaTrpAspPheValLysGluAsnTrpAsnLysLeuValHisLysPheHisLeu 959
QY 2813 GGCTCATATGACATAAGGATCATCTCTCGCACACAGCTCACTTTCTTCTTCCCAAGAT 2872
Db 960 GlySerTyrThrIleGlnSerIleValAlaGlySerThrHisLeuPheSerThrLysThr 979
QY 2873 AAGTTGCAAGAGGTGAACCTATTTTGAATCTCTTGAGGCTCAAGGATCATCTCTGAT 2932
Db 980 HisLeuSerGluValGlnGluPheGluAsnGlnSerGluAlaThrLeuGlnLeuArg 999
QY 2933 ATTTTCAACTGTTCTGGAACGATACCAAAAATATATAATGCTGGGAGAAATCTT 2992
Db 1000 CysValGlnGlnAlaPheGluValIleGluLeuAsnIleGlnTrpMetAlaArgAsnLeu 1019
QY 2993 CCGACTCTGAGGACTTGCTA 3013
Db 1020 LysThrLeuThrLeuTrpLeu 1026
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RESULT 5

```
US-09-949-016-6154
; Sequence 6154, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6154
; LENGTH: 957
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6154
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Alignment Scores:
Pred. No.: 3,43e-139 Length: 957
Score: 1444.00 Matches: 323
Percent Similarity: 53.07% Conservative: 178
Best Local Similarity: 34.22% Mismatches: 361
Query Match: 24.42% Indels: 82
DB: 4 Gaps: 19

US-10-039-073-2 (1-3366) x US-09-949-016-6154 (1-957)
QY 263 GTGCCATCTAGTTATCACTTCACTGAGGATCTCTGGGGCTTTTCCAGTA----- 310
Db 60 LeuProSerSer-----ThrAlaSerProSerGlyProAlaGlnAsnGlnAsp 76
QY 311 -----GCCACTAATGGGGAACGATTTCTTGGCAGGAGCTAAGGCTCCCGAGTGTG 361
Db 77 IleCysProAlaSerGluAspGluSerGlyGlnTrpLysAsnPheArgLeuProAspPhe 96
QY 362 GTCATTTCTCTCCATTATGACCTTCTTGTCCACCCCAATCTCACCTCTCTGGACTTTGTT 421
Db 97 ValAsnProValHisTyrAspLeuHisValLysProLeuLeuGluAspThrTyrThr 116
QY 422 GCATCTGAGAAGATCGAAGTCTTGTGTCAGCAATGCTACCCAGTTTATCATCTTGCACAGC 481
Db 117 GlyThrValSerIleSerIleAsnLeuSerAlaProThrArgTyrLeuTrpLeuHisLeu 136
QY 482 AAGATCTTGAATACGAATGCCACCTTCACTCAGAGGGAAGATTCAAGATACATGAAA 541
Db 137 ArgGluThrArgIleThrArgLeu-----ProGluLeuLysArg 149
QY 542 CCA---GGAAAGAAGCTGAAAGTT-----TTGAGTTTACCTCTGCTCATGAACAAAT 589
Db 150 ProSerGlyAspGlnValGlnValArgCysPheGluTyrLysLysGlnGluTyrVal 169
QY 590 GCATCTGCTGTTCCAGAGAACTTACGCTCACCTG-----AAATCTATGTGGCT 640
Db 170 ValValGluAlaGluGluLeuThrProSerSerGlyAspGlyLeuTyrLeuLeuThr 189
QY 641 ATGCACTTCCCAAGCCAGTTAGGTAGTGGCTTTGAGGGTTTATAAAGCACATACAGA 700
Db 190 MetGluPheAlaGlyTrpLeuAsnGlySerLeuValGlyPheTyrArgThrTyr- 208
QY 701 ACTCTTGGTGTGAAACAAGAATTTCTTGCAAGTAAACAGATTTTGAGCCAAACCCAGGCACGC 760
Db 209 ThrGluAsnGlyArgValLysSerIleAlaAlaThrAspHisGluProThrAspAlaArg 228
QY 761 ATGCTTTTCCCTTGGTGTGATGAACCGTTGTTCAAGCCAACTTTTCAATCAAGATACGA 820
Db 229 LysSerPheProCysPheAspGluProAsnLysAlaThrTyrThrIleSerIleThr 248
QY 821 AGAGAGCAGCAGCATATTGCACTATCAACATGCCAAAGGTTAAGACAATTTGAACCTGAA 880
Db 249 HisProLysGluTyrGlyAlaLeuSerAsnMetProValAlaLysGluLysValAsp 268
QY 881 GGAGGTCTTTTGAAGATCACTTTGAAACTACTGTAAAAATAGTACATACCTTTGTAGCC 940
Db 269 AspLysTrpThrArgThrThrPheGluLysSerValProMetSerThrTyrLeuValCys 288
QY 941 TACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACTTCATCAGGGGTCAAGGTGTC 1000
Db 289 PheAlaValHisGlnPheAspSerValLysArgIleSerAsnSerGlyLysProLeuThr 308
QY 1001 ATCTATGATCCCCAGACAAACGGAATCAAAACATTTATCTTTTGCAGGCATCACTCAAG 1060
Db 309 IleTyrValGlnProGluGlnLysHisThrAlaGluTyrAlaAlaAsnIleThrLysSer 328
QY 1061 CTACTTGAATTTTATGAAAAGTACTTTGATATCTTACTTACTCTCCCAACTCGAATTTA 1120
Db 329 ValPheAspTyrPheGluGluTyrPheAlaMetAsnTyrSerLeuProLysLeuAspLys 348
QY 1121 ATTGCTATTCCTGACTTTGCACCTGGAGCCATCGAAAATTTGGGCTCATATACATAGG 1180
Db 349 IleAlaIleProAspPheGlyThrGlyAlaMetGluAsnTrpGlyLeuIleThrTyrArg 368
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QY 1181 GAGAGCTCACTGCTTTTACCCCAAGACCTCTTCTGCTTCGATAAACTGGGTGTCACC 1240
DB 369 GluThrAsnLeuLeuTyrAspProLysGluSerAlaSerAsnGlnGlnArgValAla 388
QY 1241 AGAGTCATAGCCCACTGCGGACCACTGGTGGCACTGGTGGCACTGGTGGCACTGGTGG 1300
DB 389 ThrValValAlaHisGluLeuValHisGlnTrpPheGlyAsnIleValThrMetAspTrp 408
QY 1301 TCGAATGATATTGGCTTAAGAGGGTTTTGCAAAATACATCGAACTTATCCCTGCTTAAT 1360
DB 409 TrpGluAspLeuTrpLeuAsnGluGlyPheAlaSerPheGluPheLeuGlyValAsn 428
QY 1361 GCTACATATCCAGAGCTGCAATTT---GATGACTATTTTGAATGTGTGTTTGAAGTA 1417
DB 429 HisAlaGluThrAspTrpGlnMetArgAspGlnMetLeuLeuGluAspValLeuProVal 448
QY 1418 ATTACAAAAGATTTCATTAATTCATCCCGCTCTCTCAACACCGGAAACCCGACT 1477
DB 449 GlnGluAspAspSerLeuMetSerHisProIleValThrValThrProAsp 468
QY 1478 CAATACAGGAATGTTTCATGAAGTTTCTATAACAAGGAGCTGTGTTTGAATATG 1537
DB 469 GluIleThrSerValPheAspGlyIleSerTyrSerLysGlySerSerIleLeuArgMet 488
QY 1538 CTCAGGATTTTCTGGTGAGGAGAAATTCAGAAAGGAATTAATTCAGTACTTAAGAAG 1597
DB 489 LeuGluAspTrpIleLysProGluAsnPheGlnLysGlyCysGlnMetTyrLeuGluLys 508
QY 1598 TTCAGCTATAGAATGCTTAAGATGATGACTGTGTGAGCAGCTCTGCAATAGTTGTTA 1657
DB 509 TyrGlnPheLysAsnAlaLysThrSerAspPheTrpAlaAlaLeuGluAla----- 526
QY 1658 GAAAGTGATTTTACATCTGCTGGAGTTTGTCTATTCGGATCCCAAGATGACAAAGTAACATG 1717
DB 526 ----- 526
QY 1718 CTCGCTTTCTGGGGAAATCCAGAGTCAAGAGATGATGACTACATGGACTCTCCAG 1777
DB 527 -----SerArgLeuProValLysGluValMetAspThrTrpThrArgGln 541
QY 1778 AAAGNAATCCCTGCTGCTGTTAAACAAGCGGTGTCTACTCGAGTGCACAGGAG 1837
DB 542 MetGlyTyrProValLeuAsnVal-----AsnGlyValLys-----AsnIleThrGlnLys 558
QY 1838 CCTCTCTCCAGGGGTTTTCCAGGAAGACCTGAAATGGAGGCGCTCGCAGGAG----- 1891
DB 559 ArgPheLeuLeu-----AspProArgAlaAsnProSerGlnProSer 573
QY 1892 -----AGTACTCTGGCATATCCATTGACCTAC-----TCCACGAGTTCTTCT 1936
DB 574 AspLeuGlyTyrThrTrpAsnIleProValLysTrpThrGluAspAsnIleThrSerSer 593
QY 1937 AATGTGATCCAGACACATTCATAATCAAGACAGATCTCTGTGATCTACCTGAAAG 1996
DB 594 ValLeuPheAsnArgSerGluLysGluGlyIleThrLeuAsnSerSerAsnProSerGly 613
QY 1997 ACCAGTGGGTGAATTTAATGTGACTCAAAATGGTTTACTACATCGTTCACTATGAGGT 2056
DB 614 AsnAlaPheLeuLysIleAsnProAspHisIleGlyPheTyrArgValAsnTyrGluVal 633
QY 2057 CATGGATGGCACTAATATACAGCTGAATCAGAACACCACTCTCTCAGACCTAAG 2116
DB 634 AlaThrTrpAspSerIleAlaThrAlaLeuSerLeuAsnHisLysThrPheSerSerAla 653
QY 2117 GACAGATAGTCTGATGATGATGTTTTCAGCTAGTTGGTGGAGGAGTACCTCCTA 2176
DB 654 AspArgAlaSerLeuIleAspAlaPheAlaLeuAlaArgAlaGlnLeuLeuAspTyr 673
QY 2177 GACAAAGCTCTTGACATGACTTACTACCTCCAACTGAAGAAACAGGAGC-----CCC 2227
DB 674 LysValAlaLeuAsnLeuThrLysTyrLeuLysArgGluGluAsnPheLeuProTrpGln 693

QY 2228 GCACCTTCGAAGGTCTGAGTTACTTGAATCGTTTACCACATGATGCACAGAAGGAAT 2287
DB 694 ArgValIleSerAlaValThrTyrIleIleSerMetPhe-----GluAsp 708
QY 2288 ATTTTCAGATATCTCTGAAAACCTCAAGGTTTACCTTCTTTCAGTATTTTAAAGCCAGTGATT 2347
DB 709 AspLysGluLeuTyrProMetIleGluLeuTyrPheGlnGlnValLysProIleAla 728
QY 2348 GACAGGCAAACTGGAGTGAAGGGTCACTGCGGACAGATGCTCCGCTCGGCTCTC 2407
DB 729 AspSerLeuGlyTyrAsnAspAlaGlyAspHisValThrLysLeuLeuArgSerVal 748
QY 2408 TTGAAGCTGGGCTGTGACCTGAAACCTCTCTTGCATCCAGAAAGCTGCTGAACCTCTC 2467
DB 749 LeuGlyPheAlaCysLysMetGlyAspArgGluAlaLeuAsnAsnAlaSerSerLeuPhe 768
QY 2468 TCCAGTGGATGGAATCCAGTGGAAATTAATAATACCAACAGATGTTTAAAGATTGTG 2527
DB 769 GluGlnTrpLeu-----AsnGlyThrValSerLeuProValAsnLeuArgLeuVal 786
QY 2528 TATTCTGGGTCTCAGACAAACAGCA-----GGATGGAATTACTCTTTTAGAGCAA 2578
DB 787 TyrArgTyrGlyMetGlnAsnSerGlyAsnGluIleSerTrpAsnTyrThrLeuGluGln 806
QY 2579 TATGAATGCTCAATGTCAAGTCTGAACAAACAAATTCGTATGCTTGTCAACGAGC 2638
DB 807 TyrGlnLysThrSerLeuAlaGlnGluLysGluLysLeuLeuTyrGlyLeuAlaSerVal 826
QY 2639 AAGCATCAGGAAAGTTACTGAAGTTAATTCAACTAGGAATGGAAGGAAAGGTTTCAAG 2698
DB 827 LysAsnValThrLeuLeuSerArgTyrLeuAspLeuLeuLysAspThrAsnLeuLeuLys 846
QY 2699 ACACAGAACTGGCAGCTCTCTTCATGCGATGCCAGACGTCCAAAGGGGCGACCACTA 2758
DB 847 ThrGlnAspValPheThrValIleArgTyrIleSerTyrAsnSerTyrGlyLysAsnMet 866
QY 2759 GCATGGGATTTTGAAGAAAATTTGGACCATCTTCTGAAAAAATTTGACTTGGCTCA 2818
DB 867 AlaTrpAsnTrpIleGlnLeuAsnTrpAspTyrLeuValAsnArgTyrThrLeuAsnAsn 886
QY 2819 TATCACAATGAGATGATCATCTCTGGCAACAACAGCTCACTTTCTTCAAGGATAAGTTG 2878
DB 887 ArgAsnLeuGlyArgIleValThr---IleAlaGluProPheAsnThrGluLeuGlnLeu 905
QY 2879 CAAGAGTGAACTATTTTGAATCTCTTTCAGGCTCAAGGATCACATCTCGATATTTT 2938
DB 906 TrpGlnMetGluSerPhePheAlaLysTyrProGlnAlaGlyAlaGlyGluLysProArg 925
QY 2939 CAAACTGTTTGGAAACGATACCAAAATATAAATGCTGGAGAGAAATCTTCGACT 2998
DB 926 GluGlnValLeuGluThrValLysAsnAsnIleGluTrpLeuLysGlnHisArgAsnThr 945
QY 2999 CTGAGGACTCG 3010
DB 946 IleArgGluTrp 949

RESULT 6

US-09-949-016-7431
; Sequence 7431, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08


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; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7431
; LENGTH: 964
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7431

Alignment Scores:
Pred. No.:      8,89e-139      Length:      964
Score:          1440.00        Matches:     322
Percent Similarity: 52.97%      Conservative: 178
Best local Similarity: 34.11%    Mismatches: 362
Query Match:      24.36%       Indels:      82
DB:               4           Gaps:         19

US-10-039-073-2 (1-3366) x US-09-949-016-7431 (1-964)

QY 263 GTGCATCTAGTTATCACTTCACTGAGGATCTCGGGCTTTCCAGTA----- 310
Db  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 67 LeuProSerSer-----ThrAlaSerProSerGlyProProAlaGlnAspGlnAsp 83
Db  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 311 -----GCCACTAATGGGAGCGATTCTTGGCAGGAGCTAAGCTCCCGAGTGTG 361
Db  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 84 IleCysProAlaSerGluAspGluSerGlyGlnTrpLysAsnPheA:GLeuProAspPhe 103
Db  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 362 GTCATTCCTCCATTATGACTCTTTGTCCACCCCAATCTCACCTCTCTGGACTTTGTT 421
Db  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 104 ValAsnProValHisTyrAspLeuHisValLysProLeuLeuGluGluAspThrTyrThr 123
Db  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 422 GCATCTGAGAAGATCGAAGTCTTGTCAGCAATGCTACCCAGTTTATCATCTTCCACAGC 481
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 124 GlyThrValSerIleSerIleAsnLeuSerAlaProThrArgTyrLeuTrpLeuHisLeu 143
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 482 AAAGATCTTGAATCAGCAATGCCACCTTCTCAGTCAGGAGGAGATTCAAGATACATGAAA 541
Db  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 144 ArgGluThrArgIleThrArgLeu-----ProGluLeuLysArg 156
Db  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 542 CCA---GGAAAGAACTGAAAGTT-----TTGAGTTACCTGCTCATGAACAAT 589
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 157 ProSerGlyAspGlnValGlnValArgArgCysPheGluTyrLysLysGlnGluTyrVal 176
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 590 GCATCTGTGTTCCAGAGAACTTACCGCTCACCTG-----AAATACTATGTGGCT 640
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 177 ValValGluAlaGluGluGluLeuThrProSerSerGlyAspGlyLeuTyrLeuLeuThr 196
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 641 ATGGACTTCCAGCCAGTTAGTGTGATGGCTTTGAGGGTTTATAAAGCACATACAGA 700
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 197 MetGluPheAlaGlyTrpLeuAsnGlySerLeuValGlyPheTyrArgThrTyr--- 215
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 701 ACTCTTGTGTGTAACAAGAAATCTTGCAGTAACAGATTTTGAGCCAAACCCAGGCACGC 760
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 216 ThrGluAsnGlyArgValLysSerIleValAlaThrAspHisGluProThrAspAlaArg 235
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 761 ATGGCTTTCCTTGTGTTGATGAACCGTTGTTCAAAGCCAACTTTCAATCAAGATACGA 820
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 236 LysSerPheProCysPheAspGluProAsnLysLysAlaThrTyrThrIleSerIleThr 255
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 821 AGAGAGACGCGCATATTGCACTATCCAAATGCCAAAGGTTAGACAAATGAACACTGAA 880
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 256 HisProLysGluTyrGlyAlaLeuSerAsnMetProValAlaLysGluLysValAsp 275
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 881 GGAGGTCTTTTGGAGAGATCACTTTGAACTACTGTAAAAATGAGTACATACCTTTGTAGCC 940
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 276 AsplysTrpThrArgThrThrPheGluLysSerValProMetSerThrTyrLeuValCys 295
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 941 TACATAGTTTGTGATTTCCATCTCTGAGTGGCTTCTCACTTCATCAAGGGGTCAAGGTGCC 1000
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 296 PheAlaValHisGlnPheAspSerValLysArgIleSerAsnSerGlyLysProLeuThr 315
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1001 ATCTATGATCCCCAGACAAACGGAATCAACACATATTATGCTTTGCGGCGATCACTAAG 1060
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 316 IleTyrValGlnProGluGlnLysHisThrAlaGluTyrAlaAlaAsnIleThrLysSer 335
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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QY 1061 CTACTTGATTTTATGAAAAAGTACTTTTGATATCTACTATCTCCACTCTCCAAACTCGAATTTA 1120
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 336 ValPheAspTyrPheGluGluTyrPheAlaMetAsnTyrSerLeuProLysLeuAspLys 355
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1121 ATTGCTATTCTCGACTTTGACCTGGAGCCATGAAATAATTTGGGGCTCATATACATATAGG 1180
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 356 IleAlaIleProAspPheGlyThrGlyAlaMetGluAsnTrpGlyLeuIleThrTyrArg 375
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1181 GAGAGCTCACTGCTTTTGGACCCACAGACCTCTTCTGCTCCGATAAATCTGGGTCCACC 1240
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 376 GluThrAsnLeuLeuTyrAspProLysGluSerAlaSerSerAsnGlnGlnArgValAla 395
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1241 AGAGTCATAGCCCATGAACCTGGCGCCACCTGAGTGTGTTGGCAACCTGGTGCACAAATGG 1300
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 396 ThrValValAlaHisGluLeuValHisGlnTrpPheGlyAsnIleValThrMetAspTrp 415
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1301 TGAATGATATTTGGCTTAAAGAGGGTTTTCGAAAATACATGGAACCTTATCGCTGTTAAT 1360
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 416 TrpGluAspLeuTrpLeuAsnGluGlyPheAlaSerPhePheGluPheLeuGlyValAsn 435
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1361 GCTACATATCCAGAGCTGCAATTT---GATGACTATTTTGTGAATGTGCTTTTGAAGTA 1417
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 436 HisAlaGluThrAspTrpGlnMetArgAspGlnMetLeuLeuGluAspValLeuProVal 455
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1418 ATTACAAAAGATTCATTGAATTCATCCCGCCTTCTCCAAACCCAGCGAAACCCCGACT 1477
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 456 GlnGluAspAspSerLeuMetSerSerHisProIleValThrValThrThrProAsp 475
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1478 CAAATACAGAAATGTTTGTATGAAGTTTCTATAAACAGGAGCTGTATTTGAATATG 1537
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 476 GluIleThrSerValPheAspGlyIleSerTyrSerLysGlySerIleLeuArgMet 495
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1538 CTCAGAGATTTCTGGGTGAGGAGAAATCCACAAAGGATAATTCAGTACTTAAAGAAG 1597
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 496 LeuGluAspTrpIleLysProGluAsnPheGlnLysGlyCysGlnMetTyrLeuGluLys 1515
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1598 TTCAGCTATAGAAATGCTAAGAAATGATGACTTGTGGAGCAGCTGTGCAAAATAGTTGTTA 1657
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 516 TyrGlnPheLysAsnAlaLysThrSerAspPheTyrAlaAlaLeuGluGluAla---- 533
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1658 GAAAGTGATTTTACATCTGTGTGAGTTTGTTCATTCGATCCCAAGATGACAAGTAACATG 1717
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 533 ----- 533
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1718 CTCGCTTTCTGGGGGAAAATGCAGAGGTCAAAGAGATGATGACTACATGCACTCTCCAG 1777
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 534 -----SerArgLeuProValLysGluValMetAspThrTrpThrArgGln 548
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1778 AAAGGAATCCCTCGCTGTGTGGTTAAACAAGACGGGTGTTCACTCCGACTGCAACAGGAG 1837
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 549 MetGlyTyrProValLeuAsnVal-----AsnGlyValLys---AsnIleThrGlnLys 565
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1838 CGCTTCTCCAGGGGTTTTCAGGAGAGACCCTGAATGGAGGGCCCTCGCAGGAG----- 1891
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 566 ArgPheLeuLeu-----AspProArgAlaAsnProSerGlnProProSer 580
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1892 -----AGGTACTGTGGCATATCCCATTCACCTAC-----TCACGAGGTCTTCT 1936
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 581 AspLeuGlyTyrThrTrpAsnIleProValLysTrpThrGluAspAsnIleThrSerSer 600
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1937 AATGTGATCCACAGACACATTTCTAAATCAAAGACAGATACTCTGGATCTTACTCTGAAAAG 1996
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 601 ValLeuPheAsnArgSerGluLysGluGlyIleThrLeuAsnSerSerAsnProSerGly 620
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1997 ACAGTTGGTGAATAATTAATGGACTCAATAGTGTACTACATCGTTCTACTATGAGGT 2056
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 621 AsnAlaPheLeuLysIleAsnProAspHisIleGlyPheTyrArgValAsnTyrGluVal 640
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 2057 CATGGATGGACCAACTCATTACAGAGCTGAATCAGAACCAACACACTTCTCAGACCTAAG 2116
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 641 AlaThrTrpAspSerIleAlaThrAlaLeuSerLeuAsnHisLysThrPheSerSerAla 660
Db  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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QY 2117 GACAGTAGGCTGATTCATGATGTTTACAGTAGTTGGTGAGGAGACTGACCCCTA 2176
Db 661 AsparGalaSerLeuileAspAspAlaPheAlaLeuAlaArgAlaGlnLeuLeuAspTyr 680
QY 2177 GACAAAGCTCTTGACATGACTTACTACCTCCAAACATGAAACAAAGCAGC-----CCC 2227
Db 681 LysValAlaLeuAsnLeuThrLysTyrLeuLysArgGluGluAsnPheLeuProTrpGln 700
QY 2228 GCATCTTCGAAGGCTGAGTTACTTGGAAATCGTTTACCATGATGGACAGAGGAAT 2287
Db 701 ArgValIleSerAlaValThrTyrIleLeuSerMetPhe-----GluAsp 715
QY 2288 ATTTTCAGATATCTCTGAAACCTCAAGCGTTTACCTTCTTCAGTATTTTAAAGCAGGATT 2347
Db 716 AspLysGluLeuTyrProMetIleGluGluTyrPheGlnGlyValValLysPheProIleAla 735
QY 2348 GACAGGCAAAAGCTGGAGTGACAAAGGCTCAGCTGGACAGGATCTCGCTCGGCTCTC 2407
Db 736 AspSerLeuGlyTrpAsnAspAlaGlyAspHisValThrLysLeuLeuLysArgSerVal 755
QY 2408 TTGAAGCTGGCTGTGACCTGAACCATGCTCTTCATCCAGAAAGCTGCTGAATCTTC 2467
Db 756 LeuGlyPheAlaCysLysMetGlyAspArgGluAlaLeuAsnAsnAlaSerSerLeuPhe 775
QY 2468 TCCAGTGATGGAATCCAGTCGGAATTAATATATACACAGATGTTTAAAGATTGTG 2527
Db 776 GluGlnTrpLeu-----AsnGlyThrValSerLeuProValAsnLeuArgLeuVal 793
QY 2528 TATTCGTGGGGCTCAGACACAGCA-----GGATGAAATTACCTTTTAGAGCAA 2578
Db 794 TyrArgTyrGlyMetGlnAsnSerGlyAsnGluIleSerTrpAsnTyrThrLeuGln 813
QY 2579 TATGAACCTGTCAATGCTGAAACAAACAAATTTCTGTATGCTTTGTCAACGAGC 2638
Db 814 TyrGlnLysThrSerLeuAlaGlnGluLysGluLysLeuLeuTyrGlyLeuAlaSerVal 833
QY 2639 AAGCATCAGAAAGTTACTGAAGTTAATTGAACATAGGAATGGAAGGAAGTTATCAAG 2698
Db 834 LysAsnValThrLeuLeuSerArgTyrLeuAspLeuLysAspThrAsnLeuIleLys 853
QY 2699 ACACAGAACTTGGCAGCTCTCCTCATGCGATTGGCCAGAGCTCCAAAGGGGAGCACTA 2758
Db 854 ThrGlnAspValPheThrValIleArgTyrIleSerTyrAsnSerTyrGlyLysAsnMet 873
QY 2759 GCATGGGATTTTGAAGAAATTTGGACCCATCTTCTGAAATAATTTGACTTGGGCTCA 2818
Db 874 AlaTrpAsnTrpIleGlnLeuAsnTrpAspTyrLeuValAsnArgTyrThrLeuAsnAsn 893
QY 2819 TATGACATAAGGATGATCATCTCTGGCACACAGCTCACTTTTCTCCAGGATAGTTG 2878
Db 894 ArgAsnLeuGlyArgIleValThr---IleAlaGluProPheAsnThrGluLeuGlnLeu 912
QY 2879 CAAGAGGTGAACATATTTTGAATCTCTTGAGGCTCAAGGATCATCTGGATATTTT 2938
Db 913 TrpGlnMetGluSerPhePheAlaLysTyrProGlnAlaGlyAlaGlyGluLysProArg 932
QY 2939 CAAACTGTTCTGGAACACCAACCAATAATAATAATGCTCGGAGCAAGAACTTCCCGACT 2998
Db 933 GluGlnValLeuGluThrValLysAsnAsnIleGluTrpLeuLysGlnHisArgAsnThr 952
QY 2999 CTGAGGACTTGG 3010
Db 953 IleArgGluTrp 956
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RESULT 7

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US-09-139-802-201
; Sequence 201, Application US/09139802
; Patent No. 6180084
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
; TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
```

```
; TITLE OF INVENTION: Same
; FILE REFERENCE: P-LJ 3203
; CURRENT APPLICATION NUMBER: US/09/139,802
; EARLIER FILING DATE: 1998-08-25
; EARLIER APPLICATION NUMBER: 08/926,914
; EARLIER FILING DATE: 1997-09-10
; EARLIER APPLICATION NUMBER: 08/710,067
; EARLIER FILING DATE: 1996-09-10
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 201
; LENGTH: 967
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-139-802-201

Alignment Scores:
Pred. No.: 1,07e-120 Length: 967
Score: 1264.50 Matches: 325
Percent Similarity: 46.62% Conservative: 158
Best Local Similarity: 31.37% Mismatches: 386
Query Match: 21.39% Indels: 167
DB: 3 Gaps: 26

US-10-039-073-2 (1-3366) x US-09-139-802-201 (1-967)
QY 203 AGAGGATTTTACTGCTTAACAGCCATC-----TTGCCCAA 238
Db 3 LysGlyPheTyrIleSerLysSerLeuGlyIleLeuGlyIleLeuGlyValAlaAla 22
QY 239 ATATGCAATTTGTTCTCAGTTCCTCAGTCCCATCTAGTTATCTACTTCACCTGAGGATCCTGGG 298
Db 23 ValCysThrIleIleAlaLeuSerValValTyrSerGlnGluLysAsnLysAsnAlaAsn 42
QY 299 GCTTTCCAGTAGCC----- 313
Db 43 SerSerProValAlaSerThrThrProSerAlaSerAlaThrThrAsnProAlaSerAla 62
QY 314 ---ACTAATGGGAAACGATTTCTTGGCAGAGCTTAAGCTCCCGAGTGTGCTTCTTCT 370
Db 63 ThrThrLeuAspGlnSerLysAlaTrpAsnArgTyrArgLeuProAsnThrLeuLysPro 82
QY 371 CTCCATTTAGCTCTTGTGTCACCCCAATCTCACCTCTCTGGAC----- 415
Db 83 AspSerTyrGlnValThrLeuArgProTyrLeuThrProAsnAspArgGlyLeuTyrVal 102
QY 416 TTTGTGTCATCTGAGAAGATCGAAGTCTTGTGTCAGCAATGCTTACCAGTTTATCATCTTG 475
Db 103 PheLysGlySerSerThrValArgPheThrCysLysGluAlaThrAspValIleIleIle 122
QY 476 CACAGCAAGATCTTGAATCAGCAATGCCACCTTTCAGTCAGAGAGAAAGATTCAAGATAC 535
Db 123 HisSerLysLysLeuAsnTyrThr----- 130
QY 536 ATGAACCCAGAAAGAACTGAAAGTTTGTAGTTAC-----CCTGCTCAT 580
Db 131 LeuSerGlnGlyHisArgValValLeuArgGlyValGlyGlySerGlnProProAspIle 150
QY 581 GAACAAATTCACCTGCTGGTTCCA---GAGAAATCTACGCTCCTCAGCTGAAA----- 628
Db 151 AspLysThrGluLeuValGluProThrGluTyrLeuValValHisLeuLysGlySerLeu 170
QY 629 -----TACTATGTGCTATGAGCTTCCAAAGTTCAGGATAGGTAGGTGCTTT 673
Db 171 ValLysAspSerGlnTyrGluMetAspSerGluPheGluGlyGluLeuAlaAspAspLeu 190
QY 674 GAAGGTTTTATAAAGCACATACAGAACTCTTGGTGTGGAACACAGAAATTTCTTGCACATA 733
Db 191 AlaGlyPheTyrArgSerGluTyrMetGlu---GlyAsnValArgLysValValAlaThr 209
QY 734 ACAGATTTTGGCCAAACCCAGGACGATGCTTCCCTTCTTGTGTAACCGTGTGTTTC 793
Db 210 ThrGlnMetGlnAlaAlaAspAlaArgLysSerPheProCysPheAspGluProAlaMet 229
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	Db	387 AspHisCysPheProGluTyrAspIleThrGlnPheValSerAlaAspTyrThrArg	406
	Qy	1418 ATTACAAA---GATTCAATGAATTCATCCGCCCTATCTCCAAGCACGGGAAACCCC	1474
	Db	407 AlaGlnGluLeuAspAlaLeuAspAenSerHisProileedGluValSerValGlyHisPro	426
	Qy	1475 ACTCAATACAGGAAATGTGGTAGAAGTTTCTATAACAAGGAGCTTGATATTTTGAAT	1534
	Db	427 SerGluValaspGluilePheaspAlaileSerTySerlysGlyAlaSerValilleAer	446
	Qy	1535 ATGCTCAAGGATTTCTCGGTGAGGAGNAATTCAGAAAGGAATAATTCAGTACTTAAGA	1594
	Db	447 MetLeuHisAspTyrIleGlyAspPheLysGlyMetAenMetyrLeuThr	466
	Qy	1595 AAGTTTCAGCTATAGAAATGCTAAGATCATCTGTGGAGCAGTCTGTCAAATAGTTGT	1654
	Db	467 LysPheGlnGlnLysAenAlaalaThrGluaspleuTrpGluslerLeuGluAenAla---	485
	Qy	1655 TTAGAAAGTGATTTTACATCTGTGTGGAGTTTGTCTTCGGATCCCAAGATGCACA	1714
	Db	485 -----	485
	Qy	1715 ATGCTCGCTTTCTGGGGAAAAATGCAGAGGTCAAGAGATGATGACTACATCGACTCTC	1774
	Db	486 -----SerGlyLysProileAlaalaValMetAenThrTrpThrLys	499
	Qy	1775 CAGAAAGGAATCCCCCTGCTGTGTGTTAAA-----CAAGACGGGTGTTCACTC	1822
	Db	500 GlnMetGlyPheProleuIleTyrValGluAlagluInValGluasPaspArgLeuLeu	519
	Qy	1823 CGACTGCAACAGGACGCTTCTCCAGGG-----GTTTTCCAGGAAGACCCTGAA	1873
	Db	520 ArgLeuserGlnLysPheCysAlaGlyGlySerTyrValGlyGluAaspCysProGln	539
	Qy	1874 TGGAGGGCCCTCGAGGAGAGGTACTCTGCGCATATCCATTTGACCTACTCCAGAGTTCT	1933
	Db	540 TrpMet-----ValProileThrIleSerThrSerGlu	550
	Qy	1934 TCT---AATGTGATCCACAGACACATCTTAAATCAAAGACAGAT-----ACTCTG	1981
	Db	551 AspProAenGlnAlaLysLeuLysIleleuMetAspLysProGluMetAenValValLeu	570
	Qy	1982 GATCTTACCTGMAAAGACCAGTTGGTGCAATTTAATGTGGACTCAATGTACTACATC	2041
	Db	571 LysAenValLysProAspGlnTrpValLysLeuAenLeuglyThrValGlyPheTyrArg	590
	Qy	2042 GTTCACTATGAGGCTCATGNTGGGACCAACTCATTCACAGCTGAATCAGAACACACA	2101
	Db	591 ThrGlnTyrSerSerAlaMetLeuGluSerLeuLeuProglyIleArgAap-----Leu	608
	Qy	2102 CTCTTCACAGCTAAGGACAGAGTAGGTCTGATTCATCATGTCTGTTTACGTAGTTGGTGA	2161
	Db	609 SerLeuProValaspArgLeuGlyeUglnAasnAspLeuPheSerLeuAlaAargAla	628
	Qy	2162 GGGAGACTGACCCCTAGACAAAGCTCTTTGACATGACTTTACTCTCCAAACATGAACA	2221
	Db	629 GlyIlelle-----	631
	Qy	2222 AGCCCCGACTCTTCGAAGGCTCGAGTTACTTGGNATCGTTTTTACCACATGATGGACAG	2281
	Db	632 -----SerThrValGluValLeuLysValMetGluAlaPheValAenGluProAenTyr	649
	Qy	2282 AGGAATATTTTCAGATATCTCT-----	2302
	Db	650 ThrValTrpSerAspLeuSerCysAenLeuGlyIleleuSerThrLeuLeuSerHisThr	669
	Qy	2303 -----GAAAACTCAAGCGTTTACTCTTTCAGTATTTTAAAGCCAGTGATTCACAG	2353
	Db	670 AspPheTyrGluGluileGlnPheValLysAaspValPheSerProIleGlyGluAarg	689
	Qy	2354 CAAGCTGAGTGACAG-----GGCTAGCTGGGACAGAGTGTCTCCCTCGGCT	2404
	Db	690 LeuGlyTApapProLysProGlyGluGlyHisleu-AspAlaLeuLeuArgGlyLeu	708

QY 2405 CTCCTGTAAGCTGGCGTGTGAACCAATGCCTCTTCATCCAGAAAGCTGCTGAACCTC 2464
: : ||| : : : : :
Db 709 ValLeuGlyLysLeuGlyLysAlaGlyHisLysAlaThrLeuGluGluAlaArgArg 728
2465 TTCCTCCAGTCGATCGAATCAGTGGAATAAATATACACAGATGTTTTAAAGATT 2524
||| : : : : :
Db 729 PheLysAspHisValGlu-----GlyLysGlnIleLeuSerAlaAspLeuArgSerPro 746
2525 GTGTATTCTGTG-----GGTGTCCAGACAACAGCAGGATGGAATTTACCTTTTA 2572
||| ||| ||| ||| ||| : : : : :
Db 747 ValTy rLeuThrValLeuLysHisGlyAspGlyThrLeu-----AspIleMetLeu 764
2573 GAGCAATATGAACCTGTCAATGTCAAGTCTGACAAAAACAAAATTTCTGTATGCTTTGTCA 2632
: : : : : : : : : : :
Db 765 LysLeuHisLysGlnAlaAspMetGlnGluGlyLysAsnArgIleGluArgValLeuGly 784
2633 ACGAGCAAGCATCAGGAAAAAGTTACTGAAGTTAATTAAGTAGGAATGGAAGAAAGGTT 2692
: : : : : : : : : : :
Db 785 AlaThrLeuLeuProAspLeuIleGlnLysValLeuThrPheAlaLeuSerGluGluVal 804
2693 ATCAAGACACAGAATCTGGCAGCTCTCTTCATGCGATTGCCAGACGTCCTCAAAG---GGG 2749
: : : : : : : : : : :
Db 805 ---ArgProGlnAspThrValSerValIleGlyValAlaGlyGlySerLysHisGly 823
2750 CAGCAACTAGCATGGATTTTGTAAAGAGAAAAATTCGACCCTCTTCTGAAAAAATTTGCAC 2809
: : : : : ||| : : : : :
Db 824 ArgLysAlaAlaTrpLysPheIleLysAspAsnTrpGluGluLeuTy rAsnArgTy rGln 843
2810 TTGGGCTCATATGACATGAAGATGATCATCTCTGGCACACAGCTCATTCTTCTTCCCAAG 2869
: : : : : : : : : : :
Db 844 ---GlyGlyPheLeuIleSerArgLeuIleLysLeuSerValGluGlyPheAlaValAsp 862
2870 GATAAGTTGCAAGAGGTCAAACTATTTTTCGATCTCTTGAGGCTCAAGGATCATCATCTG 2929
: : : : : ||| : : : : :
Db 863 LysMetAlaGlyGluValLysAlaPheGluSerHisProAlaProSerAlaGluArg 882
2930 GATATTTTCAAACGTCTCTCGAACAGATAACCAAAAAATATAAAATGGCTGAGAGAAGAT 2989
||| ||| ||| ||| ||| : : : : :
Db 883 Thrile---GlnGlnCysCysGluAsnIleLeuLeuAsnAlaAlaTrpLeuLysArgAsp 901
2990 CTTCGACTCTGAGACTGTGCTGAATG 3016
: : : : : : : : : : :
Db 902 AlaGluSerIleHisGlnTy rLeuLeu 910

RESULT 10
US-08-335-844A-22
; Sequence 22, Application US/08335844A
; Patent No. 6066503
; GENERAL INFORMATION:
; APPLICANT: GRAHAM, MARGARET
; APPLICANT: SMITH, TREVOR STANLEY
; APPLICANT: MUNN, EDWARD ALBERT
; APPLICANT: KNOX, DAVID PATRICK
; APPLICANT: OLIVER, JOANNA JANE
; APPLICANT: NEWTON, SUSAN ELIZABETH
; TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING
; TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE PREPARATION OF
; TITLE OF INVENTION: VACCINES AGAINST HELMINTH INFECTIONS
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Earnst & Kurz
; STREET: Suite 701-E, 555 Thirteenth St., N.W
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:


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Db 931 LeuIysAsnLeuTyrLysAsn---AspLysArgAlaArgGluTyrGlyAlaPheGlyGly 949
Qy 2945 GTTCTGGAAACGATACCAAAATATAAAATGGCTGGAGAGAAATCTTCCGACTCTG 3001
Db 950 AlaIleGluArgSerGluHisArgValIysTrpIleGluLysHisPheArgLysLeu 968

RESULT 11
US-09-129-366-22
; Sequence 22: Application US/09129366
; Patent No. 6534638
; GENERAL INFORMATION:
; APPLICANT: GRAHAM, MARGARET
; APPLICANT: SMITH, TREVOR STANLEY
; APPLICANT: MUNN, EDWARD ALBERT
; APPLICANT: KNOX, DAVID PATRICK
; APPLICANT: OLIVER, JOANNA JANE
; APPLICANT: NEWTON, SUSAN ELIZABETH
; TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING
; TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE PREPARATION OF
; TITLE OF INVENTION: VACCINES AGAINST HELMINTH INFECTIONS
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESS: Rochwell, Figg, Ernst & Kurz
; STREET: Suite 701-E, 555 Thirteenth St., N.W
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/129.366
; FILING DATE: 05-AUG-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/335,844
; FILING DATE: 09-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB PCT/GB93/00943
; FILING DATE: 06-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9209936
; FILING DATE: 08-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, Barbara G.
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1181-241A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)783-6040
; TELEFAX: (202)783-6031
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 977 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-129-366-22

Alignment Scores:
Pred. No.: 1.91e-110 Length: 977
Score: 1165.00 Matches: 280
Percent Similarity: 49.22% Conservative: 192
Best Local Similarity: 29.20% Mismatches: 411
Query Match: 76 Indels: 76
DB: 4 Gaps: 21

US-10-039-073-2 (1-3366) x US-09-129-366-22 (1-977)
Qy 260 TCAGTGCCTAGTATCATCTTCACT-----GAGGAT 292
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Db 41 SerIleGlyLeuThrTyrTyrPheThrArgLysAlaPheAspThrThrGlyGlyAsnGly 60
Qy 293 CTTGGGGCTTTCCAGTAGCCACTAATGGGAAACGATTTCTTGGCAGGAGTAAAGCTC 352
Db 61 LysGlyAspGlnProIleValAspAspAsnSerProSerAla---GluGluLeuArgLeu 79
Qy 353 CCCAGTGTGGTCATTCCTCTCCATATGACCTCTTTGTCCAC-----CCCAATCTC 403
Db 80 ProThrThrIleLysProLeuThrTyrAspLeuValIleLysThrTyrLeuProAsnTyr 99
Qy 404 ACCTCTCTG-----GACTTT-----GTTGCATCTGAG 430
Db 100 ValAsnTyrProProGluLysAspPheAlaIleAspGlyThrValValIleAlaMetGlu 119
Qy 431 AAGATCGAAGTCTTGGTCAGCAATGCTACCCAGTTTATCATCTTGACACACAAAGATCTT 490
Db 120 ValValGlu-----ProThrThrSerIleValLeuAsnSerLysAsnIle 134
Qy 491 GAAATCACGAATGCCACCTTTCAGTCAGAGGAAAGATTCAAGATACATGAAACACGAGAAA 550
Db 135 ProVal-----IleAlaAspGlnCysGluLeuPheSerAsnAsnGlnLysLeuAspIle 152
Qy 551 GAACGTGAAAGTTTGGATTACCTGCTCATGAACAATTGCACCTGCTGGTTCAGAGAAA 610
Db 153 Glu---LysValValAspGlnProArgLeuGluLysValGluPheValLeuLysLys 171
Qy 611 CTTACGGCTCACCTGAAATACTATGTGCTATGCATTCACAGCTTCCAGCCAAAGTTAGGTGGC 670
Db 172 LeuGluLysAsnGlnLysIleThrLeuLysIleValTyrIleGlyLeuIleAsnAspMet 191
Qy 671 TTTGAAGGGTTTATATAAGACACATACAGAACTCTTGGTGGTGAACAAGAAATCTTTGCA 730
Db 192 LeuGlyGlyLeuTyrArgThrThrTyrThrAspLysAspGlyThrThrLysIleAlaAla 211
Qy 731 GTAACAGATTTTGAGCCAAACCCAGGACCGCATGGCTTCCCTTCTGCTTTGTATGAACCGTTG 790
Db 212 CysThrHisMetGluProThrAspAlaArgLeuMetValProCysPheAspGluProThr 231
Qy 791 TTCAAAGCCCAACTTTTCAATCAAGATACGAAGAGAGAGAGAGCATATTTGCATCTCAAC 850
Db 232 PheLysAlaAsnTrpThrValThrValIleHisProLysGlyThrSerAlaValSerAsn 251
Qy 851 ATGCCAAAGGTTAAGACAATTGAACCTTGAAGAGAGTCTTTTGAAGATCACTTTGAAACT 910
Db 252 GlyIleGluLysGlyGluGlyGluValSerGlyAspTrpValThrThrArgPheAspPro 271
Qy 911 ACTGTAAATAGTAGTACATACCTTTGTAGCTCATAGTTTGTGATTTCCACTCTCTAGT 970
Db 272 ThrProArgMetProSerTyrLeuIleAlaLeuValIleSerGluPheLysTyrIleGlu 291
Qy 971 GGCTTCACTTCATCAGGGGTCAAGGTGTCATTCATGCATCCCGACCAACAAACGGAATCAA 1030
Db 292 AsnTyrThrLysSerGlyValArgPheArgIleProAlaArgProGluAlaMetLysMet 311
Qy 1031 ACACATTATGCTTTGAGGATCACTGAAGCTACTTATTTATTTATGAAAAATCTTTGAT 1090
Db 312 ThrGluTyrAlaMetIleAlaGlyIleLysCysLeuAspTyrTyrGluAspPheGly 331
Qy 1091 ATCTACTATCCACTCTCCAAACCTGGATTAAATTCGTATTCTCTGATTTGACCTGGAGCC 1150
Db 332 IleLysPheProLeuProLysGlnAspMetValAlaLeuProAspPheSerSerGlyAla 351
Qy 1151 ATGGAATAATGGGGCTTCATTACATATAGGAGAGCGTCACCTGCTTTTGTGACCCCAAGACC 1210
Db 352 MetGluAsnTrpGlyLeuIleThrTyrArgGluGlySerValLeuTyrAspGluAsnLeu 371
Qy 1211 TCTTCTGCTTCCGATAAACTGTGGTCCACAGAGTCTATAGCCCATAGCACTGAACCTGGCAGC 1270
Db 372 TyrGlyProMetAsnLysGluArgValAlaGluValIleAlaHisGluLeuAlaHisGln 391
Qy 1271 TGGTTTGGCACTTGGTCAAAATGGAATGGTGAATGATATTTGGCTTAAGGAGGTTTT 1330
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Db 392 TrpPheGlyAsnLeuValThrMetLysTrpTrpAspAsnLeuTrpLeuAsnGluGlyPhe 411
Qy 1331 GCAAAATACATGAACTTATCCTGTTAAATGCTACATATCCAGAGCTG---CAATTTGAT 1387
Db 412 AlaSerPheValGluTyrIleGlyAlaAspPheIleSerAspGlyLeuTrpGluMetLys 431
Qy 1388 GACTATTTTGAATGTGTGTTT---GAAGTAATTTACAAAGATTCATTGAATTCATCC 1444
Db 432 AspPhePheLeuLeuAlaProTyrThrSerGlyIleThrAlaAspAlaValAlaSerSer 451
Qy 1445 CGCCCTATCTCCAAACCGGCAACCCGAGCTCAAAATACAGAAATGTTTTCATGAAGTT 1504
Db 452 HisProLeuSerPheArgIleAspLysAlaAlaAspValSerGluAlaPheAspIle 471
Qy 1505 TCCTATAACAGGAGCTGTTATTTTGAATATGCTCAAGGATTTTCTGGGTGAGGAGAA 1564
Db 472 ThrTyrArgLysGlyAlaSerValLeuGlnMetLeuLeuAsnLeuValGlyAspGluAsn 491
Qy 1565 TTCCAGAAAGGAATATTCAGTACTTAAGAGTTTCAGCTATAGAAATGCTAAGATGAT 1624
Db 492 PheLysGlnSerValSerArgTyrLeuLysLysPheSerTyrAspAsnAlaAlaGlu 511
Qy 1625 GACTTGTGAGCAGCTGTGCAATAGTTGTTTGAAGAGTGATTTTACATCTCGTGGAGTT 1684
Db 512 AspLeuTrpAlaAlaPhe-----AspGluThrValGlnGlyIle 524
Qy 1685 TGCTATTCGGATCCCAAGATGACAAAGTAAATGCTCGCTTCTCGGGGAAAAATCCAGAG 1744
Db 525 -----ThrGlyProAsn-----GlyGlyProLeuLys 533
Qy 1745 GTCAAGAGATGATGACTATACATGAGTCTCCAGAAAGGATCCCTGCTGCTGTTAA 1804
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Qy 1805 CAA---GAGCGGTGTCTACCTCGACTGCAACAGGAGCGTCTCTCCAGGGGTTTTCCAG 1861
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Db 574 LysGluProGluLysTyrArgHisProThrTyrGlyPheLysTyrAspValProLeuTrp 593
Qy 1919 TACTCCAGAGTCTTCTNATGTGATCCACAGACATCTTAAATCAAGACAGATACT 1978
Db 594 TyrGlnGluAspGluGlnValLysArgThrTrpLeuLysArgGluGluProLeuTyr 613
Qy 1979 CTGGATCTACCTGAAAGACCACTGGTGGTGAATTTAATGTGGACTCAATGTTACTTAC 2038
Db 614 PheHisValSerAsnSerAspSerValValAlaAsnAlaGluArgAlaPheCys 633
Qy 2039 ATCGTTCTACTATGAGGCTCATGATGGGACCACTCATACACAGCTGAATCAGAACCCAC 2098
Db 634 ArgSerAsnTyrAspAlaAsnGlyTyrArgAsnIleMetArgArgLysGlnAsnHis 653
Qy 2099 ACATCTTCCAGACCTTAAGACAGAGTAGTCTGATTCATGATGTGTTTCAGCTAGTTGGT 2158
Db 654 LysValTyrGlyProArgThrArgAsnAlaLeuIleSerAspAlaPheAlaAlaAla 673
Qy 2159 GCAGGAGAGTACCCCTGACAAAAGCTCTTGACATGACTTACTACTCCACATCAACA 2218
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Qy 2219 AGCAGCCCGCCTCTCTCGAAGCTGTGATGTTACTTGGAAATCGTTTATCCATCATGATGAC 2278
Db 694 AspTyrLeuProTyrLysGluAlaIleSer-----GlyPheAsnThrIleLeuAsp 710
Qy 2279 AGAAGGAATATTTTCAGATATCTTGAAACCTCAAGCGTTACTTCTTCAGTATTTTAAAG 2338
Db 711 PhePheGlySerGluProGlnSerGlnTrpAlaSerGluTyrMetArgLysLeuMetLys 730
Qy 2339 CCAGTGATTTGACAGGCAAGC-----TGGAGTGACAGAGGCTCA 2377
Db 731 ProIleTyrAspLysSerSerIleLysPheIleAlaGluAsnTyrLysAspSerLeu 750
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Qy 2438 CTTTGCATCCAGAAAGCTGCTGAACCTCTTCTCCAG-----TGG 2476
Db 771 GluCysLeuGluGluMetLysLeuPheAspLysGluValMetLysCysGlnProGly 790
Qy 2477 ATGGAATCCAGTGGAAAAATTAATATACCAACAGATGTTTAAAGATGTGTATTCTGTG 2536
Db 791 GlnGlnAlaThrAspCysValLysValThrAlaProLeuArgLysThrValTyrCysTyr 810
Qy 2537 GGTGCTCAGACA-----ACAGCAGGATGGAATACCTTTTAGACCAATATGAATGTCA 2590
Db 811 GlyValGlnGluGlyGlyAspGluAlaPheAspLysValMetGluLeuTyrAsnAlaGlu 830
Qy 2591 ATGTCNAGTGTGACAAAACAAAATTCGTATGCTTGTCAACGACGACGATCAGGAA 2650
Db 831 GlnValGlnLeuGluLysAspSerLeuArgGluAlaLeuGlyCysHisLysAspValThr 850
Qy 2651 AAGTTACTGAAGTTAAATTTGAATAGGAATGAA-----GGAAAGGTTTATCAAGACACAG 2704
Db 851 AlaLeuLysGlyLeuLeuMetLeuAlaLeuAspArgAsnSerSerPheValArgLeuGln 870
Qy 2705 AACTTGGCAGCTCTCTTCATGCTCCAGATGCGCAGAGCTCCAAAGGGGACCAACTAGCATGG 2764
Db 871 AspAlaHisAspValPheAsnIleValSerArgAsnProValGlyAsnGluLeuLeuPhe 890
Qy 2765 GATTTTGAAGAAAATTTGACCCCTCTCTGAAAAAATTTTGACTTGGGCTCATATGAC 2824
Db 891 AsnPheLeuThrGluArgTyrGluGluLeuLeuGluSerLeuSerIleArgHisArgSer 910
Qy 2825 ATAAGGATGATCATCTCTGGCACAACAGCTCACTTTCTTCCAGGATAAGTTGCAAGAG 2884
Db 911 ValAspArgValIleLysAlaCysThrArgGlyLeuArgSerArgGluGlnValGlnGln 930
Qy 2885 GTGAAACTATTTTGAATCTCTTGGAGCTCAAGGATCAGATCTGGATATTTTCAAACT 2944
Db 931 LeuLysAsnLeuTyrLysAsn---AspLysArgAlaArgGluTyrGlyAlaPheGlyGly 949
Qy 2945 GTTCTGGAAACGATAACCAAAAATATAAATGCTGGAGAGAAATCTTCCGACTCTG 3001
Db 950 AlaIleGluArgSerGluHisArgValLysTrpIleGluLysHisPheArgLysLeu 968
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RESULT 12

US-08-335-844A-24

; Sequence 24, Application US/08335844A

; Patent No. 6066503

; GENERAL INFORMATION:

; APPLICANT: GRAHAM, MARGARET

; APPLICANT: SMITH, TREVOR STANLEY

; APPLICANT: MUNN, EDWARD ALBERT

; APPLICANT: KNOX, DAVID PATRICK

; APPLICANT: OLIVER, JOANNA JANE

; APPLICANT: NEWTON, SUSAN ELIZABETH

; TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING

; TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE PREPARATION OF

; TITLE OF INVENTION: VACCINES AGAINST HELMINTH INFECTIONS

; NUMBER OF SEQUENCES: 73

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Rothwell, Figg, Ernst & Kurz

; STREET: Suite 701-E, 555 Thirteenth St., N.W

; CITY: Washington

; STATE: D. C.

; COUNTRY: U.S.A.

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/335,844A
FILING DATE: 09-JAN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB PCT/GB93/00943

FILING DATE: 06-MAY-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9209936

FILING DATE: 08-MAY-1992

ATTORNEY/AGENT INFORMATION:

NAME: WALKER, Barbara W.

REGISTRATION NUMBER: 35,400

REFERENCE/DOCKET NUMBER: 1181-223A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)783-6040

TELEFAX: (202)783-6031

INFORMATION FOR SEQ ID NO:

SEQUENCE CHARACTERISTICS:

LENGTH: 972 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-335-844A-24

Alignment Scores:

Pred. No.:	1,68e-105	Length:	972
Scores:	1117, 00	Matches:	279
Percent Similarity:	48.93%	Conservative:	199
Best Local Similarity:	28.56%	Mismatches:	391
Query Match:	18.89%	Indels:	108
DB:	3	Gaps:	25

US-10-039-073-2 (1-3366) x US-08-335-844A-24 (1-972)

Qy	260	TCAGTGCACCTAGTATACCTTCACT-----GAGGATCCTGGG	298
Db	32	SerIleGlyLeuThrTyrPheThrArgLysAlaPheAspThrSerGluLysProGly	51
Qy	299	GCT-----TTCCAGTAGCCACTTAATGGGAACGA	328
Db	52	LysAspAspThrGlyLysAspLysAspAsnSerProSerAlaAla-----	67
Qy	329	TTTCCTGGCAGGAGCTAAGGCTCCCAAGTGTGTCATCTCTCCATTATGACCTCTTT	388
Db	68	-----GluLeuLeuLeuProSerAsnIleLysProLeuSerTyrAspLeuThr	83
Qy	389	GTC-----CACCCCAATCTCACCTCTCTGGACTTTGTT	421
Db	84	IleLysThrTyrLeuProGlyTyrValAspPheProProGluLysAsnLeuThrPheAsp	103
Qy	422	GCATCTGAGAGATCGAAGTCTGTGTGACGAATGCTACCCAGTTTATCATCTTCGACAGC	481
Db	104	GlyArgValGluIleSerMetValIleGluProThrLysSerIleValLeuAsnSer	123
Qy	482	AAAGATCTTGAATCAGCAATGCCACCTTCAGTCAGAGGAGGATTCAGATACATGAAA	541
Db	124	LysLysIleSerValIle-----ProGlnGluCysGluLeuValSer	137
Qy	542	CCAGAAAGAACGTGAAGTTTGTAGT-----TACCTGTCTCATGAACAATGGCA	592
Db	138	GlyAspLysLysLeuGluIleGluSerValLysGluHisProArgLeuGluLysValGlu	157
Qy	593	CTGCTGGTTCCAGAGAACTTACGCTCACCTGAAATACTATGTGGCTATGGACTTCCAA	652
Db	158	PheLeuIleLysSerGlnLeuGluLysAspGlnGlnIleLeuLeuLysValGlyTyrIle	177
Qy	653	GCCAAGTTAGTGGCTTTGAAGGTTTTATAAAGCACATACAGAATCTTTGGTGGT	712
Db	178	GlyLeuIleSerAsnSerPheGlyGlyIleTyrGlnThrTyrThrThrProAspGly	197
Qy	713	GAACAGAAATCTTGGAGTAACAGATTTTGAGCCACCCAGGACCGATGGCTTTCCT	772
Db	198	ThrProLysIleAlaAlaValSerGlnAsnGluProIleAspAlaArgMetValPro	217

Qy	773	TGCTTTGATGAACCGTTGTTTCAAGGCCAACTTTTCAATCAAGATACGAGAGAGCAGG	832
Db	218	CysMetAspGluProLysTyrLysAlaAsnThrValThrValIleHisProLysGly	237
Qy	833	CATATTGCATCTCAACATGCCCCAAGGTTAAG---ACAATTGAACCTTGAAGGAGGCTTT	889
Db	238	ThrLysAlaValSerAsnGlyIleGluValAsnGlyAspGlyGluIleSerGlyAspTyr	257
Qy	890	TTGGAAGATCATTGAAACTACTGTAAATAAGTACATACCTTTGTAGCTACATAGTT	949
Db	258	IleThrSerLysPheLeuThrThrProArgMetSerTyrLeuLeuAlaValMetVal	277
Qy	950	TGTGATTTCCACTCTCTGAGTGGCTTCATCAGGGGTCAAGGTGTCATCTATGCA	1009
Db	278	SerGluPheGluTyrIleGluGlyGluThrLysThrGlyValArgPheArgIleTrpSer	297
Qy	1010	TCCCCAGACAAACGGAATCAACACATTATGCTTTGCAGGCATCATCTGAAGTACTTGTAT	1069
Db	298	ArgProGluAlaLysLysMetThrGlnTyrAlaLeuGlnSerGlyIleLysCysIleGlu	317
Qy	1070	TTTTATGAAAGTACTTTGATATCTACTATCTCCACTCTCCAACTGGATTTAATGCTATT	1129
Db	318	PheTyrGluAspPhePheAspIleArgPheProLeuLysLysGlnAspMetIleAlaLeu	337
Qy	1130	CCTGACTTTGCACCTGGAGCCATGGAAAATTGGGGCTCATTTACATATAGGAGACGTCA	1189
Db	338	ProAspPheSerAlaGlyAlaMetGluAsnTrpGlyLeuIleThrTyrArgGluAsnSer	357
Qy	1190	CTGCTTTTTCACCCCAAGACCTCTCTGCTTCCGATAAATCTGGGTCCACAGAGTCATA	1249
Db	358	LeuLeuTyrAspAspArgPheTyrAlaProMetAsnLysGlnArgIleAlaIleVal	377
Qy	1250	GCCCATGAAGTGGCGCAGTGGTGTGCAACTGTGTCAATGGAATGGTGAATGAT	1309
Db	378	AlaHisGluLeuAlaHisGlnTrpPheGlyAspLeuValThrMetLysTrpTrpAspAsn	397
Qy	1310	ATTGCGTTAAGGAGGTTTTCGAAAATACATGCAACTTATC---GCTGTTAATGCTTACA	1366
Db	398	LeuTrpLeuAsnGluGlyPheAlaArgPheThrGluPheIleGlyAlaGlyGlnIleThr	417
Qy	1367	TATCCAGAGCTGCAATTTGATGACTATTTTTTG---AATGTGTTTTTGAAGTAATTACA	1423
Db	418	GlnAspAspAlaArgMetArgAsnTyrPheLeuIleAspValLeuGluArgAlaLeuLys	437
Qy	1424	AAAGATTCATGAATTCATCCCGCTCTCTCCAAACCCAGCGGAAACCCGACTCAATA	1483
Db	438	AlaAspSerValAlaSerSerHisProLeuSerPheArgIleAspLysAlaIleGluVal	457
Qy	1484	CAGAAATGTTGATGAAGTTTCTTATTAACAAGGAGCTTGTATTTTGAATATGCTCAAG	1543
Db	458	GluGluAlaPheAspAspIleThrTyrAlaLysGlyAlaSerValLeuThrMetLeuArg	477
Qy	1544	GATTTTCTGGGTGAGGAGAAATTCACAGAAAGAAATTAATTCAGTACTTTAAAGAGTTCCG	1603
Db	478	AlaLeuIleGlyGluLysHisLysHisAlaValSerGlnTyrLeuLysLysPheSer	497
Qy	1604	TATAGAAATGCTAAGATGATGACTTGTGAGCAGCTGTGTCATAATAGTTTGTAGAAAGT	1663
Db	498	TyrSerAsnAlaGluAlaThrAspLeuTrpAlaValPheAspGluValValThrAspVal	517
Qy	1664	GATTTTACATCTGCTGGAGTTTGTCTTCATTCGGATCCCAAGATGACAAGTAACATGCTCGCC	1723
Db	518	GluGlyProAspGly-----LysProMetLysThr-----	528
Qy	1724	TTTCTGGGGGAAATCGCAGGTCAAAGAGATGATGACTACATGAGTCTCCAGAAAGGA	1783
Db	529	-----GluPheAlaSerGlnTrpThrThrGlnMetGly	539
Qy	1784	ATCCCTCTGCTGGTTAAACAA---GACGGGTGTTTCACTCCGACTGCAACAGAGCGC	1840
Db	540	PheProValIleSerValAlaGluPheAsnSerThrThrLeuLysLeuThrGlnSerArg	559

QY 1841 TTC---CTCCAGGGGGTTTTCAGGAAGACCCCTGAATGAGGGCCCTCGCAGAGAGGTAC 1897
Db TyrGluAlaAsnLysAspAlaValGluLysGluLysTyrArgHisProLysTyrGlyPhe 579
QY 1898 CTGTGCGCATATCCCAATTGACCTACTCCACGAGTCTTCTTAATGTGATCCACACACACATT 1957
Db LysTrpAspIleProLeuTrpTyrGlnGluGlyAspLysLysGluIleLysArgThrTrp 599
QY 1958 CTAATAACAAAGACAGATCTCTGATCTTACCTGAAAGACACAGTGGTGAAATTT--- 2014
Db LeuArg---ArgAspGluProLeuTyrLeuHisValSerAspAlaGlyAlaProPheVal 618
QY 2015 ---AATGTGGACTCAATGTGTACTACATCGTTCACTATGAGGGTCATGGATGGACCAA 2071
Db ValAsnAlaAspArgTyrGlyPheTyrArgGlnAsnHisAspAlaAsnGlyTrpLysLys 638
QY 2072 CTCATTACACAGCTCAATCAGAACACACACACTCTCAGACCTTAAGCAGAGTAGGTCTG 2131
Db IleIleLysGlnLeuLysAspAsnHisGluValTyrSerProArgThrArgAsnValIle 658
QY 2132 ATTCATGATGTGTTTCAGCTAGTGTGTCAGGGAGACTGACCTAGACAAAGCTCTTGAC 2191
Db IleSerAspAlaPheAlaAlaAlaThrAspAlaIleGluTyrGluThrValPheGlu 678
QY 2192 ATGACTTACTACTCAACATGAACAGACAGCCCCGCACTT-----CTCGAAGGT 2242
Db LeuLeuAsnTyrAlaGluLysGluThrGluTyrLeuProLeuGluIleAlaMetSerGly 698
QY 2243 CTGAGCTTACTTGAATCGTTTACCACATGATGGACAGAGGAATATTCAGATATCTCT 2302
Db IleSerIleLeuLysTyrPheProThrGluProGlu-----Ala 712
QY 2303 GAAACACCTCAACGGTTACCTCTTCAGTATTTTAAGCCAGTGAATTCAGACGCAAAAGC--- 2359
Db LysProAlaGlnThrTyrMetMetAsnIleLeuLysProMetTyrGluLysSerIle 732
QY 2360 -----TGGAGTGACAGGGGCTCAGCTCTGGGACAGGATGCTCGCGTCG 2401
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QY 2462 CTCTTC---TCCAGTGTGATGAATCCAGTGGAAAAATTAATATACCAACAGATGTTTTA 2518
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Db GlyAspTyrAlaSerAspLysValMetGluLeuTyrThrAlaGluThrLeuAlaLeuGlu 830
QY 2606 CAAAAAATTTCTGTATGCTTTGTCAACGACAGCATCAGGAAAAAGTTA-----CTG 2659
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QY 2660 AAGTTAATTGAATAGGAATGAAGAAAGGTTATCAAGACACAGAACTTGGCAGCTCTC 2719
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QY 2720 CTTTCGATGCGATGCGCAGCTGCAAGGGCAGCACTAGCATGGGATTTGTAGAGAA 2779
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QY 2780 AATTGACCCCATCTCTGAAAAAATTTGACTTGGGCTCATATGATCAAGGATGATCATC 2839
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QY 2840 TCTGGCACACAGCTCAGCTTTTCTTCCAGGATTAAGTTGCAAGAGGTGAAACTATTTT 2899

Db 911 ProAlaCysThrSerGlyIleArgSerGlnGlnGlnIleAspGlnLeuLys----- 927
QY 2900 GAATCTCTTGAAGCTCAAGGATCAT-----CTGGATATTTTCAAACTGTTCTG 2950
Db ---AsnLeuGlnLysAsnGlyMetAsnAlaArgGlnPheGlyAlaPheAspLysAlaIle 946
QY 2951 GAAACGATAACCAAAATATAAATGCTGCTGAGAGAAATCTTCCGACTCTG 3001
Db GluArgAlaGlnAsnArgValAspTrpIleLysHisPheGlnLysLeu 963
RESULT 13
US-09-129-366-24
; Sequence 24, Application US/09129366
; Patent No. 6534638
; GENERAL INFORMATION:
; APPLICANT: GRAHAM, MARGARET
; APPLICANT: SMITH, TREVOR STANLEY
; APPLICANT: MUNN, EDWARD ALBERT
; APPLICANT: KNOX, DAVID PATRICK
; APPLICANT: OLIVER, JOANNA JANE
; APPLICANT: NEWTON, SUSAN ELIZABETH
; TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING
; TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE PREPARATION OF
; TITLE OF INVENTION: VACCINES AGAINST HELMINTH INFECTIONS
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz
; STREET: Suite 701-E, 555 Thirteenth St., N.W
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/129,366
; FILING DATE: 05-AUG-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/335,844
; FILING DATE: 09-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB PCT/GB93/00943
; FILING DATE: 06-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9209936
; FILING DATE: 08-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, Barbara G.
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1181-241A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)783-6040
; TELEFAX: (202)783-6031
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 972 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-129-366-24
Alignment Scores:
Pred. No.: 1.68e-105 Length: 972
Score: 1117.00 Matches: 279
Percent Similarity: 48.93% Conservative: 199
Best Local Similarity: 28.56% Mismatches: 391
Query Match: 18.89% Indels: 108
DB: 4 Gaps: 25

[illegible]

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; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/335,844A
; FILING DATE: 09-JAN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB PCT/GB93/00943
; FILING DATE: 06-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9209936
; FILING DATE: 08-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: WALKER, Barbara W.
; REGISTRATION NUMBER: 35,400
; REFERENCE/DOCKET NUMBER: 1181-223A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)783-6040
; TELEFAX: (202)783-6031
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 972 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-335-844A-23

Alignment Scores:
Pred. No.: 9 46e-104 Length: 972
Score: 1100.00 Matches: 284
Percent Similarity: 47.02% Conservative: 190
Best Local Similarity: 28.17% Mismatches: 390
Query Match: 18.61% Indels: 144
DB: 3 Gaps: 26

US-10-039-073-2 (1-3366) x US-08-335-844A-23 (1-972)
QY 233 CCCAAATATGCATTGTTTCTTCAGTTC-----TCAGTGCCA 268
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15 ProIleSerLeuLeuCyethrLeuPheValLeuAlaAValGlyLeuSerIleGly 34
269 TCTAGTTATCACTTCACT-----GAGGAT 292
:||||:|||||
35 LeuThrTyThrPheThrArgylsAlaPheAspThrThrGlnLysGluGlnLysAspAsp 54
293 CCTGGGGCT-----TTCCAGTAGCCACTAATGGGGAACGATTCCTCTGG 337
||| ||| |||
55 SerGlyGlyLysGluLysAspIleSerProSerAla----- 66
338 CAGGAGCTAAGGCTCCCGAGTGTGGTCATTCTCTCCATTATGACCTCTTTGTC----- 391
||||| :|||::: |||:||||| |||
67 GluGluLeuLeuLeuProThrAsnIleLysProValSerTyrAspLeuAsnIleLysThr 86
392 -----CACCCCAATCTCACCTCTCTGGACTTTGTTGCATCTGAG 430
||| ||| ||| |||
87 TyrLeuProGlyTyrValAsnPheProProGluLysAsnLeuThrPheAspAlaHisVal 106
431 AAGATCGAAGTCTTGCTGACGAATGCTACCCAGTTTATCATCTTGCACACGAAGATCTT 490
:||||:||||:||||| |||:||||:||||| |||
107 GluIleAlaMetValValValGluProThrAsnSerIleValLeuAsnSerLysLysIle 126
491 GAAATCACGAATGCCACCCTTCAGTCAGAGAAGATTCAAGATACATGAACACGAGAAA 550
:|: :|: :|: :|:
127 ThrLeu-----AlaGlnGlyGlyCysGluLeuPheSerGlyAsnGln 140
551 GAACTGAAAGTTTGTAGTTACCTGCTCATGAA-----CAAAATGCATCTGGTT 601
:||||: ||| |||
141 LysLeuAspIleGluSerValLysMetGlnGluAqtLeuAspLysLeuGluIleThrLeu 160

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QY 2978 CTGGAGAGAGATCTTCCGACTCTG 3001
Db :::::||::|
956 IleLysLysHisPheHisArgLeu 963

Search completed: September 26, 2005, 07:54:48
Job time : 188.682 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 26, 2005, 06:10:40 ; Search time 88.8106 Seconds
(without alignments)
6246.842 Million cell updates/sec

Title: US-10-039-073-3
Perfect score: 5062
Sequence: 1 atgttcattcttctgcaat.....ggctaattggttaataactaa 2883

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model
-Q=/cgn2_1/usPTO spool p/US10039073/runat_26092005_070410_21316/app_query.fasta_1.6606
-DB=PIR -QFMT=faTaban -SUPPIX=rpr -MINMATCH=0.1 -LOOPECL=0 -LOOPEXT=0 -LIST=45
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-DOCALIGN=200 -THR SCORE=spt -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10039073 @CGN 1 1 317 @runat_26092005_070410_21316 -NCPU=6 -ICPU=3
-NO.MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : 1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					Description	
Result No.	Score	Match	Length	ID		
1	1999	39.5	1006	2	A59384	oxytocinase/insuli
2	1999	39.5	1025	2	A59383	oxytocinase/insuli
3	1771	35.0	916	2	I55441	vp165 - rat
4	1440	28.4	957	2	A47531	glutamyl aminopept
5	1390.5	27.5	945	2	S30398	aminopeptidase N h
6	1327	26.2	1025	2	I59331	thyrotropin-releas
7	1312	25.9	965	2	A32852	membrane alanyl am
8	1269	25.1	963	2	A53984	membrane alanyl am
9	1264.5	25.0	967	2	A30325	membrane alanyl am
10	1214	24.0	920	2	T10052	aminopeptidase (EC
11	1176	23.2	805	2	S07099	membrane alanyl am
12	1151	22.7	884	2	T39637	hypothetical prote
13	1116	22.0	844	2	S37794	aminopeptidase ysc
14	1067	21.1	856	2	S46750	aminopeptidase AAP

ALIGNMENTS

RESULT 1

A59384
oxytocinase/insulin-responsive aminopeptidase, variant 2 [imported] - human
C:Species: Homo sapiens (man)
C:Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 20-Apr-2001
C:Accession: A59384
R:Rasmussen, T.E.; Pedraza-Diaz, S.; Hardre, R.; Lausteen, P.G.; Carrion, A.G.; Kristens
Eur. J. Biochem. 267, 2297-2306, 2000
A:Title: Structure of the human oxytocinase/insulin-regulated aminopeptidase gene and lo
A:Reference number: A59384; MUID:20223264; PMID:10759854
A:Accession: A59384
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1006 <STO>
A:Cross-references: GB:CA894753; NID:98574036; PIDN:CA894753.1
C:Superfamily: membrane alanyl aminopeptidase

Alignment Scores:
Pred. No.: 1-25e-127 Length: 1006
Score: 1999.00 Matches: 400
Percent Similarity: 61.81% Conservative: 160
Best Local Similarity: 44.15% Mismatches: 310
Query Match: 39.49% Indels: 36
DB: 2 Gaps: 6

US-10-039-073-3 (1-2883) x A59384 (1-1006)

Qy	160	CCAGTAGCCACTAATGGGAACGATTTCTTGGCAGGAGCTAAGGCTCCCGAGTGGTC	219
Db	134	ProPhealathraenGlyLeuPheProTipAlaGlnileargLeuProThrAlaVal	153
Qy	220	ATTCTCTCCATTATGACCTCTTTGCCACCCCACTCCTCTCGGACTTTGTGCA	279
	:::	:::	:::
Db	154	ValProLeuargtyrGluLeuSerLeuHisProAsnLeuThrSerMetThrPheArgGly	173
Qy	280	TCTGAGAGATCGAAGTCCTGGTCAGCAATGCTATCATCTTGCACAGCAA	339
Db	174	SerValThrIleSerValGlnAlaLeuGlnValThrTrpAsnIlelleLeuHisSerThr	193

15	1047.5	20.7	882	2	T39789
16	1039	20.5	986	2	T24668
17	1031	20.4	990	2	JC8058
18	899.5	17.8	873	2	T05189
19	895.5	17.7	849	2	JC7959
20	891.5	17.7	849	2	JU0191
21	888.5	17.6	785	2	S73098
22	875	17.3	844	2	S47274
23	873	17.2	846	2	A86663
24	871.5	17.2	784	2	B90442
25	870	17.2	843	2	S38364
26	868	17.1	844	2	JC4054
27	865	17.1	848	2	B97960
28	864	17.1	848	2	E95092
29	856	16.9	846	2	JN0324
30	856	16.9	846	2	S23157
31	837	16.5	1016	2	T30942
32	832	16.4	1016	2	T30943
33	820	16.2	1009	2	T18533
34	810.5	16.0	783	2	T37457
35	770	15.2	780	2	T37456
36	705	13.9	747	2	T23882
37	702	13.9	786	2	T23883
38	692	13.7	899	2	H88572
39	683	13.5	885	2	S42841
40	630	12.4	1071	2	T18597
41	626	12.4	919	2	S42842
42	498	9.8	946	2	S48397
43	450	8.9	862	2	G87094
44	425	8.4	861	2	B70866
45	395.5	7.8	556	2	T29564

aminopeptidase - f
hypothetical prote
laeverin - human
glutamyl aminopept
lysyl aminopeptida
aminopeptidase Y (
aminopeptidase (EC
membrane alanyl am
aminopeptidase N (
tricorn proteinase
membrane alanyl am
membrane alanyl am
aminopeptidase N (
lysine aminopeptid
aminopeptidase (EC
aminopeptidase (EC
CytIAC toxin-bind
Tricorn proteinase
Tricorn proteinase
hypothetical prote
protein T16G12.1 (
T16G12.1 protein -
hypothetical prote
T16G12.2 protein -
hypothetical prote
probable aminopept
probable aminopept
hypothetical prote


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QY 580 CTTGACGTAAACAGATTTTGGACCAACCCAGGACCCATGGCTTCCCTTGGCTTTGATGAA 639
Db 289 PheAlaAlaThrGlnPheGluProLeuAlaAlaArgSerAlaPheProCysPheAspGlu 308
QY 640 CGGTGTTCAAAGCCAACTTTTCAATCAAGATACGACGAGAGAGCAGGCATATTGCACTA 699
Db 309 ProAlaPheLysAlaThrPheIleIleLysIleThrArgAspGluHisThrAlaLeu 328
QY 700 TCCAACTGCCAAAGGTTAAGACAATGAACCTTGAAGAGGTCTTTTGGAAAGATCACTTT 759
Db 329 SerAsnMetProLysSerSerValProThrGluGluGlyLeuIleGlnAspGluPhe 348
QY 760 GAAACTACTGTAAATGATGATACCTTGTAGCTACATAGTTGTGATTTCCACTCT 819
Db 349 SerGluSerValLysMetSerThrTyrLeuValAlaPheIleValGlyGluMetArgAsn 368
QY 820 CTGAGTGGCTTCACTTCATCAGGGGTCAAGGTGTCCATCTATGCTATGCCCAACCAACGG 879
Db 369 LeuSerGln---AspValAsnGlyThrLeuValSerValTyrAlaValProGluLysIle 387
QY 880 AATCAACACATATTGCTTTGAGGCATCACTGAAGTACTTGATTTTATGAAGAATGAC 939
Db 388 AspGlnValTyrHisAlaLeuAspThrThrValLysLeuLeuGluPheTyrGlnAsnTyr 407
QY 940 TTTGATATCTACTTCCACTCTCCAACTGGAATTAATTTGCTATTCTCGACTTTGCACCT 999
Db 408 PheGluIleGlnTyrProLeuLysLysLeuAspLeuValAlaIleProAspPheGluAla 427
QY 1000 GGAGCCATGGAAAAATTTGGGGCTCATTACATATAGGAGAGCTCACTGCTTTTGGACCC 1059
Db 428 GlyAlaMetGluAsnTrpGlyLeuLeuThrPheArgGluGluThrLeuLeuTyrAspAsn 447
QY 1060 AAGACCTCTTCTGCTTCGATAAACTGTGGGTCAACAGAGTCATAGCCCATGAATGGCG 1119
Db 448 AlaThrSerSerValAlaAspArgLysLeuValThrLysIleIleAlaHisGluLeuAla 467
QY 1120 CACGAGTGGTTGGCAACTGGTCAATGGAATGGTGAATGATATTTGGCTTTAAGAG 1179
Db 468 HisGlnTrpPheGlyAsnLeuValThrMetGlnTrpTrpAsnAspLeuTrpLeuAsnGlu 487
QY 1180 GGTTTTGCAAAATACATCACTTATCGCTGTATGCTACATATCCAGAGCTCAATTT 1239
Db 488 GlyPheAlaThrPheMetGluTyrPheSerValGluLysIlePheLysGluLeuAsnSer 507
QY 1240 GATCACTATTTTGAATGTGTGTTTGAAGTAATTAACAAAGATTCATTGAATTCATCC 1299
Db 508 TyrGluAspPheLeuAspAlaArgPheLysThrMetArgLysAspSerLeuAsnSerSer 527
QY 1300 CGCCCTATCTCCAACCGCGGAAACCCGACTCAATACAGGAAATGTTTGATGAAGTT 1359
Db 528 HisProIleSerSerSerValGlnSerSerGluGlnIleGluGluMetPheAspSerLeu 547
QY 1360 TCCTATACAGGAGGCTGTGTTTGAATGATGCTCAAGGATTTTCTGGGTGGAGAGAA 1419
Db 548 SerTyrPheLysGlyAlaSerLeuLeuMetLeuLysSerTyrLeuSerGluAspVal 567
QY 1420 TTCCAGAAGAAGTAATTCAGTACTTAAGAAGTTTCAGCTATAGAAAATGCTAAGAATGAT 1479
Db 568 PheGlnHisAlaIleLeuTyrLeuHisAsnHisSerTyrAlaAlaIleGlnSerAsp 587
QY 1480 GACTTGTGGAGAGCTCTCTCAAAATAGTTGTTTGTAGAAAGTGAATTTTACATCTGGTGGAGTT 1539
Db 588 AspLeuTrpAspSerPheAsnGlu-----ValThrGlyLysLeuAsp 602
QY 1540 TGTCACTCGGATCCCAAGATGACAAGTAACATGCTCGCTTCTGGGGGAAATGACAGAG 1599
Db 596 -----ValThrGlyLysLeuAsp 602
QY 1600 GTCAAGAGATGATGACTACATGGAATCTCCAGAAAGGAATCCCTCTGCTGGTGTAA 1659
Db 603 ValLysLysMetMetLysThrTrpThrLeuGlnLysGlyPheProLeuValThrValGln 622
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QY 1660 CAAGACGGGTGTTCACTCCGACTGCAACAGAGAGCGCTTCTCCAGGGGGTTCCTCCAGAA 1719
Db 623 ArgLysGlyThrGluLeuLeuGlnGlnGluArgPhePheProSerMet----- 639
QY 1720 GACCCTCAATGGAGGCGCTGACAGAGAGGTACCTGTGGCATATCCCATTCACCTACTCC 1779
Db 640 GlnProGluIleGlnAspSerAspThrSerHisLeuTrpHisIleProIleSerTyrVal 659
QY 1780 ACGAGTTCTTCTAATGTGATCCACAGACAC-----ATTCTAAATCAAGACAGAT 1830
Db 660 ThrAspGlyArgAsnTyrSerGluTyrArgSerValSerLeuLeuAspLysLysSerAsp 679
QY 1831 ACTCTGATCTACCTGAAAGACCCAGTGGTGAATTTAATGTGGACTCAATGGTTTAC 1890
Db 680 ValIleAsnLeuThrGluGlnValGlnTrpValLysValAsnThrAsnMetThrGlyTyr 699
QY 1891 TACATCCTTCACTATGAGGTGATGGACCAACTATTACACAGCTGAATCAGAAC 1950
Db 700 TyrIleValHisTyrAlaHisAspGlyTrpAlaAlaLeuIleAsnGlnLeuLysArgAsn 719
QY 1951 CACACACTTCTCAGACCTAAGGACAGAGTAGGTCTGATTCATGATGTGTTTCAGTAGTT 2010
Db 720 ProTyrValLeuSerAspLysAspArgAlaAsnLeuIleAsnAsnIlePheGluLeuAla 739
QY 2011 GGTCCAGGAGACTGACCCCTAGACAAAGCTTTGACATGACTTACTACTCCACATGAA 2070
Db 740 GlyLeuGlyLysValProLeuGlnMetAlaPheAspLeuIleAspTyrLeuArgAsnGlu 759
QY 2071 ACAGACAGCCCGCACCTTCTGAAGGTCTGAGTTACTTTGAATCGTTTACCAATGATG 2130
Db 760 ThrHisThrAlaProIleThrGluAlaLeuPheGlnThrAspLeuIleTyrAsnLeuLeu 779
QY 2131 GACAAAGGAATATTTTCAGATATCTCTGAAACCTCAAGCGTTTACCTTTCAGTATTTT 2190
Db 780 GluLysLeuGlyHisMetAspLeuSerSerArgLeuValThrArgValHisLysLeuLeu 799
QY 2191 AGCCACTGATTGACGGCAAGCTGAGTGCACAAAGGCTCAGTCTGGGACAGATGCTC 2250
Db 800 GlnAsnGlnIleGlnGlnThrTrpThrAspGluGlyThrProSerMetArgGluLeu 819
QY 2251 CGCTCGGCTCTCTTGAAGCTGGCTGACCTGAACCATGCTCTCTGCATCCAGAAAGCT 2310
Db 820 ArgSerAlaLeuLeuGluPheAlaCysAlaHisSerLeuGluAsnCysThrThrMetAla 839
QY 2311 GCTGAATCTTCTCCAGTGGATGGAATCCAGTGGAAAAATTAATATATACCAACAGATTT 2370
Db 840 ThrLysLeuPheAspGlyTrpMetAlaSerAsnGlyThrGlnSerLeuProThrAspVal 859
QY 2371 TTAAGATTGCTGATTTCTGGGTGCTCAGACACAGCAGATGGAATTTACCTTTTAGAG 2430
Db 860 MetThrThrValPheLysValGlyAlaArgThrGluLysGlyTrpLeuPheLeuPheSer 879
QY 2431 CAATATGAATGTCAATGTCAAGTCTGAACAAACAAAATTCGTATGCTTTGTCAACG 2490
Db 880 MetTyrSerSerMetGlySerGluAlaGluLysAspLysIleLeuGluAlaLeuAlaSer 899
QY 2491 AGCAAGCATCAGGAAAAGTTA 2511
Db 900 SerAlaAspAlaHisLysLeu 906
RESULT 4
A:Title: cDNA cloning and expression of human glutamyl aminopeptidase (aminopeptidase A)
A:Reference number: A47531; MUID:94063909; PMID:8244382
A:Accession: A47531
A>Status: preliminary
glutamyl aminopeptidase (EC 3.4.11.7) - human
N:Alternate names: aminopeptidase A; differentiation antigen gp160
C:Species: Homo sapiens (man)
C:Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 09-Jul-2004
C:Accession: A47531; A48287
R:Li, L.; Wang, J.; Cooper, M.D.
Genomics 17, 657-664, 1993
A:Title: cDNA cloning and expression of human glutamyl aminopeptidase (aminopeptidase A)
A:Reference number: A47531; MUID:94063909; PMID:8244382
A:Accession: A47531
A>Status: preliminary
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A:Molecule type: mRNA
A:Residues: 1-957 <LTA>
A:Cross-references: UNIPROT:Q07075; GB:L12468; NID:g347892; PIDN:AAAL6876.1; PID:g347893
R:Nanus, D.M.; Engelstein, D.; Gastl, G.A.; Gluck, L.; Vidal, M.J.; Morrison, M.; Finsta
Proc. Natl. Acad. Sci. U.S.A. 90, 7069-7073, 1993
A:Title: Molecular cloning of the human kidney differentiation antigen gp160: human amin
A:Reference number: A48287; MUID:93348214; PMID:8346219
A:Accession: A48287
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-217, A, 219-957 <NAN>
A:Cross-references: GB:L14721; NID:g291853; PIDN:AAA3522.1; PID:g291854
C:Genetics:
A:Gene: GDB:ENPEP
A:Cross-references: GDB:L38283; OMIM:L38297
A:Map position: 17pter-17p12
A:Superfamily: membrane alanyl aminopeptidase
C:Keywords: aminopeptidase; glycoprotein; transmembrane protein

Alignment Scores:
Pred. No.: 9.85e-90 Length: 957
Score: 1440.00 Matches: 322
Percent Similarity: 52.97% Conservative: 178
Best Local Similarity: 34.11% Mismatches: 362
Query Match: 28.45% Indels: 82
DB: 2 Gaps: 19

US-10-039-073-3 (1-2883) x A47531 (1-957)

Qy	118	GTGCATCTAGTATACCTTCACTGAGAGATCTCTGGGCTTTCCAGTA-----	165
Db	60	LeuProSerSer-----ThrAlaSerProSerGlyProProAlaGlnAaspGlnAasp	76
Qy	166	-----GCCACTAATGGGACGATTTCCCTGGCAGAGCTAAGGCTCCCGAGTGTG	216
Db	77	IleCysProAlaSerGluAaspGluSerGlyGlnTrpLysAenPheArgLeuProAaspPhe	96
Qy	217	GTCAATCTCTCCATTATGACCTCTTTGTCACCCCAATCTCACCTCTCTGGAGTTGTT	276
Db	97	ValAsnProValHisTyrAepLeuHisValysProLeuLeuGluAaspThrTyrThr	116
Qy	277	GCATCTGAGAAGTCGAAGTCTTGGTCAGCAATGCTACCGATTTATCATCTTGCACAGC	336
Db	117	GlyThrValSerIleSerIleAsnLeuSerAlaProThrArgTyrLeuTrpLeuHisLeu	136
Qy	337	AAAGATCTTGAATCAGCATGCCACCTTCAGTCAGAGNAGATTCAAGATACATGAA	396
Db	137	ArgGluThrArgIleThrArgLeu-----ProGluLeuLysArg	149
Qy	397	CCA---GGAAAAGAACTGAAAGTT-----TTGAGTTACCTGCTCATGAACAAATT	444
Db	150	ProSerGlyAaspGlnValGlnValArgArgCysPheGluTyrLysLysGlnGluTyrVal	169
Qy	445	GCATCTGCTGTTCCAGAGAACTTACGCCCTACCTG-----AAATACTATGTGGCT	495
Db	170	ValValGluAlaGluGluLeuLeuThrProSerSerGlyAaspGlyLeuTyrLeuLeuThr	189
Qy	496	ATGAGCTTCCAGCAAGTTAGGTGATGGCTTTGAAGGTTTATATAAAGCACAATACAGA	555
Db	190	MetGluPheAlaGlyTrpLeuAenGlySerLeuValGlyPheTyrArgThrThrTyr---	208
Qy	556	ACTCTTGGTGGTGAACAACAAATTTCTTGAGTACAGATTTTGAGCCCAACCCAGGACGC	615
Db	209	ThrGluAenGlyArgValysSerIleValAlaThrAaspHisGluProThrAaspAlaArg	228
Qy	616	ATGCTTTCCCTGCTTGTGATGAACCGTGTGTTCAAGCCCAACTTTTCAATCAAGATACGA	675
Db	229	LysSerPheProCysPheAaspGluProAsnLysLysAlaThrTyrThrIleSerIleThr	248
Qy	676	AGAGAGAGCGGATATTGACATATCCAAATGCCAAAGGTTAAGACAATTGAACTTGAA	735
Db	249	HieProLysGluTyrGlyAlaLeuSerAsnMetProValAlaLysGluLeuSerValAasp	268

Qy	736	GGAGGCTCTTTTGGAGATCAGTCTTTGAAACTACTGTAAATAGTACATACCTTGTAGCC	795
Db	269	AspLysTrpThrArgThrThrPheGluLysSerValProMetSerThrTyrLeuValCys	288
Qy	796	TACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCATTCATCAGGGTCAAGGTGTC	855
Db	289	PheAlaValHisGlnPheAaspSerValLysArgIleSerAenSerGlyLysProLeuThr	308
Qy	856	ATCTATGCATCCCGACAGCAACCGAATCAACACATATTGCTTTGACGGCATCACTGAAG	915
Db	309	IleTyrValGlnProGluGlnLysHisThrAlaGluTyrAlaAlaAenIleThrLysSer	328
Qy	916	CTACTTGATTTTATGAAAAGTACTTTGATATCTACTATCTCACTCTCAAACTGGATT	975
Db	329	ValPheAaspTyrPheGluGluTyrPheAlaMetAsnTyrSerLeuProLysLeuAaspLys	348
Qy	976	ATTGCTATTCTCTGACCTTGGACCTGGAGCATCGGAAATTTGGGGCTCATATATAGG	1035
Db	349	IleAlaIleProAaspPheGlyThrGlyAlaMetGluAenTrpGlyLeuIleThrTyrArg	368
Qy	1036	GAGACGCTACTGCTTTTGACCCCAAGACCTCTCTGCTTCCGATAAATCTGGGTCCACC	1095
Db	369	GluThrAsnLeuLeuTyrAaspProLysGluSerAlaSerSerAsnGlnArgValAla	388
Qy	1096	AGAGTCATAGCCCCATGAATCGCGCACACAGTGGTTTGGCAACCTGGTCAATGGAATGG	1155
Db	389	ThrValValAlaHisGluLeuValHisGlnTrpPheGlyAsnIleValThrMetAaspTrp	408
Qy	1156	TGGAATGATATTTGGCTTAAGAGGTTTTCGAAATATACATGGAATCTTCGCTGTTAAT	1215
Db	409	TrpGluAaspLeuTrpLeuAenGluGlyPheAlaSerPhePheGluPheLeuGlyValAsn	428
Qy	1216	GCTACATATCCAGAGCTGCNAATTT---GATGACTATTTTGGATGTGCTTTTGAAGTA	1272
Db	429	HisAlaGluThrAaspTrpGlnMetArgAaspGlnMetLeuLeuGluAaspValLeuProVal	448
Qy	1273	ATTACAAAAGATTCATTGAAATTCATCCCGCTTATCTCCAAACGAGCGGAAACCCGACT	1332
Db	449	GlnGluAaspAaspSerLeuMetSerSerHisProIleIleValThrValThrProAasp	468
Qy	1333	CAAAATACAGAAATGTTGATGAAGTTTCTTATACAGGAGCTGTATTTGATATATG	1392
Db	469	GluIleThrSerValPheAaspGlyIleSerTyrSerLysGlySerSerIleLeuAargMet	488
Qy	1393	CTCAAGATTTCTCGGTGAGGAGAAATCCACAAAGGAATAATTCAGTACTTAAAGAAG	1452
Db	489	LeuGluAaspTrpIleLysProGluAenPheGlnLysGlyCysGlnMetTyrLeuGluLys	508
Qy	1453	TTCAGCTATAGAAATGCTAAGATGATGACTTTGTGGAGCAGCTGTGCAATAGTTGTTA	1512
Db	509	TyrGlnPheLysAsnAlaLysThrSerAaspPheTrpAlaAlaLeuGluAlaAala	536
Qy	1513	GAAGTGATTTTACATCTCGTGAGTTTGTTCATTCGGATCCCAAGATGACAGTAACATG	1572
Db	526	-----	526
Qy	1573	CTCGCTTTTCGGGGAAAATGCAGAGGTCAAGAGATGATGACTACATGCTCTCCAG	1632
Db	527	-----SerArgLeuProValLysGluValMetAaspThrTrpThrArgGln	541
Qy	1633	AAAGGAATCCCTCGTGTGGTTAAACAAGACGGGTGTTTCACTCCGACTGCACACAGGAG	1692
Db	542	MetGlyTyrProValLeuAenVal-----AsnGlyValLys---AsnIleThrGlnLys	558
Qy	1693	CGTTTCTCCAGGGGGTTTTCAGGAAGACCTGGAATGAGGGCCCTCGAGGAG-----	1746
Db	559	ArgPheLeuLeu-----AaspProArgAlaAasnProSerGlnProProSer	573
Qy	1747	-----AGGTACTGTGGCATATCCCATTTGACCTAC-----TCCACAGTCTTCT	1791
Db	574	AepLeuGlyTyrThrTrpAsnIleProValLysTrpIleThrGluAaspAsnIleThrSerSer	593
Qy	1792	AATGTATCCACAGACACATTTCTAAATCAAGACAGATACTCTGGATCTTACCTGAAAG	1851


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Db      594  ValLeuPheAsnArgSerGluLysGluGlyLeuThrLeuAsnSerSerAsnProSerGly 613
Qy      1852 ACCAGTGGGTGAATTTAATGTGGACTCAAATGTTACTATCATCTGTTCACTATGAGGGT 1911
Db      614  AsnAlaPheLeuLysIleAsnProAspHisIleGlyPheTyrArgValAsnTyrGluVal 633
Qy      1912 CATGATGGGACCAACTCATTCATACAGCTGAATCAAGAACCAACACACTTCTCAGACCTAAG 1971
Db      634  AlathrTrpAspSerIleAlaThrAlaLeuSerLeuAsnHisLeuThrPheSerSerAla 653
Qy      1972 GACAGAGTAGTCTCATCATGATGTTTACAGCTAGTGTGGTCAGGAGACTGACCCCTA 2031
Db      654  AspArgAlaSerLeuIleAspAspAlaPheAlaLeuAlaArgAlaGlnLeuLeuAspTyr 673
Qy      2032 GACAAAGCTTGTACATCTTACTACTCCTCAACATGAACAAGCAGC-----CCC 2082
Db      674  LysValAlaLeuAsnLeuThrLysTyrLeuLysArgGluGluAsnPheLeuProTrpGln 693
Qy      2083 GCATCTTCGAGGCTCGAGTCTAGTACTTGAATCGTGTATTTACCATGATGCAGACAGGAAT 2142
Db      694  ArgValIleSerAlaValThrTyrIleIleSerMetPhe-----GluAsp 708
Qy      2143 ATTTCCAGATATCTCTGAACAACTCAAGGTTACCTTCTTCAGTATTTTAAAGCCAGTGATT 2202
Db      709  AspLysGluLeuTyrProMetIleGluTyrPheGlnGlyGlnValLysProIleAla 728
Qy      2203 GACAGGCAAAAGCTGGAGTGACAAGGGCTCAGTCTGGGAGCAGGATGCTCCGCTCGGCTCTC 2262
Db      729  AspSerLeuGlyTrpAsnAspAlaGlyAspHisValThrLysLeuLeuArgSerSerVal 748
Qy      2263 TTGAAGCTGGCTGTGACTGAACCATGCTCCTTGGCATCCAGAAAGCTGTGAATCTTTC 2322
Db      749  LeuGlyPheAlaCysLeuMetGlyAspArgGluAlaLeuAsnAsnAlaSerSerLeuPhe 768
Qy      2323 TCCAGTCGATGGAATCCAGTGGGAAATTAATATACCAACAGATGTTTTAAAGATGTG 2382
Db      769  GluGlnTrpLeu-----AsnGlyThrValSerLeuProValAsnLeuArgLeuLeuVal 786
Qy      2383 TATTCTGTGGGTGCTCAGACCAACAGCA-----GGATGGAAATTACTTTTAGAGCAA 2433
Db      787  TyrArgTyrGlyMetGlnAsnSerGlyAsnGluIleSerTrpAsnTyrThrLeuGluGln 806
Qy      2434 TATGAATGTCAATGTCAAGTGTGTAACAACAATAATCTGTATGCTTTGTCAACGAGC 2493
Db      807  TyrGlnLysThrSerLeuAlaGlnGluLysGluLysLeuLeuTyrGlyLeuAlaSerVal 826
Qy      2494 AAGCATCAGGAAAGTTACTGAAGTTAATTGAAGTAAGTAAGGAAGGAAGGTTATCAAG 2553
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Qy      2554 ACACAGAACTTGGCAGCTCTCTTCATCGGATTGCCAGCGCTCCAAAGGGGCGACCACTA 2613
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Qy      2734 CAAGAGGTGAACATATTATTTTGAATCTCTTGGGCTCAAGGATCACATCTCGATATTTT 2793
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Qy      2794 CAACCTGTTTGGAAACGATACCAACAAATAATAAATCGCTGGAGAGAAATCTCCGACT 2853
Db      926  GluGlnValLeuGluThrValLysAsnAsnIleGluTrpLeuLysGlnHisArgAsnThr 945
Qy      2854 CTGAGGACTTGG 2865
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Db      946  IleArgGluTrp 949
RESULT 5
S30398
aminopeptidase N homolog BP-1/6C3 - mouse
N:Alternate names: surface antigen BP-1/6C3
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: S30398
R:Wu, Q.; Lahti, J.M.; Air, G.M.; Burrows, P.D.; Cooper, M.D.
A:Title: Molecular cloning of the murine BP-1/6C3 antigen: a member of the zinc-dependen
A:Reference number: S30398; MUID:90139003; PMID:1689065
A:Accession: S30398
A:Molecule type: mRNA
A:Residues: 1-945 <WUQ>
A:Cross-references: UNIPROT:P16406; EMBL:M29961; NID:g191947; PIDN:AAB47732.1; PID:g3091
C:Superfamily: membrane alanyl aminopeptidase
C:Keywords: disulfide bond; glycoprotein; homodimer; membrane protein; phosphoprotein; s
Alignment Scores:
Pred. No.: 2,23e-86 Length: 945
Score: 1390.50 Matches: 322
Percent Similarity: 51.69% Conservative: 168
Best Local Similarity: 33.97% Mismatches: 373
Query Match: 27.47% Indels: 85
DB: 2 Gaps: 20
US-10-039-073-3 (1-2883) x S30398 (1-945)
Qy      76  ACAGCCATCTTGGCCCCCAATATGCAATTTGTTCTCAGTTCTCAGTGCCATCTAGTTATCAC 135
Db      60  ThrAlaLeuProProGln-----AspGlnAsnValCysProAspSer----- 73
Qy      136  TTCACCTCAGGATCTCGGGCTTTCCAGTAGTCCACTAATGGGAACGATTCCTTCTGGCAG 195
Db      74  -----GluAsp-----GluSerGlyGlu-----TrpLys 81
Qy      196  GAGCTAAGGCTCCCGAGTGTGTCATCTCTCCATATGACCTTTTGTCCACCCCAAT 255
Db      82  AsnPheArgLeuProAspPheIleAsnProValHisTyrAspLeuGluValLysAlaLeu 101
Qy      256  CTCACCTCTCGGACTTTGTGCATCTGAGNAGATCGAAGCTTGGTCAGCAATGCTACC 315
Db      102  MetGluGluAspArgTyrThrGlyIleValThrIleSerValAsnLeuSerLysProThr 121
Qy      316  CAGTTTATCATCTTGCACAGCAAAAGATCTTGAAATCAGAAATGCCACCTTCAGTCAG 375
Db      122  ArgAspLeuTrpLeuHisIleArgGluThrLysIleThrLysLeu----- 136
Qy      376  GAAGATTCAAGATACATGAACCAACGAGAAAGAA-----CTGAAAGTTTGTAGT 423
Db      137  -----ProGluLeuArgArgProSerGlyGluGlnValProIleArgCysPheGlu 154
Qy      424  TACCTGCTCATGAACAAATTGCACTGCTGTTCCAGAGAACTT-----ACGCCT 474
Db      155  TyrLysLysGlnGluTyrValValIleGlnAlaGluAspLeuAlaIaThrSerGly 174
Qy      475  CACCTGAAATACTATGTGGCTATGAGCTTCCAAAGCAAGTTAGGTGATGCTTTGAAGGG 534
Db      175  AspSerValTyrArgLeuThrMetGluPheLysGlyTrpLeuAsnGlySerLeuValGly 194
Qy      535  TTTTATAAAGACATACAGAACTCTTGGTGGTGAACAAGAAATCTTTCAGTAAACAGAT 594
Db      195  PheTyrLysThrThrTyrMetGlu---AspGlyGlnIleArgSerIleAlaAlaThrAsp 213
Qy      595  TTTGAGGCAACCCAGGACCGATGCTTCCCTGCTTGTGATGATGACCGTGTTCAAAGCC 654
Db      214  HisGluProThrAspAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 233
Qy      655  AACTTTTCAATCAAGATACGACGAGCAGGCGATATTCACCTATTCACCAATGCCAAAG 714
Db      234  ThrTyrSerIleSerIleIleHisProLysGluTyrSerAlaLeuSerAsnMetProGlu 253
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1270 GTAATTAACAAGAATTCATGTAATTCATCCCGCCCTATCTCCTCAACCGGAAACCCCG 1329
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1330 ACTCAATACAGAAATGTTTGATGAAGTTTCTCTATAACAGGAGCTGTGATTTCGAAT 1389
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1390 ATGCTCAAGGATTTCTGGGTGAGGAGAAATTCAGAAAGGAATAATTCAGTACTTAAAG 1449
537 MetLeuAlaAsnPheMetGlyHisSerValPheGlnArgGlyLeuGlnAspTyrLeuThr 556
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595 GlnMetGlyTyrProValIleThrIleLeuGlyAsnMetThrAlaGluAsnArgIleLeu 614
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317 TrpValThrAspHisPheSerGlnThrProLeuMetSerThrTyrTyrLeuAlaTrpAla 336
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QY 436 ---GAACAAATTCACCTCGTGGTCCAGAGAAACTTACCGCTCACCTGAAATACATATGTG 492
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Qy 2767 GCTCAA-----GGATCAGATCTGGATATATTTTCAAATGTTCTGGAAACGATAACAAA 2820
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Qy 2821 AATATAAATCGCTGGAGAGAACTTCCGACTCTGAGGACTTGGCTAATGGTTAATACT 2880
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RESULT 8
A53984
membrane alanyl aminopeptidase (EC 3.4.11.2) - pig
N;Alternate names: aminopeptidase N; microsomal aminopeptidase N; surface glycoprotein C
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 09-Oct-1994 #sequence revision 15-Oct-1994 #text_change 09-Jul-2004
C;Accession: A53984; S24020; S05040; S13177
R;Delmas, B.; Gelfi, J.; Kut, E.; Sjoestrom, H.; Noren, O.; Laude, H.
J. Virol. 68, 5216-5224, 1994
A;Title: Determinants essential for the transmissible gastroenteritis virus-receptor interaction
A;Reference number: A53984; MUID:94309188; PMID:7913510
A;Accession: A53984
A;Molecule type: mRNA
A;Residues: 1-963
A;Cross-references: UNIPROT:P15145; GB:Z29522; NID:G525286; PIDN:CAA82641.1; PID:G525287
R;Delmas, B.; Gelfi, J.; L'Haridon, R.; Vogel, L.K.; Sjoestrom, H.; Noren, O.; Laude, H.
Nature 357, 417-420, 1992
A;Title: Aminopeptidase N is a major receptor for the entero-pathogenic coronavirus TGEV
A;Reference number: S24020; MUID:92278435; PMID:1350661
A;Accession: S24020
A;Status: preliminary
A;Molecule type: protein
A;Residues: 2-31 <DE2>
R;Olisen, J.; Sjoestrom, H.; Noren, O.
FEBS Lett. 251, 275-281, 1989
A;Title: Cloning of the pig aminopeptidase N gene. Identification of possible regulatory
A;Reference number: S05040; MUID:89325681; PMID:2568950
A;Accession: S05040
A;Molecule type: DNA
A;Residues: 1-294 <OLS>
A;Cross-references: EMBL:X16088
R;See, H.; Reithmeier, R.A.F.
Biochem. J. 271, 147-155, 1990
A;Title: Identification and characterization of the major stilbene- disulphonate- and co
A;Reference number: S13177; MUID:91024918; PMID:1977382
A;Accession: S13177
A;Status: preliminary
A;Molecule type: protein
A;Residues: 2-40 <SE5>
C;Genetics:
A;Introns: 200/2; 248/1
A;Note: the list of introns may be incomplete
C;Superfamily: membrane alanyl aminopeptidase
C;Keywords: aminopeptidase; glycoprotein; transmembrane protein
F;1-8/Domain: intracellular #status predicted <INT>
F;9-32/Domain: transmembrane #status predicted <TM>
F;33-963/Domain: extracellular #status predicted <EXT>

Alignment Scores: 3.88e-78 Length: 963
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Best Similarity: 31.89% Mismatches: 386
Best Local Similarity: 25.07% Indels: 130
Query Match: 2 Gaps: 28
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Db 3 LysGlyPheTyrIleSerLysAlaLeuGlyIleLeuGlyIleLeuLeuGlyValAlaAa 22
Qy 73 TTAACAGCCATCTTGGCCCCAATATGCAATTTGTTCTCAGTTCTCAGTGCCATCTAGTTAT 132
Db 23 ValAlaThrIleIleAlaLeuSerValValTyrAlaGlnGlnLysAsnLysAlaGlu 42
Qy 133 CACTTCAGTGAAGATCTGGGGCTTTCCAGTAGCCACCAATAATGGG----- 177
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Qy 178 GAACAGATTTCTTGGCAGGAGCTTAAGCTCCCGAGTGTGGTCAATCTCTCCATTATGAC 237
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Db 83 ValThrLeuArgProTyrLeuThrProAsnAlaAspGlyLeuTyrIlePheLysGlyLys 102
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Db 103 SerIleValArgLeuLeuCysGlnGluProThrAspValIleIleIleHisSerLysLys 122
Qy 343 CTTGAAATCACGAAT-----GCCACCTTCAGTCAGAGGAAGATTCAGATAC 390
Db 123 LeuAsnTyrThrThrGlnGlyHisMetValValLeuArgGlyValGlyAspSerGlnVal 142
Qy 391 ATGAACACAGGAAAA---GAACGTGAAGTTTGGAGTTACCTGCTCATCAACAAATTCGA 447
Db 143 ProGluIleAspArgThrGluLeuValGluLeuThr-----GluTyrLeuVal 158
Qy 448 CTGCTGGTTCCAGAGAACTTACGCTCACCTACCTGAAATATCTATGTGCTATGGATTCCTCA 507
Db 159 ValHisLeuLysGlySerLeuGlnProGlyHisMetTyrGluMetGluSerGluPheGln 178
Qy 508 GCCAAGTTAGTGATGGCTTTGAAGGGTTTTATAAAGCACATACACAGAACTCTTGGTGGT 567
Db 179 GlyGluLeuAlaAspAspLeuAlaGlyPheTyrArgSerGluTyrMetGlu---GlyAsn 197
Qy 568 GAAACAAGAAATCTTCAGCTAACAGATTTTGGAGCCAAACCCAGGACGATGGCTTCCCT 627
Db 198 ValLysValLeuAlaThrThrGlnMetGlnSerThrAspAlaArgLysSerPhePro 217
Qy 628 TGCTTTGATGAACCGTTGTTCAAAGCCAACTTTTCAATCAAGATACAGAGAGAGACAGG 687
Db 218 CysPheAspGluProAlaMetLysAlaThrPheAsnIleThrLeuIleHisProAsnAsn 237
Qy 688 CATATTGCACTATCCAACTATGCCAAGGTTAGACAATTTGAACCTTGAAGAGAGT----- 741
Db 238 LeuThrAlaLeuSerAsnMetProPro-----LysGlySerSerThr 251
Qy 742 ---CTTTTGGAAAGAT-----CACTTTGAAACTACTGTAAAAATTCAGT 780
Db 252 ProLeuAlaGluAspProAsnTrpSerValThrGluPheGluThrThrProValMetSer 271
Qy 781 ACATACCTTTGTAGCCCTACATAGTTTGTGATTTTCCACTCTCTGAGTGGCTTCACTTCATCA 840
Db 272 ThrTyrLeuLeuAlaTyrIleValSerGluPheGlnSerValAsnGlnThrAlaGlnAsn 291
Qy 841 GGGGTCAAGGTGTCCATCTCTATGCATCCCGACAGCAACGGAATCAACACAT-----TAT 894
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292	GlyValLeuIleArgIleTrpAlaArgProAsnAlaIleAlaGluGlyHisGlyMetTyr	311
895	GCITTTGAGGCATCACTGAAGCTACTCTGATATTTTATGAAAAAGTAGTTCTTGATATCTACTAT	954
312	AlaLeuAsnValThrGlyProIleLeuAsnPhePheAlaAsnHisTyrAsnThrSerTyr	331
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1015	TGGGGCTCATTTACATATAGGGAGACGCTCACTGCTTTTGTGACCCCAAGACCTCTTCTGCT	1074
352	TrpGlyLeuValThrTyrArgGluAsnAlaLeuLeuPheAspProGlnSerSerIle	371
1075	TCCGATAAACTGTGGGTCCACAGAGTCAATAGCCCATGAATGGCGGCACCACTGGTTGGC	1134
372	SerAsnLysGluArgValValThrValIleAlaHisGluLeuAlaHisGlnTrpPheGly	391
1135	AACTCTGTCACAAATGGAAATGTGGAAATATTTTGGCTTAAAGGAGGTTTTCGAAAATAC	1194
392	AsnLeuValThrLeuAlaIleTrpAsnAspLeuTrpLeuAsnGluGlyPheAlaSerTyr	411
1195	ATGGAACCTTATCGCTGTTAATGCTCATATCCAGAGCTGCCAATTTGATGACTATTTTTTG	1254
412	ValGluTyrLeuGlyAlaAspHisAlaGluProThrTrpAsnLeuLysAspLeuIleVal	431
1255	---AATGTGTTTTGAAGTAAATTTACAAAAGATTTCATTGAATTCATCCCGCCCTATCTCC	1311
432	ProGlyAspValTyrArgValMetAlaValAspAlaLeuAlaSerSerHisProLeuThr	451
1312	AAACGACGGAA-----ACCCCGACTCAAAATACAGGAAATGTTTGTAGTGAAGTTTCC	1362
452	ThrProAlaGluGluValAsnThrProAlaGlnIleSerGluMetPheAspSerIleSer	471
1363	TATAACAAGGAGCTGTGATTTTCAATATGCTCAAGGATTTTCTGGGTGAGGACAAATTC	1422
472	TyrSerLysGlyAlaSerValIleArgMetLeuSerAsnPheLeuThrGluAspLeuPhe	491
1423	CAGAAAGCAATAATTCAGTACTTAAAGAAGTTTCAGCTATAGAAATGCTAAGAATGATGAC	1482
492	LysGluGlyLeuAlaSerTyrLeuHisAlaPheAlaTyrGlnAsnThrThrTyrLeuAsp	511
1483	TTGTGGAGCAGCTCTGTCAAATAGTTGTTTGAAGAAGTGATTTATCATCTGGTGGAGTTGT	1542
512	LeuTrpGluHisLeuGlnLysAlaVal-----	520
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521	-----AspAlaGlnThrSerIleArgLeuPro-----AspThrVal	532
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533	ArgAlaIleMetAspArgTrpThrLeuGlnMetGlyPheProValIleThrVal-----	550
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551	AspThrLysThrGlyAsnIleSerGlnLysHisPheLeu-----LeuAspSerGluSer	568
1723	CCTGAATGGAGGGCCCTGCAGGAGAGGTACTCTGTGGCATATCCCATTTGACCTACTCCACG	1782
569	AsnValThrArgSerSerAlaPheAspTyrLeuTrpIleValProIle-----SerSer	586
1783	AGTTCTTCTAATGTGATCCACAGAC-----	1809
587	IleLysAsnGlyValMetGlnAspHisTyrTrpLeuArgAspValSerGlnAlaGlnAsn	606
1810	---ATTCTAAATCAAAGACAGATACTCTGGATCTACCTGAAAAAGACCACTGGGTGAAA	1866
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1867	TTTAAATGTGACTCAAAATGGTTACTATCATGTTCACTATGAGGGTCATGATGGGACCA	1926
619	LeuAsnValAsnValThrGlyTyrPheGlnValAsnTyrAspGluAspAsnTrpArgMet	638

RESULT 9

A30325

membrane alanyl aminopeptidase (EC 3.4.11.2) precursor - human

N;Alternate names: aminopeptidase N; cell surface glycoprotein CD13

C;Species: Homo sapiens (man)
 C;Date: 02-Feb-1990 #sequence revision 02-Feb-1990 #text change 09-Jul-2004
 C;Accession: A30325; I39442; S35688; S56098; S56099
 R;Look, A.T.; Ashmun, R.A.; Shapito, L.H.; Peiper, S.C.
 J. Clin. Invest. 83, 1299-1307, 1989
 A;Title: Human myeloid plasma membrane glycoprotein CD13 (gp150) is identical to aminopeptidase N
 A;Reference number: A30325; MUID:89198086; PMID:2564851
 A;Accession: A30325
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-967 <LO>
 A;Cross-references: UNIPROT:P15144; UNIPROT:Q9UCE0; GB:M22324; NID:g178535; PIDN:AAA5171
 R;Olsson, J.; Cowell, G.M.; Konigshofer, E.; Danielsen, E.M.; Moller, J.; Laustsen, L.; H
 FEBS Lett. 238, 307-314, 1988
 A;Title: Complete amino acid sequence of human intestinal aminopeptidase N as deduced fr
 A;Reference number: S01658; MUID:89005706; PMID:2901990
 A;Accession: S01658
 A;Molecule type: mRNA
 A;Residues: 1-85, 'R', '87-535, 'E', 537-602, 'M', 604-886, 'P', 888-967 <OLS>
 A;Cross-references: EMBL:X13276
 R;Shapito, L.H.; Ashmun, R.A.; Roberts, W.M.; Look, A.T.
 J. Biol. Chem. 266, 11999-12007, 1991
 A;Title: Separate promoters control transcription of the human aminopeptidase N gene in
 A;Reference number: I39442; MUID:91268079; PMID:1675638
 A;Accession: I39442
 A;Molecule type: DNA
 A;Residues: 1-15 <R>
 A;Cross-references: GB:M55522; NID:g178532; PIDN:AAA83399.1; PID:g178533
 R;Nunez, L.; Amigo, L.; Rigotti, A.; Pugliesi, L.; Mingrone, G.; Greco, A.V.; Nervi, F.
 FEBS Lett. 329, 84-88, 1993
 A;Title: Cholesterol crystallization-promoting activity of aminopeptidase-N isolated fro
 A;Reference number: S35688; MUID:93359071; PMID:8102610
 A;Accession: S35688
 A;Molecule type: protein
 A;Residues: 2-18 <NUN>
 R;Watanabe, Y.; Iwaki-Egawa, S.; Mizukoshi, H.; Fujimoto, Y.
 Biol. Chem. Hoppe-Seyler 376, 397-400, 1995
 A;Title: Identification of an alanine aminopeptidase in human maternal serum as a membra
 A;Reference number: S56098; MUID:96066273; PMID:7576235
 A;Accession: S56098
 A;Molecule type: protein
 A;Residues: 2-20 <WAT>
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 A;Status: preliminary
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 A;Gene: GDB: ANPEP; CD13; PEPN
 A;Cross-references: GDB:118728; OMIM:151530
 A;Map position: 15q25-15q26
 C;Superfamily: membrane alanyl aminopeptidase
 C;Keywords: aminopeptidase; glycoprotein; transmembrane protein

Alignment Scores:
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 Score: 1264.50 Matches: 325
 Percent Similarity: 46.62% Conservative: 158
 Best Local Similarity: 31.37% Mismatches: 386
 Query Match: 24.98% Indels: 167
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US-10-039-073-3 (1-2883) x A30325 (1-967)

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 Db 306 ProSerAlaIleAlaAlaGlyHisGlyAspTyrAlaLeuAsnValThrGlyProIleLeu 325
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 Db 386 IleAlaHisGluLeuAlaHisGlnTyrPheGlyAsnLeuValThrIleGluTyrPasn 405


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Db 466 AlaGlnIleSerGluLeuPheAspAlaIleSerTyrSerLysGlyAlaSerValLeuArg 485
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Db 634 TyrAspGluGluAenTrpArgLysIleGlnThrGlnLeuGlnAenArgAspHisSerAlaIle 653
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|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 2083 GCACCTTCGAAGGCTCAGTCTACTTGAATCGTTTACCACATCATGATGCAGCAGGAAGGAT 2142
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 694 ProTrpGluAlaAlaLeuSerSerLeuSerTyrPheLysLeuMetPheAspArg-----711
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
```

```
2143 ATTTCAATATCTCTGAAACCTCAAGCGTTACTCTTCTCAGTATTTTAAAGCCAGTGATT 2202
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 712 ---SerGluValTyrGlyProMetLysAenTyrLeuLysGlnValThrPheLeuPhe 730
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 2203 -----GACAGGCAAGCTGGAGTGAC---AAGGGCTCAGTCTGGGACAGG 2244
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 731 IleHisPheArgAenAenThrAenAenTrpArgGluIleProGluAenLeuMetAspGln 750
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 2245 ATGCTCGCTCGGCTCTCTTGAAGCTGGCTGTGACCTGACCAACCATGCTCTTGTGATCCAG 2304
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 751 TyrSerGluValAenAlaIleSerThrAlaCysSerAenGlyValProGluCysGluGlu 770
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 2305 AAAGCTGCTGAATCTCTCCAGTGGATGCCAGTCCAGTGGAAAAATTAATATATACCAACA 2364
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 771 MetValSerGlyLeuPheLysGlnTrpMetGluAenProAenAenAenProIleHisPro 790
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 2365 GATGTTTTAAAGATTGTGTAT-----TCTGTGGTGCTCAGACACAGCAGGATGGAAT 2418
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 791 AsnLeuArgSerThrValTyrCysAenAlaIleAlaGlnGlyGluGluTrpAsp 810
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 2419 TACCTTTTAGAGCAATATGAATGTCTCAATGTCTCAAGTCTGAAACAAACAAATTTCTGTAT 2478
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 811 PheAlaTrpGluGlnPheArgAenAlaThrLeuValAenGluAlaAspLysLeuArgAla 830
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 2479 GCTTTGTCAAGCAGCAGCATCAGAAAACTTACTGAAGTTAATTAAGTAACTAGGAATGGAA 2538
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 831 AlaLeuAlaCysSerLysGluLeuTrpIleLeuAenArgTyrLeuSerTyrThrLeuAen 850
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 2539 GGAAGGTTTATCAAGACACAGAACTTGGCAGCTCTCTTCATGCGATTGCCAGACGCTCA 2598
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 851 ProAspLeuIleArgLysGlnAspAlaThrSerThrIleIleSerIleThrAenAenVal 870
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 2599 AAGGGGACGCACTAGCATCGGATTTTGAAGAAATTTGGACCCCATCTTCTGAAAAAA 2658
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 871 IleGlyGlnGlyLeuValTrpAspPheValGlnSerAenTrpLysLysLeuPheAenAsp 890
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 2659 TTTGACTTGGCTCATATGACATAAGGATCATCTCTCGCACACAGCTCAGCTTTTCT 2718
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 891 TyrGlyGlySerPheSerPheSerAenLeuGlnAlaValThrArgArgPheSer 910
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 2719 TCAAGGATAAGTTGCAAGAGGTGAACATATTTTGAATCTCTTGAGGCTCAA-----2772
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 911 ThrGluTyrGluLeuGlnGlnLeuGluGlnPheLysLysAspAenGluGluThrGlyPhe 930
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 2773 GGATCATCATCGATATTTTCAAACTGTTCTGGAACAGATAACCAAAAAATATAAATGG 2832
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 931 GlySerGlyThrArgAlaLeuGluGlnAlaLeuGluLysThrLysAlaAenIleLysTrp 950
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 2833 CTGGAGAGAAATCTTCGACTCTGAGGACTTGGCTAATGTTAATCT 2880
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 951 ValLysGluAenLysGluValValLeuGlnTrpPheThrGluAenSer 966
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||

RESULT 10
T10052
aminopeptidase (EC 3.4.11.-) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10052
J;Constam, D.B.; Tobler, A.R.; Rensing-Ehl, A.; Kemler, I.; Hersh, L.B.; Fontana, A.
R; Biol. Chem. 270, 26931-26939, 1995
A;Title: Puromycin-sensitive aminopeptidase sequence analysis, expression, and functions
A;Reference number: Z16922; MUID:96070789; PMID:7592939
A;Accession: T10052
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-920 <CON>
A;Cross-references: UNIPROT:Q11011; EMBL:U35646; NID:gl184160; PIDN:AACS2409.1; PID:gl118
A;Note: puromycin-sensitive
C;Superfamily: membrane alanyl aminopeptidase
C;Keywords: aminopeptidase; metalloprotein; zinc

Alignment Scores: 2.06e-74 Length: 920
Pred. No.:
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Score:	1214.00	Matches:	305
Percent Similarity:	49.84%	Conservative:	167
Best Local Similarity:	32.21%	Mismatches:	353
Query Match:	23.98%	Indels:	122
DB:	2	Gaps:	26
US-10-039-073-3 (1-2883) x TL0052 (1-920)			
Qy	163	GTAGCCACTAATGGGCAACGATTCCTCTGGCAGGAGCTAAGGCTCCCGCAGTGTGTCATT	222
Db	43	LeuAlaAlaMetProGluLysArgProPheGlu-----ArgLeuProAlaGluValSer	60
Qy	223	CCTCTCCATTATGACCTCTTTGTGCACCCCAATCTCACTCTCTGGACCTTTGTTCATCT	282
Db	61	ProIleAsnTyrSerLeuCysLeuLysProAspLeu-----LeuAspPheThrPheGlu	78
Qy	283	GAGAGATCGAAGCTTGG-----GTCAGCAATGCTACCCAGTATTATCATCTTCGCACAGC	336
Db	79	GlyLysLeuGluAlaAlaAlaGlnValArgGlnAlaThrAsnGlnIleValMetAsnCys	98
Qy	337	AAAGATCTTGAATACACGAATGCCACCCCTTCAGTCAGAGGAAGATTCGAAGATACATGAAA	396
Db	99	AlaAspIleAspIleIleThrAlaSerTyrAlaProGluGlyAspGluGluIleHisAla	118
Qy	397	CCAGGA-----AAAGAACTGAAAGTTTTCAGTTTACCTGCTCATGAA	438
Db	119	ThrGlyPheAsnTyrGlnAsnGluAspGluLysValThrLeuSerPheProSerThrLeu	138
Qy	439	CAAAATGCACTGCTGGTTCAGAGAAACTTACGCTCACTGAAATCTATGTGGCTATG	498
Db	139	GlnThrGly-----ThrGlyThrLeuLys-----Ile	147
Qy	499	GACTTCCAAAGCAAAGTTAGGTGATGGCTTTCGAAGGGTTTTATAAAAGCACATACAGA	558
Db	148	AspPheValGlyGluLeuAsnAspLysMetLysGlyPheTyrArgSerArgTyrThrThr	167
Qy	559	CTTGGTGGTGAACAAGAATTCCTTCGAGTAACAGATTTTGAAGCAACCCAGGACGCATG	618
Db	168	ProAlaGlyGluValArgTyrAlaAlaValThrGlnPheGluAlaThrAspProArgArg	187
Qy	619	GCTTTCCCTTCGTTTGATGAACCGTTGTTCAAAGCCAACTTTTCAATCAAGATACGAAGA	678
Db	188	AlaPheProCysTyrAspGluProAlaIleLysAlaThrPheAspIleSerLeuValVal	207
Qy	679	GAGAGCAGGCATATTCGACTATCAACATGCCAAAGGTT-----AAGACAATTGAAC	732
Db	208	ProLysAspArgValAlaLeuSerAsnMetAsnValIleAspArgLysProTyrProAsp	227
Qy	733	GAAGGAGGTCTTTTGGAGATCACTTTTCAAACTACTGTATAAAATGAGTACATACCTTG	792
Db	228	AspGluAsnLeuValGluValLysPheAlaAlaArgThrProValMetSerThrTyrLeu	247
Qy	793	GCCTACATAGTTTGTGATTTCCACTCTCTGTAGTGGCTTCATCTCATCAGGGGTCAAG	852
Db	248	AlaPheValValGlyGluTyrAspPheValGluThrArgSerLysAspGlyValCysVal	267
Qy	853	TCCATCTATGCATCCCCAGACAAACGGAAATCAACACATATTATGCTTTCGAGGCATCA	912
Db	268	ArgValTyrThrProValGlyLysAlaGluGlnGlyLysPheAlaLeuGluValAlaAla	287
Qy	913	AAGCTACTTGATTTTATGAAAAGTACTTTTGATATCTACTATCCACTCTCCAAACTGG	972
Db	288	LysThrLeuProPheTyrLysAspTyrPheAsnValProTyrProLeuProLysIleAsp	307
Qy	973	TTAATTGCTATTCTGACTTTTGGCACTTGGAGCCATGGAAAATTTGGGCGCTCATTTAC	1032
Db	308	LeuIleAlaIleAlaAspPheAlaAlaGlyAlaMetGluAsnTyrGlyLeuValThrTyr	327
Qy	1033	AGGAGACGTCACCTGCTTTTGGCCCAAGACCTCTTCTGCTTCGATAACTGTGGGTC	1092
Db	328	ArgGluThrAlaLeuLeuIleAspProLysAsnSerCysSerSerArgGlnTyrVal	347
Qy	1093	ACCAGAGTCATAGCCCATGAATCGGCGCACAGTGGGTTTGGCACTGGTCCACAATGAA	1152

Db 651 ThrValTrpSerAspLeuSerCysAsnLeuGlyIleLeuSerThrLeuLeuSerHisThr 670
Qy 2158 -----GAAACCTCAAGGTTACCTCTTCAGTATTTTAAAGCCAGTGTACAGG 2208
Db 671 AspPheTyrGluGluIleGlnPheValIysAspValPheSerProIleGlyGluArg 690
Qy 2209 CAAGCTCGAGTGAAG-----CGCTCAGTCTGGGACAGATCTCGCTCGGCT 2259
Db 691 LeuGlyTrpAspProIysProGlyGluGlyHisLeu---AspAlaLeuLeuArgGlyLeu 709
Qy 2260 CTCTTGAAGCTGGCTGTGACCTGAACATGCTCTTGCATCCAGAAAGCTGTGAATC 2319
Db 710 ValLeuGlyIysLeuGlyIysAlaGlyHisIysAlaThrLeuGluGluAlaArgArg 729
Qy 2320 TTCTCCAGTGGATGGAATCCAGTGGAAATTAATAATATACCAACAGATGTTTAAAGATT 2379
Db 730 PheIysGluHisValGlu-----GlyIysGlnIleLeuSerAlaAspLeuArgSerPro 747
Qy 2380 GTGTATTCTGTGGGTCTCAGACACAGCAGCA-----TGAATTACCTTTTAGAGCAA 2433
Db 748 ValTyrLeuThrValLeuIysHisGlyAspGlyAlaThrLeuAspIleMetLeuIysLeu 767
Qy 2434 TATGAATGTCATGTCAGTGTCAAGTGTCAACAAACAAATTCGTATGCTTTGTCAACGAGC 2493
Db 768 HisIysGlnAlaAspMetGlnGluIysAsnArgIleGluArgValLeuGlyAlaThr 787
Qy 2494 AAGCATCAGGAAAGTTACTGAAGTTAATTGAACCTAGGAATGGAAGGAAAGTTATCAAG 2553
Db 788 LeuSerProGluLeuIleGlnIysValLeuThrPheAlaLeuSerGluGluVal---Arg 806
Qy 2554 ACACAGAACTGGCGACTCTCTTCATCGGATGTCAGATGCCAGACGTCCTCAAG---GGCGAGCMA 2610
Db 807 ProGlnAspThrValSerValIleGlyValAlaGlyIysSerLysHisGlyArgIys 826
Qy 2611 CTAGCATGGATTTTGAAGAAATTTGACCCCATCTTCTGAAATAATTTGACTTGGCG 2670
Db 827 AlaIaIaTrpLysPheIleGlyAsnAsnTrpGluGluLeuHisAsnArgTyrGln---Gly 845
Qy 2671 TCATATGATCAAGGATGATCATCTCTGGCACACACAGCTCATCTTTCTTCCAAGGATAAG 2730
Db 846 GlyPheLeuIleSerArgLeuIleIysLeuSerValGluGlyPheAlaValAspIysMet 865
Qy 2731 TTGCAGAGGTGAACACTATTTTGAATCTCTTGAGGCTCAAGGATCATCATCTGGATATT 2790
Db 866 AlaGlyGluValIysAlaPhePheGluSerHisProAlaProSerAlaGluArgThrIle 885
Qy 2791 TTTCAAACTGTTCTGGAACGATACCAACAAATATATAAATGCTGGAGAAATCTTCCG 2850
Db 886 ---GlnGlnCysCysGluAsnIleLeuLeuAsnAlaIaIaTrpLeuIysArgAspAlaAsp 904
Qy 2851 ACTCTGAGGACTTGGCTAATG 2871
Db 905 SerIleHisGlnTyrLeuLeu 911
RESULT 11
S07099
membrane alanyl aminopeptidase (EC 3.4.11.2) - rabbit (fragments)
N:Altermate names: leukemia antigen CD13; microsomal aminopeptidase N
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Sep-1991 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C:Accession: S07099; B25985
R:Noren, O.; Dabelsteen, E.; Hoyer, P.E.; Olsen, J.; Sjoestrom, H.; Hansen, G.H.
PDBS Lett. 259, 107-112, 1989
A:Title: Onset of transcription of the aminopeptidase N (leukemia antigen CD 13) gene at
A:Reference number: S07099; PMID:90092508; PMID:2574692
A:Accession: S07099
A:Molecule type: mRNA
A:Residues: 15-805 <NOR>
R:Peracchi, H.; Maroux, S.; Bonicel, J.; Desmuelle, P.
Biochim. Biophys. Acta 684, 133-136, 1982
A:Title: The amino acid sequence of the hydrophobic anchor of rabbit intestinal brush bo
A:Reference number: A90640; PMID:82113673; PMID:6120002

A:Accession: B25985
A:Molecule type: Protein
A:Residues: 1-14 <PER>
A:Note: this sequence represents the detergent-released form; a proteinase-released form
C:Superfamily: membrane alanyl aminopeptidase
C:Keywords: aminopeptidase; glycoprotein; membrane protein; surface antigen; zinc
F:70,98,391,409,463,487,573,656/Binding site: carboxylate (asn) covalent #status pred
F:223,224,227/Binding site: zinc (His, Glu, His) #status predicted
Alignment Scores:
Pred. No.: 7,54e-72 Length: 805
Score: 1176.00 Matches: 279
Percent Similarity: 51.33% Conservative: 147
Best Local Similarity: 33.61% Mismatches: 326
Query Match: 23.23% Indels: 78
DB: 2 Gaps: 22
US-10-039-073-3 (1-2883) x S07099 (1-805)
Qy 502 TTCCAAGCCAAAGTTAGTGATGGCTTTGAAGGGTTTATATAAGCACATACAGAACTCTT 561
Db 16 PheGlnGlyGluLeuAlaAspAspLeuAlaGlyPheTyrArgSerGluTyrMetGlu--- 34
Qy 562 GGTGGTGAACCAAGATTCTTCAGTAACA-----GATTTTGAGCCAAACCCAGGCACGC 615
Db 35 GlyAsnValArgIysValValAlaThrThrGlnMetGlnMetGlnAlaAlaAspAlaArg 54
Qy 616 ATGGCTTTCCCTTCCTTTGATGAACCGTTGTTCAAGCCAACTTTTCAATCAAGATACGA 675
Db 55 LysSerPheProCysPheAspGluProAlaSerIysAlaThrPheAsnIleThrLeuIle 74
Qy 676 AGAGAGACGAGCATATTGCATATCCAAACATG---CCAAAGGTTAAGACAAATGAACATT 732
Db 75 HisProArgAspTyrThrAlaLeuSerAsnMetLeuProArgSerSerThr----- 91
Qy 733 GAAGGAGCTCTTTGGAGAT-----CACTTTGAACACTACTGTAAA 774
Db 92 -----AlaLeuProGluAspProAsnTrpThrValThrGluPheHisThrTrpProIys 109
Qy 775 ATGAGTACATACCTTGTAGCCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACT 834
Db 110 MetSerThrTyrLeuLeuAlaTyrIleValSerGluPheThrAsnIleGluAlaGlnSer 129
Qy 835 TCATCAGGGTCAAGGTGTCATCTATGCATCCCGACAGAAACCGAATCAACACAT--- 891
Db 130 ProAsnAsnValGlnIleArgIleTrpAlaArgProSerAlaIleSerGluGlyHisGly 149
Qy 892 ---TATGCTTTGACGGCATCACTGAAGCTACTTCATTTTATGAAAGTACTTTGATATC 948
Db 150 GlnTyrAlaLeuAsnValThrGlyProIleLeuAsnPhePheAlaAsnHisTyrAsnThr 169
Qy 949 TACTATCCACTCTCCAAACTGGATTAAATTGCTATTCTCTGACTTTGCACCTGGAGCCATG 1008
Db 170 ProTyrProLeuGluIysSerAspGlnIleGlyLeuProAspPheAsnAlaGlyAlaMet 189
Qy 1009 GAAATTTGGGCGCTCATATACATATAGGAGACGTCATCTGCTTTTGGACCCCAAGACCTCT 1068
Db 190 GluAsnTrpGlyLeuValThrTyrArgGluSerAlaLeuLeuPheAspProLeuValSer 209
Qy 1069 TCTGCTTCCGATAAATCTGGTCCAGAGTCAATAGCCCATGACTGGCCGCCACGAGTGG 1128
Db 210 SerIleSerAsnIysGluArgValValThrValValAlaHisGluLeuAlaHisGlnTrp 229
Qy 1129 TTTGGCAACCTGGTCAACAATGGAAATGGTGAATGATATTTGGCTTTAAGGAGGGTTTGTCA 1188
Db 230 PheGlyAsnLeuValThrValAspTrpTrpAsnAspLeuTrpLeuAsnGluGlyPheAla 249
Qy 1189 AAATACATGAACATTATCGCTGTTTAATGCTACATATCCAGAGTGCATTTGATGACTAT 1248
Db 250 SerTyrValGluTyrLeuGlyAlaAspTyrAlaGluProThrTrpAsnLeuLeuAspLeu 269
Qy 1249 TTT---TTGATGTGTGTTTGAAGTAATTACAAAGATTCATTAATTCATCCGCCCT 1305

QY 202 AGGCTCCCGAGTGGTCTCTCCATTATGACCTCTTGTGTCACCCCAATCTCACC 261
 Db 15 ArgLeuProThrPheAlaGluProThrHisTyrAsnValArgLeuSerProCysLeuAsn 34
 QY 262 TCTCGGACTTTGGTGCATCTGAGAAGATCGAAGTCTGGTCAGCAATGCTACCCAGTTT 321
 Db 35 GlnPheSerPheAspGlyHisAlaThrIleAspValThrIleLysGluAlaThrAspVal 54
 QY 322 ATCATCTTGCACAGCAAGATCTTGAATTCAGAAATGCCACCTTTCACTCAGAGGAAGAT 381
 Db 55 LeuLysValHisAlaGlnSerLeuLeuIleGlnSerValSerLeuIleThrGln----- 72
 QY 382 TCAAGATACATGAACCCAGAAAGAACTGAAGTTTGGATTACCTGCTCATGAACAA 441
 Db 73 -----ProGlyAspAlaSerLysSerLeuGluThrSerTyrAspAspLys 87
 QY 442 ATTGCACCTGCTG-----GTTCCAGAGAAACTTAGCCCTCACCTGAAATACTATG 492
 Db 88 LeuAsnIleLeuThrIleLysLeuProThrThrMetGlnProGln--LysValGlnLeu 106
 QY 493 GCTATGGACTTCCAGCCCAAGTTAGGTGATGGCTTTGAAGGTTTATAAAGCACATAC 552
 Db 107 AspPheLysPheValGlyGluLeuAsnAspLysMetArgGlyPheTyrArgSerGlnTyr 126
 QY 553 AGAACTCTTGGTGGTGAACACAGAATCTTGCAGTAACAGATTTTGAGCCCAACCCAGCA 612
 Db 127 LysAspLysAsnGlyThrGluLysPheLeuAlaSerThrGlnPheGluSerThrTyrAla 146
 QY 613 CGCATGGCTTCCCTTGTCTTGCATCAACCGTTGTTCAAGCCCAACTTTTCAATCAAGATA 672
 Db 147 ArgTyrAlaPheProCysPheAspGluProIleTyrLysAlaThrPheAspValThrLeu 166
 QY 673 CGAAGAGAGACGAGCATATTGCATCTATCCAACTGCCAAAGGTT---AAGACAATTGAA 729
 Db 167 GluValGluAsnHisLeuThrAlaLeuSerAsnMetAsnValIleSerGluThrProThr 186
 QY 730 CTGGAAGGAGGCTTTTGGAGATCACCTTGGAACTACTGTAAATACAGTACATACCTT 789
 Db 187 AlaAspGlyLysArgLysAlaValThrPheAlaThrSerProLysMetSerSerTyrLeu 206
 QY 790 GTAGCTACATAGTTTGTGATTCTTCCACTCTGAGTGGCTTCACCTTCATCAGGGGTCAAG 849
 Db 207 ValAlaPheAlaValGlyGluLeuGluTyrIleSerAlaGlnThrLysSerGlyValGlu 226
 QY 850 GTGTCCATCTATGCATCCCGACAGCAACCGGAATCAACACATATTGCTTTTCAGCGCATCA 909
 Db 227 MetArgValTyrThrValProGlyLysLysGluGlnGlyGlnTyrSerLeuAspLeuSer 246
 QY 910 CTGAAGCTACTGATTTTATGAAAGTACTTTGATATCTACTATCTCAGCTCTCCAACTG 969
 Db 247 ValLysCysIleAspTrpTyrAsnGluTrpPheAspIleLysTyrProLeuProLysCys 266
 QY 970 GATTAAATTTGCTATCTCCTGCTTTCACCTCGAGCCATGGAAATTTGGGGCTCATTACA 1029
 Db 267 AspLeuIleAlaIleProAspPheSerMetGlyAlaMetGluAsnTrpGlyLeuValThr 286
 QY 1030 TATAGGAGAGCGTCACTGCTTTTGGACCCCAAGACCTTCTGCTTCCGATAAACTGTGG 1089
 Db 287 TyrArgGluIleAlaLeuLeuValAspProGlyValThrSerThrArgGlnLysSerArg 306
 QY 1090 GTCACCAAGCATAGCCCATGAACTGGCGCACCGAGTGGTTTGGCACTCGTCAATG 1149
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 QY 1210 GTTAATGCTACATATCCAGAGCTGCAATTTTGATGACTATTTTGTGAAT---GTGTGTTTT 1266
 Db 347 ValGlyAlaAsnCysProGluPheLysIleTrpLeuHisPheLeuAsnAspGluLeuAla 366
 QY 1267 GAAGTAATTACAAAGATTCATTGAAATTCATCCCGCCCTATCTCCAAACCAAGCGGAACC 1326

Db 367 SerGlyMetGlyLeuAspAlaLeuArgAsnSerHisProIleGluValGluIleAspAsn 386
 QY 1327 CCGACTCAAAATACAGGAAATGTTTTCATGAAGTTCCTTATACAAAGGAGCTTGTATTATTG 1386
 Db 387 ProAsnGluLeuAspGluIleTyrAspSerIleThrTyrAlaLysSerAsnSerValAsn 406
 QY 1387 AATATGCTCAAGGAATTTTCTGGGTGAGGAGAAAATTCAGAAAGGAATAATTCAGTACTTA 1446
 Db 407 ArgMetLeuCysTyrTyrLeuSerGluProValPheGlnLysGlyLeuArgLeuTyrLeu 426
 QY 1447 AAGAAGTTACGATATAGAAATCTAAGAAATGATGACTTGTGAGCAGCTCTCAAAATAGT 1506
 Db 427 LysArgPheGlnTyrSerAsnAlaValThrGlnAspLeuTrpThrAlaLeuSerGluAla 446
 QY 1507 TGTTTAGAAAGTGAATTTTACATCTGGTGGAGTTTGTTCATTCGGATCCCAAGATGACAAGT 1566
 Db 447 Ser----- 447
 QY 1567 AACATGCTCGCTTTCGGGGGAAAATGCGAGAGTCAAAAGATGATGACTACATATGACT 1626
 Db 448 -----GlyGlnAsn-----ValAsnGluLeuMetSerGlyTyrThr 459
 QY 1627 CTCCAGAAAGAAATCCCTCTGCTGGTGGTT-----AAACAAGACGGGTGTCTCA----- 1674
 Db 460 GlnGlnMetGlyPheProValLeuLysValSerGlnArgGlnAspGlyAsnAsnArgIle 479
 QY 1675 CTCCGACTGCAACAGGAGCGCTTCTCCAGGGGTTTTCCAGGAAGACCCCTGAATGGAGG 1734
 Db 480 LeuThrValGluGlnArgArgPheIleSerAsp---GlyGlyGluAspPro----- 495
 QY 1735 GCCCTGCGAGAGAGGTACCTGTGGCATATCCCATGACCTACTCTCC-----ACGAGTTCT 1788
 Db 496 -----LysAsnSerGlnTrpGlnValProIleThrValAlaValGlySerSerPro 512
 QY 1789 TCTAATGTGATCCACACACACATTTCTAAATCAAAAGACAGAT-----ACTCTGGATCTA 1842
 Db 513 SerAspValLysAlaArgPheLeuLeuLysGluLysGlnGlnGluPheThrIleGluGly 532
 QY 1843 CCTGAAAGACCAAGTTCGGTGAAATTTAATGTCGACTCAAAATGCTTACTACATCGTTCAC 1902
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 QY 1903 TATGAGGCTCATGATGGGACCAACTCATTCACAGCTGAATACAGAACACACACTTCTC 1962
 Db 553 TyrSer-----AspGluMetLeuThrAlaMetLeuProAspIleAlaSerArg 568
 QY 1963 AGACCTAAG-----GACAGAGTAGTCTGATTCATGATGTTTTCAGTCTAGTTGGTGCA 2016
 Db 569 ArgMetProValLeuAspArgPheGlyLeuIleAsnAspLeuSerAlaLeuLeuAsnThr 588
 QY 2017 GGGAGACTGACCCCTAGACAAAGCTCTTGACATGACTTACTACCTCCCAACATGAAACAAGC 2076
 Db 589 GlyArgValSerIle-----AlaGlnPheValGlnValAlaAlaSer 602
 QY 2077 AGCCCC-----GCATTTCTCGAAGTCTGAGTTACTTGT 2109
 Db 603 SerAlaLysGluAspGluTyrValValTrpGlyAlaIleAspGluGlyMetSerLysLeu 622
 QY 2110 GAATCGTTTTTACCACATGATGGACAGGAGGAATATTTTCAGATATCTCTGAAAACTCAAG 2169
 Db 623 LeuAlaCysAlaArgGluMetSer-----GluAspThrLeuLysSerAlaLys 638
 QY 2170 CGTTACCTCTTCTGATTTTAAAGCCAGTGT-----ATTGACAGCAAGC 2214
 Db 639 GlnLeuValValLysMetPheGluGlnThrGlyAlaGluLeuGlyPheAlaGluGlnAla 658
 QY 2215 TGGAGTGACAAAGGGCTCAGTCTCGGACAGAGATGCTCGCTCGCTCTCTTTGAAGCTGGCC 2274
 Db 659 GlyGluAspSerGlnLysMet-----MetLeuArgSerLeuValGlnAlaArgLeu 675
 QY 2275 TGTGACCTGAACCATGCTCTCTTCATCCAGAAAGCTGCTGAACTCTCTCCAGTGATG 2334

Db 676 AlaargalaGlyHisGlnProThrIleAspLysPheThrGlnMetPheAsnAspPheLeu 695
Qy 2335 GAATCCAGTGGAAATTAATATATACCAACAGATGTTTTAAAGATGTGTATCTCTGGGT 2394
Db 696 GlulysGlyThrProIleHis-----ProAspIleArgLeuAlaThrPheGlyValVal 713
Qy 2395 GCTCAG-----ACAACAGCAGGAGTGAATTTACCTTTTAGAGCAATATGAAGTGTCAATG 2448
Db 714 AlaArgTyrGlyGlyLysGluGlyPheAspLysLeuMetAsnLeuArgGluThrThr 733
Qy 2449 TCAAGTCTGACAAACAAATTTCTGTATGCTTTTGTACAGCAGCAAGCATCAGGAAAG 2508
Db 734 PheGlnGluIleGluArgGlnThrMetValAlaMetSerGlnThrProGluGluSerLeu 753
Qy 2509 TTACTGAAGTTAAATGTAAGTAGGAATGGAAGAGGTTATCAAGACACAGAACTTGGCA 2568
Db 754 LeuAlaGlnLeuPheGluTyrGlyPheGluLysAsnLysValArgProGlnAspGlnLeu 773
Qy 2569 GCTCTCTTCATCGATGTCGACAGCTCCAAAGGGGCGCAACTAGCATGGGATTTTGTGTA 2628
Db 774 TyrLeuPheLeuGlyThrGlyAlaThrHisMetGlyGlnGlnTyrAlaTPrLysTyrPhe 793
Qy 2629 AGACAAATGGACCCATCTCTGAAAAATTT---GACTTGGCTCATATGACATGAAG 2685
Db 794 CysGluHisIleLysGluPheLeuAspLysTyrGlyGlyAlaAsnSerSerLeuPheGln 813
Qy 2686 ATGATCATCTCTGCGACACACAGCTCACTTTCTTCCAAAGGATAGTTGCAAGAGTGAAA 2745
Db 814 ArgCysLeuLysPheAlaGlyGluSerPheGlyAsnGluLysArgAlaValGluPheGln 833
Qy 2746 CTATTTTT-----GAATCTCTTGAGGCTCAAGGATCAGATCCTGGAT 2787
Db 834 AspPhePheCysAsnCysAsnValLeuSerAspThrAspArgGlnThrLeuAlaAArgPro 853
Qy 2788 ATTTTCAAAGTCTGGAACCAATACCAAAATATATAAATCGCTGGAGAGAT 2844
Db 854 IleGlyGlnThrVal---GluAlaIleArgLeuAsnAlaArgLeuLeuGluSerAsn 871
RESULT 13
S37794
aminopeptidase yscII (EC 3.4.11.-) - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YKL157w; protein YKL611
C;Species: Saccharomyces cerevisiae
C;Date: 03-May-1994 #sequence revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: S37794; S37987; S44571; S19642
R;Vandenbol, M.; Bolle, P.; Dion, C.; Portetelle, D.; Hilger, F.
submitted to the EMBL Data Library, September 1993
A;Description: DNA sequencing of a 36.2 Kb fragment located between the FAS1 and LAP4 loci of yeast 10, 35-40, 1994
A;Reference number: S37786
A;Accession: S37794
A;Molecule type: DNA
A;Residues: 1-844 <VAN>
A;Cross-references: UNIPROT:P32454; EMBL:Z26877; NID:g407482; PIDN:CAA81497.1; PID:g407482
A;Experimental source: strain S288C
R;Vandenbol, M.; Bolle, P.A.; Dion, C.; Portetelle, D.; Hilger, F.
submitted to the Protein Sequence Database, March 1994
A;Reference number: S37976
A;Accession: S37987
A;Molecule type: DNA
A;Residues: 1-844 <VA2>
A;Cross-references: EMBL:Z28157; NID:g486272; PIDN:CAA81999.1; PID:g486273; MIPS:YKL157w
A;Experimental source: strain S288C
R;Vandenbol, M.; Bolle, P.A.; Dion, C.; Portetelle, D.; Hilger, F.
Yeast 10, 35-40, 1994
A;Title: DNA sequencing of a 36.2 kb fragment located between the FAS1 and LAP4 loci of yeast 10, 35-40, 1994
A;Accession: S44571
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-844 <VAN>
A;Cross-references: EMBL:Z26877; NID:g407482; PIDN:CAA81497.1; PID:g407491
A;Experimental source: strain S288C
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1993

R;Garcia-Alvarez, N.; Cueva, R.; Suarez-Rendueles, P.
Eur. J. Biochem. 202, 993-1002, 1991
A;Title: Molecular cloning of soluble aminopeptidases from Saccharomyces cerevisiae. Seq
A;Reference number: S19642; MUID:92111552; PMID:1765107
A;Accession: S19642
A;Molecule type: DNA
A;Residues: 1-163, 'V', 165-441, 'E', 443-843, 'VNRDRDVVNKYLKNGYY', <GAR>
A;Cross-references: EMBL:X63998; NID:g3367; PIDN:CAA45403.1; PID:g3368
C;Genetics:
A;Gene: SGD:APE2; LAP1
A;Cross-references: SGD:S0001640; MIPS:YKL157w
A;Map position: 11L
C;Superfamily: membrane alanyl aminopeptidase
C;Keywords: aminopeptidase; glycoprotein; metalloprotein; zinc
F;290,622/Binding site: carbonylate (Asn) (covalent) #status predicted
F;305,309/Binding site: zinc (His) #status predicted
F;306/Active site: Glu #status predicted

Alignment Scores:
Pred. No.: 8,92e-68 Length: 844
Score: 1116.00 Matches: 281
Percent Similarity: 50.45% Conservative: 171
Best Local Similarity: 31.36% Mismatches: 372
Query Match: 22.05% Indels: 72
DB: 2 Gaps: 24

US-10-039-073-3 (1-2883) x S37794 (1-844)

Qy 187 CTTTGCAGAGCTAAGGCTCCAGTGGTGTCTCTCTCCATATGACCTTTTGTG 246
Db 6 ProAsnArgGluIle---LeuProAspAsnValProLeuHisTyrAspLeuThrVal 24
Qy 247 CACCCCAACTCACCCTCTCGGACTTTTGTGCATCTGAGAAGATCGAAGCTTTGGTCAGC 306
Db 25 GluProAspPheLysThrPheLysPheGluGlySerValLysIleGluLeuLysIleAsn 44
Qy 307 AAT---GCTACCCAGTTTATCATCTTTCACACAGCAAGATCTTGAATACGAAATGCCACC 363
Db 45 AsnProAlaIleAspThrValThrLeuAsnThrValAspThrAspIleHisSerAlaLys 64
Qy 364 CTTCACTCAGAGGAGATTCAAGATACATGAACACAGGAAAGAACTGAAGTTTGTAGT 423
Db 65 IleGlyAspValThrSerSer-----GlutIleSer 75
Qy 424 TACCTGCTCATCAACAAATTTGCACCTGCTGTTTCCAGAGAAACTTACGCCTCACCTGAAA 483
Db 76 GluGluGluGlnGlnValThrPheAlaPheProLysGlyThrMetSerSerPheLys 95
Qy 484 TACTATGTGGCTATGGAC-----TTCCAAGCCAAAGTTAGGTGATGGCTTTGAAGGGTTT 537
Db 96 GlyAsnAlaPheLeuAspIleLysPheThrGlyIleLeuAsnAspAsnMetAlaGlyPhe 115
Qy 538 TATAAAGACACATACAGA---ACTCTTGGTGTGAACAACAAGATTCTTCAGTAAACAGAT 594
Db 116 TyrArgAlaLysTyrGluAspLysLeuThrGlyLysTyrMetAlaThrThrGln 135
Qy 595 TTTGAGCCCAACCCAGCAGCATGGCTTTCCCTTGTCTTTGTATGAACCGTTGTTCAAAGCC 654
Db 136 MetGluProThrAspAlaArgAlaPheProCysPheAspGluProAsnLeuLysAla 155
Qy 655 AACTTTTCAATCAAGATACGAGAGAGAGCAGGCATATTGCACTATCCAAACATGCCAAAG 714
Db 156 SerPheAlaIleThrLeuValSerAspProSerLeuThrHisLeuSerAsnMet---Asp 174
Qy 715 GTTAAAGCAATTTGAATCTGAGAGGCTCTTTTGGAGAGATCAGCTTTGAAACTACTGTAAA 774
Db 175 ValLysAsnGluTyrValLysAspGlyLysValThrLeuPheAsnThrThrProLys 194
Qy 775 ATGAGTACATACCTTGTAGCTACATAGTTTGTGATTTCCACTCTCTAGTGGCTTCACT 834
Db 195 MetSerThrThrLeuValAlaPheIleValAlaGluLeuLysTyrValGluSer---Lys 213
Qy 835 TCATCAGGGGTCAAGGTGTCCATCTATGCATCCCCAGACAAACGGAATCAACACATTTAT 894

A;Accession: S46750
A;Molecule type: DNA
A;Residues: 1-856 <DUZ>
A;Cross-references: UNIPROT:P37898; EMBL:U00062; NID:g488162; PIDN:AAB68919.1; PID:g488162
R;Caprioglio, D.R.; Padilla, C.; Werner-Washburne, M.
J. Biol. Chem. 268, 14310-14315, 1993
A;Title: Isolation and characterization of AAP1. A gene encoding an alanine/arginine and
A;Reference number: S48291; MUID:93300827; PMID:8100228
A;Accession: S48291
A;Molecule type: DNA
A;Residues: 107-549, 570-645, 'E', 647-652 <CAP>
A;Cross-references: EMBL:L12542
C;Genetics:
A;Gene: SGD:AAP1
A;Cross-references: SGD:S0001089; MIPS:YHR047c
A;Map position: 8R
C;Superfamily: membrane alanyl aminopeptidase
C;Keywords: aminopeptidase

Alignment Scores:
Pred. No.: 1.88e-64 Length: 856
Score: 1067.00 Matches: 282
Percent Similarity: 48.46% Conservative: 159
Best Local Similarity: 30.99% Mismatches: 381
Query Match: 21.08% Indels: 88
DB: 2 Gaps: 23

US-10-039-073-3 (1-2883) x S46750 (1-856)

Qy	205	CTCCCCAGTGGTGCATCTCTCCATATGACCTCTTTGTCCACCCCAATCTCACCTCT	264
Db	6	LeuProAsnValThrProLeuHisTyrAspIleThrLeuGluProAsnPheArgAla	25
Qy	265	CTGGACTTTGTCATCTGAGAGATCGAAGTCTTGTGTCAGC-----AATGCT	312
Db	26	PheThrPheGluGlySerLeuLysIleAspLeuGlnIleAsnAspHisSerIleAsnSer	45
Qy	313	ACCAGGTTT-----ATCATCTGCACAGCAAGATCTTGAATCAGCAATGCC	360
Db	46	ValGlnIleAsnTyrLeuGluIleAspPheHisSerAlaArgIleGluGlyValAsnAla	65
Qy	361	ACCCTTCAGTCAGGGAAGATTCAAGATACATGAAACCAGGAAGAAAGTGTG	420
Db	66	IleGluValAsnLysAsnGluAsnGln-----	74
Qy	421	AGTTACCTGCTCATGAACAAATTGCACTGCTGTTCCA-----GAGAACTT	468
Db	75	-----GlnLysAlaThrLeuValPheProAsnGlyThrPheGluAsnLeu	89
Qy	469	ACGCCTCACCTGAATACTATGTGGCTATGGACTTCCAGCCCAAGTTAGGTGATGGCTTT	528
Db	90	GlyProSerAlaLysLeuGluIle-----PheSerGlyIleLeuAsnAspGlnMet	107
Qy	529	GAGGGTTTATAAAGACATACAGA---ACTCTGGTGGTGAACAAAGAAATCTTTGCA	585
Db	108	AlaGlyPheTyrArgAlaLysTyrThrAspLysValThrGlyGluThrLysTyrMetAla	127
Qy	586	GTAACAGATTTCGACCAACCCAGGCACGATGGCTTTCCCTTGTGATGACCGCTTG	645
Db	128	ThrThrGlnMetGluAlaThrAspAlaArgArgAlaPheProCysPheAspGluProAsn	147
Qy	646	TTCAAAGCCAACTTTTCAATCAAGATACGAAGAGAGAGAGGAGGATATTGCACTATCCAAC	705
Db	148	LeuLysAlaThrPheAlaValThrLeuValSerGluSerPheLeuThrHisLeuSerAsn	167
Qy	706	ATGCCAAAGGTTAAGACAAATTGAAGAGAGGCTTTTGGGAAGATCACTTTGAAACT	765
Db	168	Met---AspValArgAsnGluThrIleLysGluGlyLysTyrThrThrPheAsnThr	186
Qy	766	ACTGTAAATAGATACATACCTTGTAGCCTACATAGTTGTGATTTCCACTCTCTCAGT	825
Db	187	ThrProLysMetSerThrTyrLeuValAlaPheIleValAlaAspLeuArgTyrValGlu	206

Qy	826	GGCTTCACCTTCATCAGGGGTCAAGGTGTCATCTATCATCTCCCGACAGCAAAACGGAATCAA	885
Db	207	Ser---AsnAsnPheArgIleProValArgValTyrSerThrProGlyAspGluLysPhe	225
Qy	886	ACACATATGCTTTGAGGAGCATCAAGACTACTTGAATTTTATGAAAGTACTTTGAT	945
Db	226	GlyGlnPheAlaAlaAsnLeuAlaAlaArgThrLeuArgPhePheGluAspThrPheAsn	245
Qy	946	ATCTACTATCCACTCTCCAACTGGATTAAATTTGCTATTCTCTGACTTTCCACCTGAGCC	1005
Db	246	IleGluTyrProLeuProLysMetAspMetValAlaValHisGluPheSerAlaGlyAla	265
Qy	1006	ATGGAATAATTGGGCTCATATACATATAGGAGAGCGTCACTGCTTTTTCACCCCAAGACC	1065
Db	266	MetGluAsnTyrGlyLeuValThrTyrArgValIleAspLeuLeuAspIleGluAsn	285
Qy	1066	TCCTTCGCTTCGATAAACTGTGGGTCAACAGATCATAGCCCATGAATCTGGGCGCACAG	1125
Db	286	SerSerLeuAspArgIleGlnArgValAlaGluValIleGlnHisGluLeuAlaHisGln	305
Qy	1126	TGCTTTGGCAACCTGGTCAATGGAATGCTGGAATGATATTGGCTTAAGGAGGCTTTT	1185
Db	306	TrpPheGlyAsnLeuValThrMetAspTrpTrpGluGlyLeuTrpLeuAsnGluGlyPhe	325
Qy	1186	GCAAAATACATGGAACCTTATCGCTGTTAATGTCTACATATCCAGAGCTGCAA---TTTGAT	1242
Db	326	AlaThrTrpMetSerTrpTyrSerCysAsnLysPheGlnProGluTrpLysValTrpGlu	345
Qy	1243	GACTATTTTGAATGTGTTTGAAGTAATTAACAAAGATTCATTAATTCATCCCGC	1302
Db	346	GlnTyrValThrAspAsnLeuGlnArgAlaLeuAsnLeuAspSerLeuArgSerSerHis	365
Qy	1303	CTATCTCCAAACCCGCGAAGCCCGACTCAATACAGAAATGTTTCATGAAGTTTC	1362
Db	366	ProIleGluValProValAsnAsnAlaAspGluIleAsnGlnIlePheAspAlaIleSer	385
Qy	1363	TATAACAAGGAGCTTGTATTGTAATATGCTCAAGGATTTTCTGGGTGAGGAGAAATTC	1422
Db	386	TyrSerLysGlySerSerLeuLeuArgMetIleSerLysTrpLeuGlyGluGluThrPhe	405
Qy	1423	CAGAAAGGAATTAATTCAGTACTTAAAGAAGTTCAGCTATAGAAATCTAAGAAATGATGAC	1482
Db	406	IleLysGlyValSerGlnTyrLeuAsnLysPheLysTyrGlyAsnAlaLysThrGlyAsp	425
Qy	1483	TTGTGGAGCAGTCTGTCAAAATAGTTGTTAGAAAGTGAATTTTACATCTCTGGAGTTGT	1542
Db	426	LeuTrpAspAlaLeu-----AlaAspAlaSerGlyLysAspValCys	439
Qy	1543	CATTGGATCCCAAGATGACAAAGTAACATGCTCGCCTTTCTGGGGGAAAATGCAGAGTC	1602
Db	439	-----	439
Qy	1603	AAAGAGATGATGACTACATGGAATCTCCAGAAAGGATCCCTCTGCTGGTGTAAACAA	1662
Db	440	---SerValMetAsnIleTrpThrLysArgValGlyPheProValLeuSerValLysGlu	458
Qy	1663	GACGGGTGCTCACTCCGACTCAACAGGAGCGCTCTCTCCAG---GGGGTTCCTCAGGAA	1719
Db	459	HisLysAsnLysIleThrLeuThrGlnHisArgTyrLeuSerThrGlyAspValLysGlu	478
Qy	1720	GACCTCGAATGGAGGGCCCTGCAGGAGAGGTACCTGTGGCATATCCCATTTGACCTACTCC	1779
Db	479	GluGluAspThrIle-----TyrProIleLeuLeuAlaLeuLysAspSer	494
Qy	1780	ACGAGTTCTTCAATGTGATCCACAGACATCTTAAATCAAAAGACATACTCTGGAT	1839
Db	495	ThrGlyIleAspAsnThrLeu-----ValLeuAsnGluLysSerAlaThrPheGlu	511
Qy	1840	CTACCTGAAAAGACACCATGTTGGGTGAATTTAATGTGGACTCAATGGTTTACTACACTGTT	1899
Db	512	Leu---LysAsnGluGluPhePheLysIleAsnGlyAspGlnSerGlyIlePheIleThr	530
Qy	1900	CACTATGAGGGTCAATGGATGGGACCAACTCATTTACACAGCTGAATCAGAACCAACACTTT	1959

Db 531 SerTyrSerAspGluArgTrpAlaLysLeuSerLysGlnAlaAsn-----Leu 546
QY 1960 CTCACAGCTTAAAGCAGAGTAGTCTGATTTTCATGATGTTTCACAGTAGTTGGTGACGGG 2019
Db 547 LeuSerValGluAspArgValGlyLeuValAlaAspAlaLysAlaLeuSerAlaSerGly 566
QY 2020 AGACTGACCTTAGACAAAGCTCTTGCATGACTTACTACCTCCACATGAACAAAGCAGC 2079
Db 567 TyrThrSerThrAsnPheLeuAsnLeuLeuSerAsnTrpLysAsnGluAspSerPhe 586
QY 2080 -----CCGCACCTTCTGAAGGCTGAGTACTTGGATCTTTTACCATCATGATG 2130
Db 587 ValValTrpGluGlnIleAsnSerLeuSerAlaLeuLysSerThrTrpValPhe--- 605
QY 2131 GACAGAAGGAATATTTCAGATATCTCTGAAACCTCAAGCGTTACTTCTTCAGTATTTT 2190
Db 606 -----GluProGluAspIleLeuAsnAlaLeuAspLysPheThrLeuAspLeuVal 622
QY 2191 AAGCAGGTGATTGACAGGCAAGCTGGAGT-----GACAAGGGCTCAGTCTGGACAGG 2244
Db 623 LeuAsnLysLeuSerGluLeuGlyTrpAsnIleGlyGluAspSerPheAlaIleGln 642
QY 2245 ATGCTCCGCTCGGCTCTTGAAGCTGGCTGTGACCTGAACCATGCTCTTGCATCCAG 2304
Db 643 ArgLeuLysValThrLeuPheSerAlaAlaCysThrSerGlyAsnGluLysMetGlnSer 662
QY 2305 AAAGCTGCTGAATCTCTCCAGTGGATGGAATCCAGTGGAAATTAATAATATACCAACA 2364
Db 663 IleAlaValGluMetPheGluGlyTrp---AlaAsnGlyAsnLysGlnAlaIleProAla 681
QY 2365 GATGTTTTAAAGATTGTGTATTCTCTGGGTGCTCAGACAACAGCAGGATGGAATPAC--- 2421
Db 682 LeuPheLysAlaValAlaPheAsnThrValAlaArgLeuGlyGlyGluAsnAsnTyrGlu 701
QY 2422 ---CTTTAGACCAATATGAAGTCAATGCTCAAGTGTGCTGACAAACAAATACTGTAT 2478
Db 702 LysIlePheAsnIleTyrGlnAsnProValSerSerGluLysIleAlaLeuArg 721
QY 2479 GCTTTGTCAACGACGACATCAGGAAAGTTTACTGAAGTTAATTGAACCTAGGAATGAA 2538
Db 722 AlaLeuGlyArgPheGluAspLysGluLeuLeuGluArgThrLeuSerTyrLeuLeuAsp 741
QY 2539 GGAAGGTTATCAAGACACAGAACTTGGCAGCTCTCTTCAATGCGAATGCCAGCGTCCA 2598
Db 742 GlyThrValLeu---AsnGlnAspPheTyrIleProMetGlnGlyIleArgValHisLys 760
QY 2599 AAGGGCAGCACTAGCATGGATTTTGTAGAGAAATTTGACCCCATCTCTGAAAAA 2658
Db 761 LysGlyIleGluArgLeuTrpAlaTrpMetGlnGluHisTrpAspGluIleAlaLysArg 780
QY 2659 TTTGACTTGGGCTCATATGACATNAGGATGATCATCTCTGGCACAACAGCTCCTTTCT 2718
Db 781 LeuGlnProGlySerProValLeuGlyValLeuThrLeuGlyLeuThrAsnPheThr 800
QY 2719 TCCAAGGATAAGTTGCAAGAGGTGAACCTATTTTGAATCTCTTGGAGCTCAAGGATCA 2778
Db 801 SerPheGluAlaLeuGluLysIleSerAlaPheTyrSerArgLysValThrLysGlyPhe 820
QY 2779 CATCTGGATATTTTCAAACTGTTCTGGAACGATAACCAAAATATAAAATGCTGGAG 2838
Db 821 AspGlnThrLeuAlaGln---AlaLeuAspThrIleArgSerLysAlaGlnTrpValSer 839
QY 2839 AAGAATCTTCCGACTCTGAGGACTTGGCTA 2868
Db 840 ArgAspArgGluIleValAlaThrTyrLeu 849

RESULT 15

T39789

aninopeptidase - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: T39789

R:Seeger, K.; Harris, D.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1999
A:Reference number: Z21816
A:Accession: T39789
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-882 <SSE>
A:Cross-references: UNIPROT:Q9USX1; EMBL:AL122033; PIDN:CAB58971.1; GSPDB:GN00067; SPDB:
A:Experimental source: strain 972h-; cosmid c1921
C:Genetics:
A:Gene: SPDB:SPBC1921.05
A:Map position: 2
C:Superfamily: membrane alanyl aminopeptidase

Alignment Scores:

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Percent Similarity:	47.67%	Conservative:	162
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Query Match:	20.69%	Indels:	91
DB:	2	Gaps:	24

US-10-039-073-3 (1-2883) x T39789 (1-882)

QY 205 CTCCCCAGTGTGTCATCTCTCCATATGACCTCTTTGTCCACCCCAATCTCACCTCT 264
Db 20 LeuProLysAsnValLysProIleHisTyrAspLeuTyrProAspLeuGluThr 39
QY 265 CTGGACTTTTGTGCATCTGAGNAGATCGAAGTCTTGTGTCAGCAATGCTACCCAGTTTATC 324
Db 40 PheThrTyrGlyGlyLysValValValThrLeuAspValLeuGluAspSerAsnSerIle 59
QY 325 ATCTTGACACGAAAGATCTTGAATCAGCAATGCCACCTTTCAGTCAGAGGAAGATCA 384
Db 60 ThrLeuHisGlyIleAsnLeuArgIleLeuThrAlaAlaLeuGluTyrGlySerGlnThr 79
QY 385 AGATCATGAACACGAGAAAGAACTGAAAATTTTGATTTTACCTGCTCATGAACAAAT 444
Db 80 ValTrpAlaSerGlu-----ValSerTyr-----GlyAspGluArgIle 92
QY 445 GCACGTGCTGTTCCAGAGAAACTTACGCTCACCTGAAATACTATGTGGCTATGGACTTC 504
Db 93 ValLeuGlnPheProSerThrValProAlaAsnSerValAlaValLeuThrLeuProPhe 112
QY 505 CAAGCCAACTAGGTAGTGGCTTTGAAGGGTTTTTATAAAGCACATACAGAACTCTTGGT 564
Db 113 ThrAlaArgIleSerSerGlyMetGluGlyPheTyrArgSerSerTyrValAspSerAsp 132
QY 565 GGTGAACACAGAAATCTTGCAGTAACAGATTTTGAGCAACCCAGGACGATGCTTTC 624
Db 133 GlyAsnThrLysTyrLeuAlaThrThrGlnMetGluProThrSerAlaArgAlaPhe 152
QY 625 CCTGCTTTCATGAACCGTTGTTCAAAGCCAACTTTTCAATCAAGATACGAAGAGAGAGC 684
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QY 685 AGGCATATTGACCTATCCACATGCCAAGGTTTAAGCAATTTGAAGAGGCTTT 744
Db 173 AsnTyrThrIleLeuSerAsnMetAsnAlaValGluGlu---ThrValLysAspGlyLeu 191
QY 745 TTGGAAGATCACTTTGAACTACTGTAAAATAGTACATACCTTTGTAGCTACATAGTT 804
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QY 805 TGTGATTTCCACTCTCTGAGTGGCTTCACCTTCATCA-----GGGCTCAAGGTG 852
Db 212 AlaGluLeuGluTyrValGluTyrPheThrProGlyLysHisCysProArgLeuProVal 231
QY 853 TCCATCTATGCATCCCGACAGCAAAACGGAATCAAAACACATTTATGCTTTTGCAGGCACTACTG 912
Db 232 ArgValTyrThrThrProGlyPheSerGluGlnGlyLysPheAlaAlaGluLeuGlyAla 251
QY 913 AAGCTACTTGATTTTATGAAAAGTACTTTTGATATCTACTATCCACTCTCCAAACTCGAT 972

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 26, 2005, 06:07:35 ; Search time 451.896 Seconds
(without alignments)
6533.911 Million cell updates/sec

Title: US-10-039-073-3
Perfect score: 5062
Sequence: 1 atgttcattcttctgcatt.....ggctaatggttaataacttaa 2883

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=UniProt -QFWT=fastcan -SUPFIX=rup -MINMATCH=0.1 -LOOPCT=0 -LOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=ptc -NORM=ext -HRAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10035073 @CEN 1 1 1214 @runat_26092005_070409_21306 -NCPU=6 -ICPU=3
-NO.MWAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5052	99.8	960	Q9HBX2	Q9hb22 homo sapien
2	5047	99.7	960	Q725K1	Q725k1 homo sapien
3	4789.5	94.6	915	Q6P179	Q6p179 homo sapien
4	2768	54.7	532	Q8TD32	Q8td32 homo sapien
5	2516.5	49.7	929	ART1_HUMAN	Q9nz08 h adipocyte
6	2512.5	49.6	941	Q6UWY6	Q6uw06 homo sapien
7	2480	49.0	930	ART1_MOUSE	Q9sqh2 mus musculus
8	2430	48.0	930	ART1_RAT	Q9jj22 rattus norv
9	2034	40.2	1003	Q6PE23	Q6pe23 brachydanio
10	2027	40.0	1025	LCAP_RAT	P97629 r leucyl-cy
11	2022	39.9	1025	Q8C129	Q8c129 mus musculus
12	1999	39.5	1025	LCAP_HUMAN	Q9uiq6 homo sapien
13	1883	37.2	694	Q8C9W5	Q8c9w5 mus musculus
14	1847	36.5	997	Q6PCG5	Q6pcg5 xenopus lae
15	1690	33.4	350	Q8WVJ4	Q8wvj4 homo sapien
16	1564	30.9	549	Q8C4S7	Q8c4s7 mus musculus

17	1455.5	28.8	942	1	AMPE_PIG	Q95334 eus scrofa
18	1444	28.5	957	1	AMPE_HUMAN	Q07075 homo sapien
19	1391.5	27.5	1012	2	Q9VFW7	Q9vfw7 drosophila
20	1391	27.5	945	1	AMPE_RAT	P50123 rattus norv
21	1390.5	27.5	945	1	AMPE_MOUSE	P16406 mus musculus
22	1389.5	27.4	1036	2	Q86P55	Q86p55 drosophila
23	1373.5	27.1	994	2	Q86NQ5	Q86nq5 drosophila
24	1371.5	27.1	991	2	Q7PQR3	Q7pq3 anopheles g
25	1367	27.0	903	2	Q8INH5	Q8inh5 drosophila
26	1367	27.0	1025	2	Q8INH6	Q8inh6 drosophila
27	1361.5	26.9	988	2	Q9VFX0	Q9vfx0 drosophila
28	1343	26.5	885	2	Q8IHC5	Q8ihc5 drosophila
29	1340	26.5	942	2	Q9VFW9	Q9vfw9 drosophila
30	1339	26.5	885	2	Q9VFW8	Q9vfw8 drosophila
31	1329.5	26.3	691	2	Q8B214	Q8bz14 mus musculus
32	1329.5	26.3	862	2	Q8IGR1	Q8igr1 drosophila
33	1327	26.2	1025	1	THDE_RAT	Q10836 rattus norv
34	1322	26.1	1024	2	Q6UWJ4	Q6uwj4 homo sapien
35	1320	26.1	1024	1	THDE_HUMAN	Q8uk06 homo sapien
36	1312	25.9	964	1	AMPN_RAT	P15684 rattus norv
37	1310	25.9	1025	1	THDE_MOUSE	Q8K093 mus musculus
38	1298	25.6	966	1	AMPN_FELCA	P79171 felis silve
39	1290.5	25.5	1007	2	Q9U0D1	Q9u0d1 aplysia cal
40	1280.5	25.3	866	2	Q9W0E4	Q9w0e4 drosophila
41	1280.5	25.3	1053	2	Q8IRH0	Q8irho drosophila
42	1280.5	25.3	1075	2	Q8IRH1	Q8irhl drosophila
43	1275	25.2	997	2	Q7QAH5	Q7qah5 anopheles g
44	1274	25.2	965	1	AMPN_RABIT	P15541 oryctolagus
45	1272.5	25.1	866	2	Q9GPG3	Q9gpg3 drosophila

ALIGNMENTS

RESULT 1
Q9HBX2 PRELIMINARY; PRT; 960 AA.
AC Q9HBX2
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DB AminoPeptidase.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Schomburg L.
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF191545; AAG28383.1; -.
DR MEROPS; M01.024; -.
DR GO; GO:0004177; F:aminopeptidase activity; IEA.
DR GO; GO:0004179; F:membrane alanyl aminopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001930; Peptidase_M1.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF01433; Peptidase_M1; 1.
DR PRINTS; PR00756; ALADIPTASE.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW AminoPeptidase.
SQ SEQUENCE 960 AA; 110461 MW; 261EFC06870D644E CRC64;

Alignment Scores:
Pred. No.: 0 Length: 960
Score: 5052.00 Matches: 960
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.80% Indels: 0
DB: 2 Gaps: 0

US-10-039-073-3 (1-2883) x Q9HBX2 (1-960)

Qy 1 ATGTTCCATTCTTCTGCAATGTTAATTCACAGAAAACCAATGTTTAACTTCACAGA 60

Db 1 MetPheHisSerSerAlaMetValAsnSerHisArgLysProMetPheAsnIleHisArg 20
QY 61 GGATTTTACTGCTTAACAGAGCATCTTCCCAATATGCAATTTGTTCTCTCAGTCTCAGTG 120
Db 21 GlyPheTyxCysLeuThrAlaIleLeuProGlnIleCysIleCysSerGlnPheSerVal 40
QY 121 CCATCTAGTTATCACTTCACTAGGATCCTGGGCTTTCCAGTAGCAGTCAATATGGGAA 180
Db 41 ProSerSerTyHisPheThrGluAspProGlyAlaPheProValAlaThrAsnGlyGlu 60
QY 181 CGATTTCTTGGCAGGAGCTAAGCTCCAGTGTGTCATTTCTCTCCATATGACCTC 240
Db 61 ArgPheProTrpGlnGluLeuArgLeuProSerValValIleProLeuHisTyAspLeu 80
QY 241 TTTCTCCACCCCAATCTCACCTCTCTGACTTTGTCATCTGAGAGATCGAAGTCTTG 300
Db 81 PheValHisProAsnLeuThrSerLeuAspPheValAlaSerGluIlyIleGluValLeu 100
QY 301 GTCAGCAATGCTACCCAGTTTATCATCTTCACAGCAAGATCTTGAATCACGAATGCC 360
Db 101 ValSerAsnAlaThrGlnPheIleLeuHisSerLysAspLeuGluIleThrAsnAla 120
QY 361 ACCCTTCAGTCAGGGAAGATTCAAGATACATGAACACGAGAAAGAACTGAAAGTTTG 420
Db 121 ThrLeuGlnSerGluGluAspSerArgTyMetLysProGlyLysGluLeuLysValLeu 140
QY 421 AGTTACCCTGCTCATGAACAAATTGCACTGCTGTCACAGAAACTTACGSCCTCACCTG 480
Db 141 SerTyProAlaHisGluGlnIleAlaLeuLeuValProGluLysLeuThrProHisLeu 160
QY 481 AAATACTATGTGGCTATGGACTTCCAAAGCCAAAGTTAGTGATGGCTTTGAAGGTTTAT 540
Db 161 LysTyTyValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTy 180
QY 541 AAAGCAATACAGAACTCTTGGTGGTGAACCAAGAAATCTTGCAGTAAACAGATTTGAG 600
Db 181 LysSerThrTyArgThrLeuGlyGlyGluThrArgIleLeuAlaValThrAspPheGlu 200
QY 601 CCAACCCAGCAGCATGGCTTTCCCTTGCTTGTGATGAACCGTTGTTCAAGCCCACTTT 660
Db 201 ProThrGlnAlaArgMetAlaPheProCysPheAspGluProLeuPheLysAlaAsnPhe 220
QY 661 TCAATCAAGATACGAAGAGAGAGCAGCATATTCACATCCAAACATGCCAAAGGTTAAG 720
Db 221 SerIleLysIleArgArgGluSerArgHisIleAlaLeuSerAsnMetProLysValLys 240
QY 721 ACAATTGAATGGAAGAGGTCTTTTGGAGAGATCATTGAAACTACTGTAAAAATGAGT 780
Db 241 ThrIleGluLeuGluGlyLeuLeuGluAspHisPheGluThrThrValLysMetSer 260
QY 781 ACATACCTGTAGCCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACCTCATCA 840
Db 261 ThrTyLeuValAlaTyIleValCysAspPheHisSerLeuSerGlyPheThrSerSer 280
QY 841 GGGGTCAAGGTGTCCATCTATGATCCCAAGCAAAACGGAAATCAAAACACATATGCTTTG 900
Db 281 GlyValLysValSerIleTyAlaSerProAspLysArgAsnGlnThrHisTyAlaLeu 300
QY 901 CAGGCATCATGAAGCTACTTGATTTTATGAAAGPACTTTTGATATCTACTATCCACTC 960
Db 301 GlnAlaSerLeuLysLeuLeuAspPheTyGluLysTyPheAspIleTyTyProLeu 320
QY 961 TCCAAATCGATTAATTTGATTTCTGATCTTTCAGTCTGGACCTGGACCAATGGAGTGGGC 1020
Db 321 SerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsnTrpGly 340
QY 1021 CTATTAATATATATGGGAGAGCTCACTGCTTTTGGACCCCAAGACCTCTCTGCTCCGAT 1080
Db 341 LeuIleThrTyArgGluThrSerLeuLeuPheAspProLysThrSerSerAlaSerAsp 360
QY 1081 AAATGTGGTCCACGAGTCATAGCCCATGAATCGCGCACAGTGGTTTGGCAACCTG 1140

Db 361 LysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeu 380
QY 1141 GTCACAATGGAATGGTGAATGATATTTGGCTTTAAGGAGGTTTTCAAAATACATCGAA 1200
Db 381 ValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyMetGlu 400
QY 1201 CTTATCGCTGTTAATGCTACATATCCAGAGCTGCAATTTTGATGACTATTTTGTGAATG 1260
Db 401 LeuIleAlaValAsnAlaThrTyProGluLeuGlnPheAspAspTyPheLeuAsnVal 420
QY 1261 TGTTTTGAAGTAATTACAAAGATTCAATTAATTCATCCGCGCTATCTCCAAACACGAG 1320
Db 421 CysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLysProAla 440
QY 1321 GAAACCCCGACTCAAAATACAGGAAATGTTTGATGAAGTTTTCCTATAAACAGGAGCTGT 1380
Db 441 GluThrProThrGlnIleGlnMetPheAspGluValSerTyAsnLysGlyAlaCys 460
QY 1381 ATTTTGAATATGCTCAAGGATTTCTGGGTGAGGAGAAATCCAGAAAGGAATAATTCAG 1440
Db 461 IleLeuAsnMetLeuLysAspPheLeuGlyGluGluLysPheGlnLysGlyIleGln 480
QY 1441 TACTTAAAGAACTTCAGCTATAGAAATGCTAAGATGATGACTTGTGGAGCAGTCTGTCA 1500
Db 481 TyLeuLysLysPheSerTyArgAsnAlaLysAsnAspLeuTrpSerLeuSer 500
QY 1501 AATAGTTGTTAAGAAAGTATTTTACATCTGGTGGAGTTTGTTCATTCGGATCCCAAGATG 1560
Db 501 AsnSerCysLeuGluSerAspPheThrSerGlyGlyValCysHisSerAspProLysMet 520
QY 1561 ACAAGTAACATGCTCGCTTCTGGGGGAAATGCAAGAGGTCAAGAGATGATGACTACA 1620
Db 521 ThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGluValLysGluMetMetThrThr 540
QY 1621 TGGACTCTCCAGAAAGGAATCCCTCTGCTGGTGGTTAAACAAGACGGGTTCACCTCCA 1680
Db 541 TrpThrLeuGlnLysGlyIleProLeuLeuValLysGlnAspGlyCysSerLeuArg 560
QY 1681 CTGCAACAGAGCGCTTCTCCAGGGGTTTTCAGGAAGACCTCAATGGAGGGCCCTG 1740
Db 561 LeuGlnGlnLysArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArgAlaLeu 580
QY 1741 CAGGAGAGGTACTGTGGCATATCCATTCGACTACTCCACGAGTTCTTCTAATGTGATC 1800
Db 581 GlnGluArgTyLeuTrpHisIleProLeuThrTySerThrSerSerSerAsnValIle 600
QY 1801 CACAGACATCTTAAATCAAGACAGATACTCGGATCTACCTGAAAGACCAAGCTTG 1860
Db 601 HisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThrSerTrp 620
QY 1861 GTGAAATTTAATGTGGACTCAATGGTTACTACATCGTTTCACTATGAGGTCATGGATGG 1920
Db 621 ValLysPheAsnValAspSerAsnGlyTyTyIleValHisTyArgGlyHisGlyTrp 640
QY 1921 GACCAACTCATTTACACAGCTGAATCAGACCAACACACTTCTCAGACCTTAAGACAGAGTA 1980
Db 641 AspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAspArgVal 660
QY 1981 GGTCTGATTCATGATGTGTTTCAGTAGTTGGTGCAGGAGACTGACCTTAGACAAAGCT 2040
Db 661 GlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAspLysAla 680
QY 2041 CTTGACATGACTTACTTACCTCCAACATGAAACAAGCAGCCCCGCACTTCTCGAAGTCTG 2100
Db 681 LeuAspMetThrTyTyTrpLeuGlnHisGluThrSerSerProAlaLeuLeuGluGlyLeu 700
QY 2101 AGTTACTTGGAAATCGTTTTACCACATGATGGACAGAGGAATATTTTCAGATATCTCGAA 2160
Db 701 SerTyLeuGluSerPheTyHisMetMetAspArgArgAsnIleSerAspIleSerGlu 720
QY 2161 AACCTCAAGCTTACCTTCTTCAGTATTTTAAAGCCAGTGAATTCACAGGCAAGCTGGAGT 2220
Db 721 AsnLeuLysArgTyLeuLeuGlnTyPheLysProValIleAspArgGlnSerTrpSer 740

QY	2221	GACAAAGGCGCTCAGTCTGGGACAGGATGCTCGGCTCGGCTCTCTTGAAAGCTGGCTGTGAC	2280
Db	741	AspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAlaCysAsp	760
QY	2281	CTGACACCATGCTCCCTGGCATCCAGAAAGCTGCTGAACCTCTTCCAGTGATGGATCC	2340
Db	761	LeuAsnHisAlaProCysGileGlnLysAlaAlaGluLeuPheSerGlnTrpMetGluSer	780
QY	2341	AGTGAAAAATTAATATATACCAACAGATGCTTTTAAAGATTGTGTATCTCTGTGGGTCTCAG	2400
Db	781	SerGlyLysLeuAsnIleProThrAspValLeuLysIleValTySerValGlyAlaGln	800
QY	2401	ACAACAGCAGGATGAATACCTTTTGTAGCAATATGAACCTGTCAATGTCAAGTGTGAA	2460
Db	801	ThrThrAlaGlyTrpAsnTyLeuLeuGluGlnTyLeuLeuSerMetSerAlaGlu	820
QY	2461	CAAAACAAAATCTGTATGCTTGTCAACGACGACATCAGGAAGCTTACTGAAGTTA	2520
Db	821	GlnAsnLysIleLeuTyAlaLeuSerThrSerLysHisGlnGluLysLeuLysLeu	840
QY	2521	ATTGAACTAGGAATCGAAGGAAAGGTTATCAAGACACAGAACTTGGCAGCTCTCCTTCAT	2580
Db	841	IleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaAlaLeuHis	860
QY	2581	GGATTGCCAGCGTCCAAAGGGCAGCAACTAGCATGGGATTTTGTGAAGAGAAATGG	2640
Db	861	AlaIleAlaArgProLysGlyGlnGlnLeuAlaTrpAspPheValArgGluAsnTrp	880
QY	2641	ACCCATCTCTGAAAAATTTGACTTGGGCTCATATGACATAGCATCATCTCTGGC	2700
Db	881	ThrHisLeuLeuLysLysPheAspLeuGlySerTyAspIleArgMetIleIleSerGly	900
QY	2701	ACACAGCTCACTTTCTTCCAAGGATAAGTTGCAAGAGTGAAACTATTTTGAATCT	2760
Db	901	ThrThrAlaHisPheSerSerLysAspLysLeuGlnGluValLysLeuPheGluSer	920
QY	2761	CTTGAGGCTCAAGGATCATCTGGATATTTTCAAACTGTTCTGGAAACGATACCAA	2820
Db	921	LeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIleThrLys	940
QY	2821	AATATAAATGGCTGAGAGNATCTTCGACTCTGAGACTTGGCTTAATGTTAATCT	2880
Db	941	AsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeuMetValAsnThr	960
RESULT 2			
Q7Z5K1			
ID	Q7Z5K1	PRELIMINARY;	PRT; 960 AA.
AC	Q7Z5K1;		
DT	01-OCT-2003 (TrEMBLrel. 25, Created)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	Leukocyte-derived arginine aminopeptidase long form variant.		
GN	Name=l-rap;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
FN	[1]		
RP	SEQUENCE FROM N.A.		
RX	PubMed=12799365; DOI=10.1074/jbc.M305076200;		
RA	Tanlaka T., Hattori A., Maeda S., Nomura Y., Nakayama H.,		
RA	Mizutani S., Tsujimoto M.;		
RT	"Human leukocyte-derived arginine aminopeptidase:The third member of		
RT	the oxytocinase subfamily of aminopeptidases.";		
RL	J. Biol. Chem. 278:32275-32283(2003).		
DR	EMBL; AB109031; BAC78818.1; -;		
DR	MEDPES; M01.024; -;		
DR	GO; GO:0004177; F:aminopeptidase activity; IEA.		
DR	GO; GO:0004179; F:membrane alanyl aminopeptidase activity; IEA.		
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.		
DR	InterPro; IPR001930; Peptidase_M1.		
DR	InterPro; IPR006025; Pept_M_Zn_BS.		

DR	Pfam; PF01433; Peptidase_M1; 1.		
KW	PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.		
KW	AminoPeptidase.		
SQ	SEQUENCE 960 AA; 110447 MW; 27898FE2107E814E CRC64;		
Alignment Scores:			
Pred. No.:	0	Length:	960
Score:	5047.00	Matches:	959
Percent Similarity:	99.90%	Conservative:	0
Best Local Similarity:	99.90%	Mismatches:	1
Query Match:	99.70%	Indels:	0
DB:	2	Gaps:	0
US-10-039-073-3 (1-2883) x Q7Z5K1 (1-960)			
QY	1	ATGTTCCATTTCTTCTGCAATGGTTAAATTCACACAGAAAAACAATGTTTAAACATTACAGA	60
Db	1	MetPheHisSerSerAlaMetValAsnSerHisArgLysProMetPheAsnIleHisArg	20
QY	61	GGATTTTACTGCTTAAACAGGCATCTTCCCCCAATATGCATTTGTTCTCAGTTCTCAGTG	120
Db	21	GlyPheTyrcysLeuThrAlaIleLeuProGlnIleCysIleCysSerGlnPheSerVal	40
QY	121	CCATCTAGTTATCACTTCACTGAGGATCCTGGGGCTTTCCAGTAGCCACTAAATGGGAA	180
Db	41	ProSerSerTyHisPheThrGluAspProGlyAlaPheProValAlaThrAsnGlyGlu	60
QY	181	CGATTTCTTGGCAGGAGCTTAAGGCTCCCGAGTGTGCTCATTTCTCCATTATGACCTC	240
Db	61	ArgPheProIrpGlnGluLeuArgLeuProSerValValIleProLeuHisTyAspLeu	80
QY	241	TTTGTCCACCCCAATCTCACTCTCGAGCTTTGTTGTCATCTGAGAGATCGAAGTCTTG	300
Db	81	PheValHisProAsnLeuThrSerLeuAspPheValAlaSerGluLysIleGluValLeu	100
QY	301	GTGACGAACTGCTACCCAGTTTATCATCTTCACAGCAAGATCTTGAATCACCAGTCCC	360
Db	101	ValSerAsnAlaThrGlnPheIleIleLeuHisSerLysAspLeuGluIleIleAsnAla	120
QY	361	ACCTTTCAGTCAGAGGAAGATTCAAGATACATGAACCAAGCAAGAACTGAAAGTTTG	420
Db	121	ThrLeuGlnSerGluGluAspSerArgTyMetLysProGlyLysGluLeuLysValLeu	140
QY	421	AGTTACCTGCTCATGAACAAATTTGCACTGCTGTTCCAGAGAACTTACCCCTCACCTG	480
Db	141	SerTyProAlaHisGluGlnIleAlaLeuValProGluLysLeuThrProHisLeu	160
QY	481	AAATACTATGCTGCTATGGACTTCCAGCCAAGTTAGTGTATGCTTTGAAGGTTTAT	540
Db	161	LysTyTyValAlaAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTy	180
QY	541	AAAGACACATACAGAACTTTGGTGGTGAACCAAGAAATTTCTGCAGTAACAGATTTTGAG	600
Db	181	LysSerThrTyArgThrLeuGlyGlyGluThrArgIleLeuAlaValThrAspPheGlu	200
QY	601	CCAAACCAGCAGCATGGCTTCCCTTCTGTTGATGAACCGTTGTTCAAGCAACTTT	660
Db	201	ProThrGlnAlaArgMetAlaPheProCysPheAspGluProLeuPheLysAlaAsnPhe	220
QY	661	TCATCAAGATACGAAGAGAGAGAGCATATTTCACCTATCCACATGCCAAAGCTTAAG	720
Db	221	SerIleLysIleArgArgGluSerArgHisIleAlaLeuSerAsnMetProLysValLys	240
QY	721	ACAAATCAACTTGAAGGAGGTCTTTTGGAAAGATCACCTTTTGAACACTCTGTAATAAGT	780
Db	241	ThrIleGluLeuGluGlyLeuLeuGluAspHisPheGluThrThrValLysMetSer	260
QY	781	ACATACCTTGTAGCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACCTCATCA	840
Db	261	ThrTyLeuValAlaTyIleValCysAspPheHisSerLeuSerGlyPheThrSerSer	280
QY	841	GGGTCAAGGTGCTCATCTATGCATCCCGACAAACGGAATCAACACATATATGCTTTG	900

Db 281 GlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyrAlaLeu 300
Qy 901 CAGGCATCACTGAAGCTACTGTTGTTTATCAAAAGTACTTTGATATCTACTATCCACTC 960
Db 301 GlnAlaSerLeuLysLeuLeuAspPheTyrGlnLysTyrPheAspIleTyrTyrProLeu 320
Qy 961 TCCAAATCGGATTTAATGCTATTCCTGACTTTCGACCTCGAGCCATCGGAAATTTGGGC 1020
Db 321 SerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsnTrpGly 340
Qy 1021 CTCATTCATATAGGAGAGCTGCTCTCTTTTACCCCAAGACCTCTCTGCTCCGAT 1080
Db 341 LeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAlaSerAsp 360
Qy 1081 AAACGTGGGTCACAGAGTCATAGCCATCAAGCTGGCGACACAGTGGTTTGGCAACCTG 1140
Db 361 LysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeu 380
Qy 1141 GTCACAATGGAATGGTGGAAATGATATTTGGCTTAAGGAGGGTTTGCAAAATACATGGAA 1200
Db 381 ValThrMetGluTrpTrpAsnAspIleTrpLeuAsnGluGlyPheAlaLysTyrMetGlu 400
Qy 1201 CTTATCCCTGTTAATGCTACATATCCAGAGCTGCAATTTGATGACTATATTTTGAATGTG 1260
Db 401 LeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeuAsnVal 420
Qy 1261 TGTTTTCAAGTAATTACAAAGATTTCATGAAATTCATCCCGCCTATCTCCAAACACAGCG 1320
Db 421 CysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLysProAla 440
Qy 1321 GAAACCCCGACTCAAAATACAGGAAATGTTTCATGAAGTTTCCATATAACAGGGAGCTTGT 1380
Db 441 GluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGlyAlaCys 460
Qy 1381 ATTTTGATATGCTCAGGAATTTCTCGGTGAGAGAAATTCAGAAAGGAATAATTCAG 1440
Db 461 IleLeuAsnMetLeuLysAspPheLeuGlyGluLysPheGlnLysGlyIleGln 480
Qy 1441 TACTTAAAGAGTTTCAGCTATAGAAATGCTAAGAAATGATGACTTGTGGACAGTCTGTCA 1500
Db 481 TyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspLeuTrpSerSerLeuSer 500
Qy 1501 AATAGTTGTTTAAAGTGAATTTTACATCTCGTGGAGTTTGTCTATTCGGATCCCAAGATG 1560
Db 501 AsnSerCysLeuGluSerAspPheThrSerGlyValCysHisSerAspProLysMet 520
Qy 1561 ACAAGTAACATGCTCGCTTCTCGGGGAAATTCAGAGAGTCAAAAGAGATGATGACTACA 1620
Db 521 ThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGluValLysGluMetThrThr 540
Qy 1621 TGGACTCTCCAGAAAGAAATCCCTCTGCTGGTGTAAACAAGACGGGTCTCACTCCGA 1680
Db 541 TrpThrLeuGlnLysGlyIleProLeuLeuValLysGlnAspGlyCysSerLeuArg 560
Qy 1681 CTGCAACAGGAGCGCTTCTCCAGGGGTTTTCAGGAAGACCCCTGAAATCGAGGGCCCTG 1740
Db 561 LeuGlnGlnGluArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArgAlaLeu 580
Qy 1741 CAGAGAGGTACCTGTGGCATATCCCATTTGACCTTCCACGAGTTCCTTAATGTGATC 1800
Db 581 GlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerThrSerSerAsnValIle 600
Qy 1801 CACAGACACATCTAAATCAAGACAGATACTCTGGATCTACTGAAAGACAGTTGG 1860
Db 601 HisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThrSerTrp 620
Qy 1861 GTGAAATTTAATGTGGACTCAAAATGGTTACTACATCGTTCACTATGAGGGTCAATGGATGG 1920
Db 621 ValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHisGlyTrp 640
Qy 1921 GACCAACTCATTCACAGCTGAATCAGAACACACACTTCTCAGACCTTAAGGACAGAGTA 1980
Db 641 AspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAspArgVal 660

Qy 1981 GGTCTGATTCATGATGTGTTTTCAGCTAGTTGGTGCAGGGAGACTGACCCCTAGACAAAGCT 2040
Db 661 GlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAspLysAla 680
Qy 2041 CTTGACATGACTTACTACCTCCAAATGAAACAAGCAGCCCCGCACTTCTCGAAGGTCTG 2100
Db 681 LeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProAlaLeuLeuGluGlyLeu 700
Qy 2101 AGTTACTTCGAAATCGTTTACCACATGATGGACAGAAAGAAATATTTTCAGATATCTCGAA 2160
Db 701 SerTyrLeuGluSerPheTyrHisMetMetAspArgArgAsnIleSerAspIleSerGlu 720
Qy 2161 AACCTCAAGCGTTTACCTTCTTCAGTATTTTAAAGCAGTGAATTCACAGGCAAAAGCTCGAGT 2220
Db 721 AsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSerTrpSer 740
Qy 2221 GACAAAGGCTCAGTCTGGACAGGATGCTCCGCTCGGCTCTCTTGAAGCTGGCTGTGAC 2280
Db 741 AspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAlaCysAsp 760
Qy 2281 CTGAACCATGCTCCTTGCATCCAGAAAGCTGCTGAACCTCTCTCCAGTGGATGGAATCC 2340
Db 761 LeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMetGluSer 780
Qy 2341 AGTGGAAAAATTAATATACCAACAGATGTTTAAAGATTGTGTATTCTGTGGGTGCTCAG 2400
Db 781 SerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrSerValGlyAlaGln 800
Qy 2401 ACAACAGCAGGATGGAATTAACCTTTTAGAGCAATATGAATCTGTCATGTCAGTCTGAA 2460
Db 801 ThrThrAlaGlyTrpAsnTyrLeuLeuGluGlnTyrGluLeuSerMetSerSerAlaGlu 820
Qy 2461 CAAAACAAAATCTGTATGCTTGTCAACAGCACAGCATCAGGAAAGTTACTGGAAGTTA 2520
Db 821 GlnAsnLysIleLeuTyrAlaLeuSerThrSerLysHisGlnGlnLysLeuLeuLysLeu 840
Qy 2521 ATTGAACCTAGGAATGGAAGAAAGGTTATCAAGACACAGAACTTGGCAGCTCTCTTCAT 2580
Db 841 IleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaLeuLeuHis 860
Qy 2581 GCGATTGCGACAGCTCCAAAGGGCAGCAACTAGCATGGGATTTTGTAAAGAGAAATGG 2640
Db 861 AlaIleAlaArgArgProLysGlyGlnGlnLeuAlaTrpAspPheValArgGluAsnTrp 880
Qy 2641 ACCCATCTTCTGAAAAATTTGACTTGGCTCATATGACATAAGGATGATCATCTCTGCC 2700
Db 881 ThrHisLeuLeuLysLysPheAspLeuGlySerTyrAspIleArgMetIleIleSerGly 900
Qy 2701 ACAACAGCTCACCTTTTCTTCCAAAGGATAAGTTGCAAGAGGTGAAACTATTTTGAATCT 2760
Db 901 ThrThrAlaHisPheSerSerLysAspLysLeuGlnGluValLysLeuPhePheGluSer 920
Qy 2761 CTTGAGGCTCAAGGATCACATCTGGATATTTTCAAACTGTTCTGTAAGACGATAACAA 2820
Db 921 LeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIleThrLys 940
Qy 2821 AATATAAATGCTGAGAGAAATCTTCGACTCTGAGGACTTGGCTAATGTTAATACT 2880
Db 941 AsnIleLysTrpLeuGlnLysAsnLeuProThrLeuArgThrTrpLeuMetValAsnThr 960

RESULT 3
Q6P179 PRELIMINARY; PRT; 915 AA.
ID Q6P179
AC Q6P179; (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE LRAP protein.
GN Name=LRAP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.


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QY 1501 AATAGTTGTTAGAAAAGTGAATTTTACATCTGGTGGAGTTGTGTCAATCCGGATCCCAAGATG 1560
DB 456 AsnSerCysLeuGluSerAspPheThrSerGlyGlyValCysHisSerAspProLysMet 475
QY 1561 ACAAGTAACTGTCGCTTCTTCGGGGGAAATATGACAGAGTCAAAAGAGATGATGACTACA 1620
DB 476 ThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGluValLysGluMetMetThrThr 495
QY 1621 TGGACTCTCCAGAAAGAAATCCCTCTGCTGGTGTAAACAAGACGGGTCTTCACTCCGA 1680
DB 496 TrpThrLeuGlnLysGlyIleProLeuLeuValLysGlnAspGlyCysSerLeuArg 515
QY 1681 CTGCAACAGGAGCGCTTCTCCAGGGGTTTCCAGGAAGACCTGAAATCGAGGGCCCTG 1740
DB 516 LeuGlnGlnGluArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArgAlaLeu 535
QY 1741 CAGGAGAGTACCTGTGGCATATCCCAATGACCTTCTCCACGAGTCTTCTTAATGTGATC 1800
DB 536 GlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerThrSerSerAsnValIle 555
QY 1801 CACAGACACATCTCAAAATCAAGACAGACTCTGATCTACTGAAAGACCACTGG 1860
DB 556 HisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThrSerTrp 575
QY 1861 GTGAAATTTAATGTGGACTCAAAATGGTTACTACATCGTTCACTATGAGGTCATGGATGG 1920
DB 576 ValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHisGlyTrp 595
QY 1921 GACCAACTCATTTACAGCTGAATCAGAACACACACTTCTCAGACTTAAGACAGAGTA 1980
DB 596 AspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAspArgVal 615
QY 1981 GGTCTGATTCATGATGTGTTTCAGCTAGTTGGTCAGGGAGACTGACCCCTAGACNAAGCT 2040
DB 616 GlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAspLysAla 635
QY 2041 CTTGACATGACTTACTACCTCCAACTCAACAGACAGCCCGCACCTTCTCGAAGGCTG 2100
DB 636 LeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProAlaLeuLeuGluGlyLeu 655
QY 2101 AGTTACTTGGAACTGTTTTACCACATGATGACAGAAAGGAATATTTCCAGATATCTCTGAA 2160
DB 656 SerTyrLeuGluSerPheTyrHisMetMetAspArgArgAsnIleSerAspIleSerGlu 675
QY 2161 AACCTCAAGCTTACCTTCTCAGTATTTTAAGCCAGTATTCACAGGCGAAAGCTCGAGT 2220
DB 676 AsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSerTrpSer 695
QY 2221 GACAAGGGCTCAGTCTGGGACAGGATGCTCCGCTCGGCTCTCTTGAAGCTGGCTGTGAC 2280
DB 696 AspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAlaCysAsp 715
QY 2281 CTGAACCATGCTCTTCATCCAGAAAAGCTGCTGAATCTTCTCCAGTGGATCGAATCC 2340
DB 716 LeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMetGluSer 735
QY 2341 AGTGGAAATTAATATACCAACAGATGTTTAAAGATTCTGTATCTGTGGTGTCTCAG 2400
DB 736 SerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrSerValGlyAlaGln 755
QY 2401 ACAACAGCAGGATGGAATTTACCTTTTATAGACAATATGAATGTCAATGTCAAGTCTGAA 2460
DB 756 ThrThrAlaGlyTrpAsnTyrLeuLeuGluGlnTyrGluLeuSerMetSerSerAlaGlu 775
QY 2461 CAAACAAAATTCGTATGCTTTCTCAACGACGACGATCATCAGGAAAGATTTACTGAATTA 2520
DB 776 GlnAsnLysIleLeuTyrAlaLeuSerThrSerLysHisGlnGluLysLeuLeuLysLeu 795
QY 2521 ATTGAACCTAGGAATGGAAGGAAGTTATCAACACAGAACTGGCAGCTCTCCTTCAT 2580
DB 796 IleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaAlaLeuLeuHis 815
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QY 2581 GCGATTGCCAGACGTCCAAAGGGCAGCAACTAGCATGGGATTTTGTAAAGAGAAAATTGG 2640
DB 816 AlaIleAlaArgArgProLysGlyGlnLeuAlaTrpAspPheValArgGluAsnTrp 835
QY 2641 ACCATCTTCTGAAAAAATTTGACTTGGGCTCATATGACATAAGGATGATCATCTCTGGC 2700
DB 836 ThrHisLeuLeuLysLysPheAspLeuGlySerTyrAspIleArgMetIleIleSerGly 855
QY 2701 ACAACAGCTCACCTTTCTTCCAGAGGATAAGTTCGAAGAGGTGAAACTATTTTGAATCT 2760
DB 856 ThrThrAlaHisPheSerLysAspLysLeuGlnGluValLysLeuPhePheGluSer 875
QY 2761 CTTGAGGCTCAAGGATCACATCTGGATATTTTCAAACTGTTCTGGAAACGATAACCAA 2820
DB 876 LeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIleThrLys 895
QY 2821 AATATAAATGGCTGGAGAGAAATCTTCGACTCTGAGACTTGGCTAATGGTTAATACT 2880
DB 896 AsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeuMetValAsnThr 915
RESULT 4
RSD32 Q8TD32 PRELIMINARY; PRT; 532 AA.
ID AC Q8TD32;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Leukocyte-derived arginine aminopeptidase short form.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21374137; PubMed=11481040;
RA Hattori A., Matsumoto K., Mizutani S., Teujimoto M.;
RA Mizutani S., Teujimoto M.;
RT "Human leukocyte-derived arginine aminopeptidase: The third member of
RT the oxytocinase subfamily of aminopeptidases.";
RL J. Biol. Chem. 0:0-0(2003).
DR EMBL; AY028805; AAK37776.1; -.
DR MEROPS; M01.024; -.
DR GO; GO:0004177; F:aminopeptidase activity; IEA.
DR GO; GO:0004179; F:membrane alanyl aminopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001930; Peptidase_M1.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF01433; Peptidase_M1; 1.
DR PRINTS; PR00756; ALADIPASE.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Aminopeptidase.
SQ SEQUENCE 532 AA; 60937 MW; DA0F4F00AD9E0D71 CRC64;
Alignment Scores:
Pred. No.: 2,19e-178 Length: 532
Score: 2768.00 Matches: 523
Percent Similarity: 99.81% Conservative: 1
Best Local Similarity: 99.62% Mismatches: 1
Query Match: 54.68% Indels: 0
DB: 2 Gaps: 0
US-10-039-073-3 (1-2883) x Q8TD32 (1-532)
QY 1 ATGTTCCATCTTCTCAATGGTTAATTCACACAGAAAACCAATGTTTAACATTACAGA 60
DB 1 MetPheHisSerSerAlaMetValAsnSerHisArgLysProMetPheAsnIleHisArg 20
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QY 61 GGATTTTACTGCTTAACAGCCATCTTGCCCAAAATATGATTTGTTCTCAGTTCTCAGTG 120
 Db 21 GlyPheTyrCysLeuThrAlaIleLeuProGlnIleCysIleCysSerGlnPheSerVal 40
 QY 121 CCATCTAGTTATCACTTCACTGAGGATCTCTGGGGCTTTCCCAAGTAGCCACCAATAGGGAA 180
 Db 41 ProSerSerTyrHisPheThrGluAspProGlyAlaPheProValAlaThrAsnGlyGlu 60
 QY 181 CGATTTCCCTGGCAGGAGCTAAGGCTCCCGCTGAGTGGTCAATTCCTCTCCATATGACCTC 240
 Db 61 ArgPheProTropGlnGluLeuArgLeuProSerValValIleProLeuHisTyrAspLeu 80
 QY 241 TTTGTCCACCCCAATCTCACCCTCTGACCTTTGTTGTCATCTGAGAAATGCAAGTCTTG 300
 Db 81 PheValHisProAsnLeuThrSerLeuAspPheValAlaSerGluLysIleGluValLeu 100
 QY 301 GTCAGCAATGCTPACCCAGTTATCATCTTGCACACCAAGATCTTGAATCAGCAATGCC 360
 Db 101 ValSerAsnAlaThrGlnPheIleIleLeuHisSerLysAspLeuGluIleThrAsnAla 120
 QY 361 ACCCTTCAGTCAGAGAAAGATTCAAGATACATGAACACCAAGAAAGAACTGAAAGTTTG 420
 Db 121 ThrLeuGlnSerGluAspSerArgTyrMetLysProGlyLysGluLeuLysValLeu 140
 QY 421 AGTTACCTGCTCATGAACAAATTCGACTGCTGGTTCCAGAGAACTTACGCTCACCTG 480
 Db 141 SerTyrProAlaHisGluGlnIleAlaLeuLeuValProGluLysLeuThrProHisLeu 160
 QY 481 AAATACTATGGCTATGGACTTCAGACTTCCAGCCAGTTAGGTGATGGCTTGAAGGTTTTAT 540
 Db 161 LysTyrTyrValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTyr 180
 QY 541 AAAACACATACAGAACTCTGGTGGTCAACAGAAATCTTGCAGTAACAGATTTTCAG 600
 Db 181 LysSerThrTyrArgThrLeuGlyGlyGluThrArgIleLeuAlaValThrAspPheGlu 200
 QY 601 CCAACCCAGCCAGCATGGCTTTCCTTTCCTTTGATGAACCGTTGTTCAAGCCCACTTT 660
 Db 201 ProThrGlnAlaArgMetAlaPheProCysPheAspGluProLeuPheLysAlaAsnPhe 220
 QY 661 TCNATCAGATACGAGAGAGCAGGATGATTCACACTTCCACATCCCAAGGTTAAG 720
 Db 221 SerIleLysIleArgArgGluSerArgHisIleAlaLeuSerAsnMetProLysValLys 240
 QY 721 ACAATTGAACCTGAAGGAGGCTTTTGAAGATCACTTTGAACTACTGTAAATAGT 780
 Db 241 ThrIleGluLeuGluGlyGlyLeuLeuGluAspHisPheGluThrValLysMetSer 260
 QY 781 ACATACCTTGTAGCCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACATTCATCA 840
 Db 261 ThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThrSerSer 280
 QY 841 GGGGTCAAGGTGTCATCTATGATCCCGACAGAAACGGAATCAACACATATGCTTTG 900
 Db 281 GlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyrAlaLeu 300
 QY 901 CAGGCATCACTGAAGCTACTGATTTTATGAAAGTACTTTGATATCTACTATCCACTC 960
 Db 301 GlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyrProLeu 320
 QY 961 TCCAACTGGATTAATTTGCTATTCTCCTGACTTTTGCACTGGAGCCATCGAAAATTTGGGC 1020
 Db 321 SerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsnTrpGly 340
 QY 1021 CTCATTACATATAGGAGACGTCACTGCTTTTGTACCCCAAGACCTCTTCTGCTTCGAT 1080
 Db 341 LeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAlaSerAsp 360
 QY 1081 AAACCTGGGTCAACAGATCATAGCCCATGACTGGCGCCAGTGGTTTGGCACTTG 1140
 Db 361 LysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeu 380

QY 1141 GTCAATGGAATGCTGAATGATATTGCTTAAGGAGGGTTTTTCCAAAATACATGAA 1200
 Db 381 ValThrMetGluTrpTrpAsnAspIleTrpLeuAsnGluGlyPheAlaLysTyrMetGlu 400
 QY 1201 CTTATCGCTGTTAATGCTACATATCCAGAGCTGCAATTTGATGACTATTTTGAATGTG 1260
 Db 401 LeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeuAsnVal 420
 QY 1261 TGTTTTGAAGTAATTACAAAAGATTCAATTGATTCATCCGCCCTTATCTCCAAACCAAGC 1320
 Db 421 CysPheGluValIleThrLysAspSerLeuAsnSerArgProIleSerLysProAla 440
 QY 1321 GAAACCCCGACTCAATACAGAAATGTTTCATGAGTTTCCATTAACAAAGGAGCTTGT 1380
 Db 441 GluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGlyAlaCys 460
 QY 1381 ATTTTGAATATGCTCAAGGATTTTCTGGTGGAGGAAATTCAGAAAGGAATAATTTCAG 1440
 Db 461 IleLeuAsnMetLeuLysAspPheLeuGlyGluGluLysPheGlnLysGlyIleIleGln 480
 QY 1441 TACTTAAAGAAAGTTTCAAGTATAGAAATGCTAAGAAATGATGATCTTGTGGAGCAGTCTGTC 1500
 Db 481 TyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspAspLeuTrpSerSerLeuSer 500
 QY 1501 AATAGTTGTTTAAAGAGTATTTTACATCTCGTGGAGTTTGTCTTCGATCCCAAGATG 1560
 Db 501 AsnSerCysLeuGluSerAspPheThrSerGlyGlyValCysHisSerAspProLysMet 520
 QY 1561 ACAAGTAACATGCTC 1575
 Db 521 ThrSerAsnMetVal 525

RESULT 5
 ART1 HUMAN
 ID ART1_HUMAN STANDARD; PRT; 929 AA.
 AC Q9NZ08; Q60278; Q8NEL4; Q8TAD0; Q9UHF8; Q9UKY2;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Adipocyte-derived leucine aminopeptidase precursor (EC 3.4.11.-) (A-LAP) (ARNS-1) (aminopeptidase PILS) (Puromycin-insensitive leucyl-specific aminopeptidase) (PILS-AP) (Type 1 tumor necrosis factor receptor shedding aminopeptidase regulator).
 DE Name=ARNS1; Synonyms=APPILS, KIAA0525;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=White adipose tissue;
 RX MEDLINE=99238715; PubMed=10220586;
 RA Hattori A., Matsumoto H., Mizutani S., Tsujimoto M.;
 RT "Molecular cloning of adipocyte-derived leucine aminopeptidase highly related to placental leucine aminopeptidase/oxytocinase.";
 RL J. Biochem. 125:931-938(1999).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Leukocyte;
 RX MEDLINE=21374137; PubMed=11481040;
 RA Hattori A., Matsumoto K., Mizutani S., Tsujimoto M.;
 RT "Genomic organization of the human adipocyte-derived leucine aminopeptidase gene and its relationship to the placental leucine aminopeptidase/oxytocinase gene.";
 RL J. Biochem. 130:235-241(2001).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC Schomburg L.;
 RT "Molecular characterization of human aminopeptidase PILS.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Cui X., Alsaaty S., Lawrence M., Combs C.A., Rouhani F.N.,

RA Levine S.J.;
RT "Identification of an aminopeptidase regulator of type I tumor
RT necrosis factor receptor shedding";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND REVISION TO 718.
RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
RA Nomura N., Ohara O.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RP [6]
RP SEQUENCE OF 62-929 FROM N.A. (ISOFORM 2).
RC TISSUE=Brain;
RX MEDLINE=38290545; PubMed=9628581;
RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
RA Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. IX.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro.";
RL DNA Res. 5:31-39(1998).
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield V.S.N., Krywinski M.I., Skalska U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RP SEQUENCE OF 25-37, AND CHARACTERIZATION.
RX MEDLINE=20512052; PubMed=11056387;
RA Hattori A., Kitatani K., Matsumoto H., Miyazawa S., Rogi T.,
RA Tsuruoka N., Mizutani S., Natori Y., Tsujimoto M.;
RT "Characterization of recombinant human adipocyte-derived leucine
RT aminopeptidase expressed in Chinese hamster ovary cells.";
RL J. Biochem. 128:755-762(2000).
CC -!- FUNCTION: May play a role in the inactivation of peptide hormones.
CC May be involved in the regulation of blood pressure through the
CC inactivation of angiotensin II and/or the generation of bradykinin
CC in the kidney.
CC -!- CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Xaa-|-
CC Xbb-, in which Xaa is preferably Leu, but may be other amino acids
CC including Met, Cys and Phe.
CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing, Named isoforms=2;
CC Name=1;
CC IsoId=Q9NZ08-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9NZ08-2; Sequence=VSP_005450;
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- PTM: N-glycosylated.
CC -!- SIMILARITY: Belongs to the peptidase M1 family.

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF106037; AAF07395.1; ALT_INIT.
DR EMBL; AY028806; AAK37777.1; ALT_INIT.
DR EMBL; AY028807; AAK37778.1; ALT_INIT.
DR EMBL; AF183569; AAF20384.1; ALT_INIT.
DR EMBL; AF222340; AAF34664.1; ALT_INIT.
DR EMBL; AB011097; BAA25451.2; ALT_INIT.
DR EMBL; BC030775; AAH30775.1; ALT_INIT.
DR IntAct; Q9NZ08; -.
DR MEROPS; M01_018; -.
DR H-InvDB; HIX0005052; -.
DR MiM; 606832; -.
DR GO; GO:0005829; C:cytosol; NAS.
DR GO; GO:0005783; C:endoplasmic reticulum; NAS.
DR GO; GO:000576; C:extracellular; IDA.
DR GO; GO:0016021; C:integral to membrane; NAS.
DR GO; GO:0005138; F:interleukin-6 receptor binding; IPI.
DR GO; GO:0004178; F:leucyl aminopeptidase activity; IDA.
DR GO; GO:0004239; F:methionyl aminopeptidase activity; NAS.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IPI.
DR GO; GO:0008270; F:zinc ion binding; NAS.
DR GO; GO:0045444; P:adipocyte differentiation; NAS.
DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . .; NAS.
DR GO; GO:0006509; P:membrane protein ectodomain proteolysis; IDA.
DR GO; GO:0050714; P:positive regulation of protein secretion; IDA.
DR GO; GO:0008217; P:regulation of blood pressure; NAS.
DR GO; GO:0045088; P:regulation of innate immune response; NAS.
DR InterPro; IPR006025; Rept_M_Zn_BS.
DR InterPro; IPR001930; Peptidase_M1.
DR Pfam; PF01433; Peptidase_M1; 1.
DR PRINTS; PS00756; ALADIPITASE.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR Alternative splicing; Aminopeptidase; Direct protein sequencing;
KW Glycoprotein; Hydrolase; Metalloprotease; Polymorphism; Protease;
KW Signal; Zinc. 1 24
FT CHAIN 25 929 Adipocyte-derived leucine aminopeptidase.
FT METAL 341 341 Zinc (catalytic) (By similarity).
FT ACT_SITE 342 342 By similarity.
FT METAL 345 345 Zinc (catalytic) (By similarity).
FT METAL 464 464 Zinc (catalytic) (By similarity).
FT ACT_SITE 426 426 Proton donor (Potential).
FT CARBOHYD 58 58 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 142 142 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 402 402 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 748 748 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 889 889 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 928 929 RM -> HDPEADATG (in isoform 2).
FT FTId=VSP_005450.
FT VARIANT 115 115 R -> P (in dBSNP:26653).
FT FTId=VAR_012779.
FT VARIANT 264 264 I -> M (in dBSNP:26618).
FT FTId=VAR_012780.
FT VARIANT 334 334 G -> D (in dBSNP:27895).
FT FTId=VAR_012781.
FT VARIANT 337 337 M -> V (in dBSNP:2287987).
FT FTId=VAR_012782.
FT VARIANT 516 516 K -> R (in dBSNP:27434).
FT FTId=VAR_012783.
FT VARIANT 718 718 Q -> E (in dBSNP:27044).
FT FTId=VAR_012784.
FT CONFLICT 502 502 G -> R (in Ref. 3).
FT CONFLICT 563 563 D -> N (in Ref. 2, 5 and 6).
FT CONFLICT 713 713 R -> Q (in Ref. 2, 5 and 6).
SQ SEQUENCE 929 AA; 105846 MW; 75C6AD58D0D70D51 CRC64;
Alignment Scores: 2.39e-161 Length: 929
Pred. No.:

Db	666	AsnGluLeuIleProMetTyrLysLeuMetGluLysArgAspMetAsnGluValGluThr	685
Qy	2161	AACTCAAGCGTTACCTTCTTCAGTATTTAAAGCCAGTGAATGACAGCAAGCTGGAGT	2220
Db	686	GlnPheLysAlaPheLeuIleArgLeuLeuArgAspLeuIleAspLysGlnThrTrpThr	705
Qy	2221	GACAAGGGCTCAGTCTGGACAGAGATCTCGCTCGGCTCTCTTGAAGCTGGCTGTGAC	2280
Db	706	AspGluGlySerValSerGluArgMetLeuArgSerGlnLeuLeuLeuLeuAlaCysVal	725
Qy	2281	CTGAACCATGCTCTTCATCCAGAAAGCTGCTGAACTCTTCTCCAGTGGATGGAATCC	2340
Db	726	HisAsnTyrGlnProCysValGlnArgAlaGluGlyTyrPheArgLysTrpLysGluSer	745
Qy	2341	AGTGGAAAAATTAAATATATACCAACAGATGTTTTAAAGATTGTGTATTCTGTGGGTGCTCAG	2400
Db	746	AsnGlyAsnLeuSerLeuProValAspValThrLeuAlaValPheAlaValGlyAlaGln	765
Qy	2401	ACAACAGCAGATGGAAATTACCTTTTAGACGAATATGCAATGTGCAAGTGTCTGAA	2460
Db	766	SerThrGluGlyTrpAspPheLeuTyrSerLysTyrGlnPheSerLeuSerSerThrGlu	785
Qy	2461	CAAAACAAAATTCGTATGCTTTGTCAACGAGCAAGCATCAGGAAAAAGTTACTGAAGTTA	2520
Db	786	LysSerGlnIleGluPheAlaLeuCysArgThrGlnAsnLysGluLysGlnTrpLeu	805
Qy	2521	ATTGAACTAGGAATTGGAAGAAAGTTATCAAGACACAGAACTTGGCAGCTCTCTTCAT	2580
Db	806	LeuAspGluSerPheLysGlyAspLysIleLysThrGlnGluPheProGlnIleLeuThr	825
Qy	2581	GCGATTGCCAGACTCCAAAGGGCGACGAATAGCATGGGATTTGTGAAGAAAAATTGG	2640
Db	826	LeuIleGlyArgAsnProValGlyTyrProLeuAlaTrpGlnPheLeuArgLysAsnTrp	845
Qy	2641	ACCATCTTCTGAAAAAATTGACTCTGGGCTCATATGACATAGGATGATCATCTCTGGC	2700
Db	846	AsnLysLeuValGlnLysPheGluLeuGlySerSerIleAlaHisMetValMetGly	865
Qy	2701	ACAACAGCTCAGCTTTCTTCCAAGATAAGTTGCAAGAGGTGAAACTATTATTTTGAATCT	2760
Db	866	ThrThrAsnGlnPheSerThrArgThrArgLeuGluGluValLysGlyPhePheSerSer	885
Qy	2761	CTTGAGGCTCAAGATCACATCTGGATATTTTCAAACGTCTTCGGAACGATAACCAA	2820
Db	886	LeuLysGluAsnGlySerGlnLeuArgCysValGlnGlnThrIleGluThrIleGluGlu	905
Qy	2821	AATATAAATGGCTGGAGAGAACTTCCGACTCTGAGGACTTGGCTA	2868
Db	906	AsnIleGlyTrpMetAspLysAsnPheAspLysIleArgValTrpLeu	921
RESULT	6		
ID	Q6UWY6	PRELIMINARY;	PRT: 941 AA.
AC	Q6UWY6;		
DT	05-JUL-2004	(TrEMBLrel. 27, Created)	
DT	05-JUL-2004	(TrEMBLrel. 27, Last sequence update)	
DE	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)	
DE	ARTS-1.		
GN	ORFNames=JNQ584;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;		
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,		
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,		
RA	Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,		
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,		
RA	Leung L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,		
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,		
RA	Vandlen R., Watanabe C., Wiand D., Woods K., Xin M.H., Yansura D.,		

RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA	Godowski P.;
RT	"The secreted protein discovery initiative (SPDI), a large-scale
RT	effort to identify novel human secreted and transmembrane proteins: a
RT	bioinformatics assessment.";
RL	Genome Res. 13:2265-2270(2003).
DR	EWBL; AY358590; AAQ88953.1; ..
DR	GO: GO:0004179; F:membrane alanyl aminopeptidase activity; IEA.
DR	GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR	InterPro; IPR001930; Peptidase M1.
DR	InterPro; IPR006025; Pept M.Zn.BS.
DR	Pfam; PF01433; Peptidase_M1_1.
DR	PRINTS; PR00756; ALADIP7ASE.
DR	PROSITE; PS00142; ZINC PROTEASE; UNKNOWN_1.
SO	SEQUENCE 941 AA; 107143 MW; C3DC8ACFCFB5BBCC CRC64;

Alignment Scores:		4.46e-161	Length:	941
Pred. No.:	Score:	2512.50	Matches:	477
	Percent Similarity:	69.34%	Conservative:	172
	Best Local Similarity:	50.96%	Mismatches:	268
	Query Match:	49.63%	Indels:	19
DB:		2	Gaps:	7

US-10-039-073-3 (1-2883) X Q6UWY6 (1-941)	
Qy	67 TACTGCTTAACGCCATCTTGCCCAAAATAGCATTTGTTCTCAGTCTTCAGTCCCATCT 126
Db	::: ::: ::: : :::
Qy	15 PheLeuLeuSerSerLeuLeuAlaLeuThrVal-----SerThrProSer 30
Qy	127 AGTTATCACTTCACTGAGGATCTCGGGCTTCCAGTAGCCACTAATGGGGAACGATTT 186
Db	
Qy	31 TrpCysGlnSerThrGlu-----AlaSerProLysArgSerAspGlyThrProPhe 47
Qy	187 CCTTGGCAGAGCTAAGGCTCCCGAGTGTGGTCACTCTCCATTATGACCTCTTTGTC 246
Db	:::::
Qy	48 ProTrpAsnLysIleArgLeuProGluTyrrValleProValHisItyrAspLeuLeu 67
Qy	247 CACCCCAATCTCACCTCTCTGGACTTTGTTGGCATCTGAGAGAGATCGAAGTCTTGGTCAGC 306
Db	:::::
Qy	68 HisAlaAsnLeuThrLeuThrPheThrGlyThrThrLysValGluIleThrAlaSer 87
Qy	307 AATGCTACCCAGTTTATCATCTTGGCAGCAAAAGATCTTGAATTCAGAAATGCCACCTT 366
Db	:::::
Qy	88 GlnProThrSerThrIleLeuHisSerHisHisLeuGlnIleSerArgAlaThrLeu 107
Qy	367 CAGTCAGGAGGATTCACATACATCAACACGAGGAAAGAACTGAAAGTTTGGAGTTAC 426
Db	:::::
Qy	108 ArgLysGlyAlaGlyGluArgLeuSerGlu-----GluProLeuGlnValLeuGluHis 125
Qy	427 CCTGCTCATGAACAAATTTGACTCTGCTGGTTCAGAGAAACTTACGCCTCACCTGAATAC 486
Db	:::::
Qy	126 ProProGlnGluGlnIleAlaLeuLeuAlaProGluProLeuValGlyLeuProTyr 145
Qy	487 TATGTGCTATGACTTCCAAAGCAAGTATAGGTGATGGCTTTGAAGGGTTTTATAAAGC 546
Db	:::::
Qy	146 ThrValValIleHisItyrAlaGlyAsnLeuSerGluThrPheHisGlyPheTyrLysSer 165
Qy	547 ACATACAGACTCTTGGTGTGTGAACCAAGATTTCTTGCAGTACAGATTTTGGCCCAACC 606
Db	:::::
Qy	166 ThrTyrArgThrLysGluGlyGluLeuArgIleLeuAlaSerThrGlnPheGluProThr 185
Qy	607 CAGCAGCATGGCTTTCCCTTGTGATGAACCGTTGTTCAAAGCAACTTTTCAATC 666
Db	:::::
Qy	186 AlaAlaArgMetAlaPheProCysPheAspGluProAlaPheLysAlaSerPheSerIle 205
Qy	667 AAGATACGAGAGAGACGACCATATTCGACTATTCACCAATGCCAAAGGTTTAGACAATT 726
Db	:::::
Qy	206 LysIleArgArgGluProArgHisLeuAlaIleSerAsnMetProLeuValLysSerVal 225
Qy	727 GAACCTGAAGGAGGTCTTTGGAGATCATCTTTGAACTACTCTTAAATAGGTACATAC 786
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Qy	226 ThrValAlaGluGlyLeuIleGluAspHisPheAspValThrValLysMetSerThrTyr 245

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QY 787 CTTGTAGCCTACATAGTTTGGATTTCCTCACTCTCTGAGTGGCTTCACTTCAATCAGGGTC 846
Db 246 LeuValAlaPheIleSerAspPheGluSerValSerLysIleThrLysSerGlyVal 265
QY 847 AAGGTGTCATCTATGATCCCGACAGAAACCGAATCAACACATATTATGCTTTGCAGCA 906
Db 266 LysValSerValAlaValProAspLysIleAsnGlnAlaAspTyrAlaLeuAspAla 285
QY 907 TCACCTGAAGCTACTGATTTTTATGAAAGTACTTTTGATATCTATATCCACTCTCCAAA 966
Db 286 AlaValThrLeuLeuGluPheTyrGluAspTyrPheSerIleProTyrProLeuProlys 305
QY 967 CTGGATTAAATGCTATTCCTGACTTTGCACCTGGAGCATGGAAAAATGGGGGCTCAATT 1026
Db 306 GlnAspLeuAlaAlaIleProAspPheGlnSerGlyAlaMetGluAsnTrpGlyLeuThr 325
QY 1027 ACATATAGGGAGAGCTCACTGCTTTTTCACCCCAAGAGCTCTTCTGCTCCGATTAACCTG 1086
Db 326 ThrTyrArgGluSerAlaLeuLeuPheAspAlaGluLysSerSerAlaSerSerLysLeu 345
QY 1087 TGGGTCAACAGAGTCATAGCCCATGAACCTGGCGCACCAAGTGGTTTGGCAACCTGTCACA 1146
Db 346 GlyIleThrValThrValAlaAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeuValThr 365
QY 1147 ATGGAATCGTGAATGATATTGGCTTAAGGAGGTTTTGCAAAATACATGAACTTATC 1206
Db 366 MetGluTrpTrpAsnAspLeuTrpLeuAsnGluGlyPheAlaLysPheMetGluPheVal 385
QY 1207 GCTGTTAATGTACATATCCAGAGCTGCAATTTGATGACTATTTTTGAATGTGTGTTTT 1266
Db 386 SerValSerValThrHisProGluLeuLysValGlyAspTyrPhePheGlyLysCysPhe 405
QY 1267 GAAAGTAATTACAAAGATTTCATTGAATTCATCCCGCCCTCTCTCCAAACACAGCGAAACC 1326
Db 406 AspAlaMetGluValAspAlaLeuAsnSerSerHisProValSerThrProValGluAsn 425
QY 1327 CCGACTCAAAATACAGAAATGTTTGATGAAGTTTCTATATAAAGGGAGCTTGATTTTG 1386
Db 426 ProAlaGlnIleArgGluMetPheAspAspValSerTyrAspLysGlyAlaCysIleLeu 445
QY 1387 AATATGCTCAAGGATTTCTGGTCAGGAGAAATCCAGAAGGAAATTAATTCAGTACTTA 1446
Db 446 AsnMetLeuArgGluTyrLeuSerAlaAspAlaPheLysSerGlyIleValGlnTyrLeu 465
QY 1447 AAGAAGTTTCAGCTATAGAAATGCTAAGAAATGATGACTTGTGGAGCAGTCTGCAAAAGT 1506
Db 466 GlnLysHisSerTyrLysAsnThrLysAsnGluAspLeuTrpAspSerMetAlaSerIle 485
QY 1507 TGTTTAGAAAGTGATTTTACATCTGGT-----GGAGTTTGTCTATTCGGATCCCAAGATG 1560
Db 486 Cys---ProThrAspGlyValLysGlyMetAspGlyPheCys---SerArgSerGlnHis 503
QY 1561 ACAAGTAACATGCTCGCCTTCTGGGGGAAATGACAGAGGTCAAGAGATGATGACTACA 1620
Db 504 SerSerSerSerHisThrPheHisGlnGluGlyValAspValLysThrMetMetAsnThr 523
QY 1621 TGGACTCTCCAGAAGGAATCCCTGCTGGTGTAAACAAGACGGGTGTTCTACTCGA 1680
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QY 1681 CTGCAACAGGAGCGCTTCTCCAGGGGGTTTTTCCAGGAAGACCCCTGAAATGGAGGGCCCTG 1740
Db 544 MetLysGlnGluHisTyrMetLysGly-----SerAspGlyAlaPro 557
QY 1741 CAGGAGAGGTACCTGTGCATATCCATGACTTCCAGCTTCTTCTTAATGTGATC 1800
Db 558 AspThrGlyTyrLeuTrpHisValProLeuThrPheIleThrSerLysSerAsnMetVal 577
QY 1801 CACAGACATTTCTAAAAATCAAGACAGATCTCTGGATCTACCTGAAAGACCAAGTTGG 1860
Db 578 HisArgPheLeuLeuLysThrLysThrAspValLeuIleLeuProGluGluValGluTrp 597
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QY 1861 GTGAAATTTAATGTGGACTCAATGGTTACTTACATCGTTCACTATGAGGTCATGGATGG 1920
Db 598 IleLysPheAsnValGlyMetAsnGlyTyrTyrIleValHisTyrGluAspAspGlyTrp 617
QY 1921 GACCAACTCATTTACACAGCTGAATCAGAACACACACTTCTCAGACCTTAAGACAGACGTA 1980
Db 618 AspSerLeuThrGlyLeuLeuLysGlyThrHisThrAlaValSerSerAsnAspArgAla 637
QY 1981 GGTCGTGATTCATGATGTTTTCAGCTAGTTGGTCGAGGAGACTGACCTTAGACAAAGCT 2040
Db 638 SerLeuIleAsnAsnAlaPheGlnLeuValSerIleGlyLysLeuSerIleGluLysAla 657
QY 2041 CTTGACATGACTTACTACTCCCAACATGAACACAGCAGCCCGCAGCTTCTCGAAGSTCTG 2100
Db 658 LeuAspLeuSerLeuTyrLeuLysHisGluThrGluLeuMetProValPheGlnGlyLeu 677
QY 2101 AGTTACTTGGAAATCGTTTTTACCACATGATGACAGAGAAGGAATATTTCAGATATCTCTGA 2160
Db 678 AsnGluLeuIleProMetTyrLysLeuMetGluLysArgAspMetAsnGluValGluThr 697
QY 2161 AACCTCAAGCGTTTACCTTCTTCACTATTTTAAAGCCAGTATTTGACAGCAAGCTGGAGT 2220
Db 698 GlnPheLysAlaPheLeuIleArgLeuLeuArgAspLeuIleAspLysGlnThrTrpThr 717
QY 2221 GACAAGCGCTCAGTCTGGACAGGATGCTCGCTCGGCTCTCTTGAAGCTGGCCTGTGAC 2280
Db 718 AspGluGlySerValSerGluGlnMetLeuArgSerGluLeuLeuLeuAlaCysVal 737
QY 2281 CTGAACCATGCTCTCTCCATCCAGAAAGCTGCTGAACCTTCTCCAGTGGATGGAATCC 2340
Db 738 HisAsnTyrGlnProCysValGlnArgAlaGluGlyTyrPheArgLysTrpLysGluSer 757
QY 2341 AGTGGAAAAATTAATATATACCAACAGATGTTTTTAAAGATTTGTGTATTTCTGTCGGTCTCAG 2400
Db 758 AsnGlyAsnLeuSerLeuProValAspValThrLeuAlaValPheAlaValGlyAlaGln 777
QY 2401 ACAACACAGAGTGAATTAACCTTTTAGACATATGAACGTGCTCAATGTCAAGTCTGCTGAA 2460
Db 778 SerThrGluGlyTrpAspPheLeuTyrSerLysTyrGlnPheSerLeuSerSerThrGlu 797
QY 2461 CAAAACAAAATCTGTATGTTCTCAACGAGCAAGCATCAGGAAAGTACTTACTGAAGTTA 2520
Db 798 LysSerGlnIleGluPheAlaLeuCysArgThrGlnAsnLysGluLysLeuGlnTrpLeu 817
QY 2521 ATTGAACATAGGAATGGAAGGAAGTTTATCAAGACACAGAACTTTGGCAGCTCTCCTCAT 2580
Db 818 LeuAspGluSerPheLysGlyAspLysIleLysThrGlnGluPheProGlnIleLeuThr 837
QY 2581 GCGATTCCAGACGCTCAAAAGGGCAGCAACTAGCATGGGATTTTGTAAAGAGAAATTTGG 2640
Db 838 LeuIleGlyArgAsnProValGlyTyrProLeuAlaTrpGlnPheLeuArgLysAsnTrp 857
QY 2641 ACCCATCTCTGAAAAATTTGATCTGGCTCATATGACATAAGGATGATCATCTCTGCG 2700
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QY 2701 ACAACACGCTCACTTTTCTTCCAGGATAAGTTGCAAGAGGTGAAACTATTTTTGAATCT 2760
Db 878 ThrThrAsnGlnPheSerThrArgThrArgLeuGluGluValLysGlyPhePheSerSer 897
QY 2761 CTTGAGGCTCAGGATCAGATCAGATGATTTTCAAATGTTTCTGGAACCATACCAAA 2820
Db 898 LeuLysGluAsnGlySerGlnLeuArgCysValGlnGlnThrIleGluThrIleGluGlu 917
QY 2821 AATATAAATCGCTGGAGAAGAACTTCTCCGACTCTGAGGACTTCGGCTA 2868
Db 918 AsnIleGlyTrpMetAspLysAsnPheAspLysIleArgValTrpLeu 933
RESULT 7
ART1_MOUSE
ID -ART1_MOUSE STANDARD; PRT; 930 AA.
AC Q9EQH2; Q9EF63;
DT 28-FEB-2003 (Rel. 41, Created)
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DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Adipocyte-derived leucine aminopeptidase precursor (EC 3.4.11.-) (A-
 LAP) (ARNS-1) (Aminopeptidase PILS) (Puromycin-insensitive leucyl-
 specific aminopeptidase) (PILS-AP) (VEGF induced aminopeptidase).
 DE Name=Artesl; Synonyms=Appilis;
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hattori A., Kitatani K., Matsumoto H., Mizutani S., Tsujimoto M.;
 RT "Molecular cloning of murine adipocyte-derived leucine aminopeptidase
 and its expression in adipocyte cell line, 3T3-L1 cells.";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21961541; PubMed=11964289; DOI=10.1182/blood.V99.9.3241;
 RA Miyashita H., Yamazaki T., Akada T., Niizeki O., Ogawa M.,
 RA Nishikawa S., Sato Y.;
 RT "A mouse orthologue of puromycin-insensitive leucyl-specific
 aminopeptidase is expressed in endothelial cells and plays an
 important role in angiogenesis.";
 RL Blood 99:3241-3249(2002).
 CC -!- FUNCTION: May play a role in the inactivation of peptide hormones.
 CC May be involved in the regulation of blood pressure through the
 CC inactivation of angiotensin II and/or the generation of bradykinin
 CC in the kidney (By similarity).
 CC -!- CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Xaa-|-
 CC Xbb-, in which Xaa is preferably Leu, but Met is also acceptable.
 CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -!- SIMILARITY: Belongs to the peptidase M1 family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.ebi.ac.uk/announcements/>
 CC or send an email to license@sib-ch).
 CC
 DR EMBL: AF227511; AAG44260.1; -;
 DR EMBL: AB047552; BAB11982.1; -;
 DR MEROPS: M01.018; -;
 DR MGD; MGI:1933403; Artesl.
 DR GO: GO:0005829; C:cytosol; ISS.
 DR GO: GO:0005783; C:endoplasmic reticulum; ISS.
 DR GO: GO:0005576; C:extracellular; ISS.
 DR GO: GO:0016021; C:integral to membrane; ISS.
 DR GO: GO:0005138; F:interleukin-6 receptor binding; ISS.
 DR GO: GO:004178; F:leucyl aminopeptidase activity; ISS.
 DR GO: GO:0004239; F:methionyl aminopeptidase activity; ISS.
 DR GO: GO:0005164; F:tumor necrosis factor receptor binding; ISS.
 DR GO: GO:0008270; F:zinc ion binding; ISS.
 DR GO: GO:0045444; P:adipocyte differentiation; ISS.
 DR GO: GO:0019885; P:antigen processing, endogenous antigen via . . .; ISS.
 DR GO: GO:0006509; P:membrane protein ectodomain proteolysis; ISS.
 DR GO: GO:0050714; P:positive regulation of protein secretion; ISS.
 DR GO: GO:0008217; P:regulation of blood pressure; ISS.
 DR GO: GO:0045088; P:regulation of innate immune response; ISS.
 DR InterPro: IPR006025; Pept_M_Zn_BS.
 DR InterPro: IPR001930; Peptidase_M1.
 DR Pfam: PF01433; Yeast_DNA_bind.
 DR PRINTS: PR00756; Peptidase_M1; 1.
 DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 KW Aminopeptidase; Glycoprotein; Hydrolase; Metalloprotease; Protease;
 KW Signal; Zinc. 1 20 Potential.
 FT SIGNAL 21 930 Adipocyte-derived leucine aminopeptidase.
 FT CHAIN 21 930

FT	METAL	342	342	342	Zinc (catalytic) (By similarity).
FT	ACT SITE	343	343	343	By similarity.
FT	METAL	346	346	346	Zinc (catalytic) (By similarity).
FT	METAL	465	465	465	Zinc (catalytic) (By similarity).
FT	ACT SITE	427	427	427	Proton donor (Potential).
FT	CARBOHYD	59	59	59	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	143	143	143	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	403	403	403	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	540	540	540	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	655	655	655	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	749	749	749	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	890	890	890	N-linked (GlcNAc. . .) (Potential).
FT	CONFLICT	540	541	541	NA -> KG (in Ref. 2).
SQ	SEQUENCE	930 AA;	106598 MW;	17430DBSEAD7668 CRC64;	

Alignment Scores:	Pred. No.:	Length:	Matches:
Score:	6,97e-159	2480.00	462
Percent Similarity:	69.73%	Conservative:	167
Best Local Similarity:	51.22%	Mismatches:	263
Query Match:	48.99%	Indels:	10
DB:	1	Gaps:	4

US-10-039-073-3 (1-2883) x ART1_MOUSE (1-930)

QY	166	GCACATAATGGGAGACGATTTCTTGGCAGGAGCTAAGCTCCCGCTCCCGATGTTGGTCATTCCT	225
DB <td>30 <td>AlaserAsnGlyAspSerPheProTrpAsnAsnMetArgLeuProGluTrpMetThrPro</td> <td>49</td> </td>	30 <td>AlaserAsnGlyAspSerPheProTrpAsnAsnMetArgLeuProGluTrpMetThrPro</td> <td>49</td>	AlaserAsnGlyAspSerPheProTrpAsnAsnMetArgLeuProGluTrpMetThrPro	49
QY <td>226 <td>CTCCATATGACCTCTTTGTCGACCCCAATCTACCTCTCTGAGCTTTGTTGGCATCTGAG</td> <td>285</td> </td>	226 <td>CTCCATATGACCTCTTTGTCGACCCCAATCTACCTCTCTGAGCTTTGTTGGCATCTGAG</td> <td>285</td>	CTCCATATGACCTCTTTGTCGACCCCAATCTACCTCTCTGAGCTTTGTTGGCATCTGAG	285
DB <td>50 <td>IleHisThrAspLeuMetIleHisAlaAsnLeuSerThrLeuThrPheTrpGlyLysThr</td> <td>69</td> </td>	50 <td>IleHisThrAspLeuMetIleHisAlaAsnLeuSerThrLeuThrPheTrpGlyLysThr</td> <td>69</td>	IleHisThrAspLeuMetIleHisAlaAsnLeuSerThrLeuThrPheTrpGlyLysThr	69
QY <td>286 <td>AAGATCGAAGTCTTGGTCAGCAATGTACCAGCTTTATCATCTTGCACACGACCAAGATCTT</td> <td>345</td> </td>	286 <td>AAGATCGAAGTCTTGGTCAGCAATGTACCAGCTTTATCATCTTGCACACGACCAAGATCTT</td> <td>345</td>	AAGATCGAAGTCTTGGTCAGCAATGTACCAGCTTTATCATCTTGCACACGACCAAGATCTT	345
DB <td>70 <td>GluValGluIleIleAlaSerArgProThrSerThrIleIleMetHisSerHisLeu</td> <td>89</td> </td>	70 <td>GluValGluIleIleAlaSerArgProThrSerThrIleIleMetHisSerHisLeu</td> <td>89</td>	GluValGluIleIleAlaSerArgProThrSerThrIleIleMetHisSerHisLeu	89
QY <td>346 <td>GAAATCAGCAATGCCACCTTTCAGTCAGAGGAGAGTTCAGATACATACAGAACCCAGGAAA</td> <td>405</td> </td>	346 <td>GAAATCAGCAATGCCACCTTTCAGTCAGAGGAGAGTTCAGATACATACAGAACCCAGGAAA</td> <td>405</td>	GAAATCAGCAATGCCACCTTTCAGTCAGAGGAGAGTTCAGATACATACAGAACCCAGGAAA	405
DB <td>90 <td>GlnIleSerLysAlaThrLeuArg-----ArgGlyAlaGlyGluMetLeuSerGluGlu</td> <td>107</td> </td>	90 <td>GlnIleSerLysAlaThrLeuArg-----ArgGlyAlaGlyGluMetLeuSerGluGlu</td> <td>107</td>	GlnIleSerLysAlaThrLeuArg-----ArgGlyAlaGlyGluMetLeuSerGluGlu	107
QY <td>406 <td>GAACTGAAAGTTTGGATTTACCTGCTCATGAACAAATTCACCTGCTGTTCCAGAGAAA</td> <td>465</td> </td>	406 <td>GAACTGAAAGTTTGGATTTACCTGCTCATGAACAAATTCACCTGCTGTTCCAGAGAAA</td> <td>465</td>	GAACTGAAAGTTTGGATTTACCTGCTCATGAACAAATTCACCTGCTGTTCCAGAGAAA	465
DB <td>108 <td>ProLeuLysValLeuGluTrpProIleHisGluGlnValAlaLeuLeuAlaGlnPro</td> <td>127</td> </td>	108 <td>ProLeuLysValLeuGluTrpProIleHisGluGlnValAlaLeuLeuAlaGlnPro</td> <td>127</td>	ProLeuLysValLeuGluTrpProIleHisGluGlnValAlaLeuLeuAlaGlnPro	127
QY <td>466 <td>CTTACGCCTCACCTGAAATACTATGTGGCTATGTGACTTCCAGCCCAAGTTAGTGTGATGC</td> <td>525</td> </td>	466 <td>CTTACGCCTCACCTGAAATACTATGTGGCTATGTGACTTCCAGCCCAAGTTAGTGTGATGC</td> <td>525</td>	CTTACGCCTCACCTGAAATACTATGTGGCTATGTGACTTCCAGCCCAAGTTAGTGTGATGC	525
DB <td>128 <td>LeuLeuAlaGlySerLeuTrpThrValIleIleAspTyrAlaAlaAsnLeuSerGluSer</td> <td>147</td> </td>	128 <td>LeuLeuAlaGlySerLeuTrpThrValIleIleAspTyrAlaAlaAsnLeuSerGluSer</td> <td>147</td>	LeuLeuAlaGlySerLeuTrpThrValIleIleAspTyrAlaAlaAsnLeuSerGluSer	147
QY <td>526 <td>TTTGAAGGGTTTATAAAGACATACAGAACTCTTTGGTGGTGAAACAGAAATCTTTGCA</td> <td>585</td> </td>	526 <td>TTTGAAGGGTTTATAAAGACATACAGAACTCTTTGGTGGTGAAACAGAAATCTTTGCA</td> <td>585</td>	TTTGAAGGGTTTATAAAGACATACAGAACTCTTTGGTGGTGAAACAGAAATCTTTGCA	585
DB <td>148 <td>PheHisGlyPheTyrLysSerThrTyrArgThrGlnGluGlyGluMetArgIleLeuAla</td> <td>167</td> </td>	148 <td>PheHisGlyPheTyrLysSerThrTyrArgThrGlnGluGlyGluMetArgIleLeuAla</td> <td>167</td>	PheHisGlyPheTyrLysSerThrTyrArgThrGlnGluGlyGluMetArgIleLeuAla	167
QY <td>586 <td>GTAACAGATTTTCAGCCCAAGCCAGGACGCTTCCCTGCTTGTGTGATGACCGCTTG</td> <td>645</td> </td>	586 <td>GTAACAGATTTTCAGCCCAAGCCAGGACGCTTCCCTGCTTGTGTGATGACCGCTTG</td> <td>645</td>	GTAACAGATTTTCAGCCCAAGCCAGGACGCTTCCCTGCTTGTGTGATGACCGCTTG	645
DB <td>168 <td>AlaThrGlnPheGluProThrAlaAlaArgMetAlaPheProCysPheAspGluProAla</td> <td>187</td> </td>	168 <td>AlaThrGlnPheGluProThrAlaAlaArgMetAlaPheProCysPheAspGluProAla</td> <td>187</td>	AlaThrGlnPheGluProThrAlaAlaArgMetAlaPheProCysPheAspGluProAla	187
QY <td>646 <td>TTCAAAGCCCAACTTTTCAATCAAGATACAGAGAGAGAGGAGCATATTTGCACTATCCAAC</td> <td>705</td> </td>	646 <td>TTCAAAGCCCAACTTTTCAATCAAGATACAGAGAGAGAGGAGCATATTTGCACTATCCAAC</td> <td>705</td>	TTCAAAGCCCAACTTTTCAATCAAGATACAGAGAGAGAGGAGCATATTTGCACTATCCAAC	705
DB <td>188 <td>LeuLysAlaSerPheSerIleLysIleLysArgAspProArgHisLeuAlaIleSerAsn</td> <td>207</td> </td>	188 <td>LeuLysAlaSerPheSerIleLysIleLysArgAspProArgHisLeuAlaIleSerAsn</td> <td>207</td>	LeuLysAlaSerPheSerIleLysIleLysArgAspProArgHisLeuAlaIleSerAsn	207
QY <td>706 <td>ATCCCAAGGTTAAGCAATTTGAACCTTGAAGAGGCTTTTGGAGAGATCATCTTTGAAACT</td> <td>765</td> </td>	706 <td>ATCCCAAGGTTAAGCAATTTGAACCTTGAAGAGGCTTTTGGAGAGATCATCTTTGAAACT</td> <td>765</td>	ATCCCAAGGTTAAGCAATTTGAACCTTGAAGAGGCTTTTGGAGAGATCATCTTTGAAACT	765
DB <td>208 <td>MetProLeuValLysSerValAsnValAlaGluGlyLeuIleGluAspHisPheAspIle</td> <td>227</td> </td>	208 <td>MetProLeuValLysSerValAsnValAlaGluGlyLeuIleGluAspHisPheAspIle</td> <td>227</td>	MetProLeuValLysSerValAsnValAlaGluGlyLeuIleGluAspHisPheAspIle	227
QY <td>766 <td>ACTGTAATAATGAGTACATACCTTTGAGCCGTACATAGTTTGTGATTTCCATCTCTCAGT</td> <td>825</td> </td>	766 <td>ACTGTAATAATGAGTACATACCTTTGAGCCGTACATAGTTTGTGATTTCCATCTCTCAGT</td> <td>825</td>	ACTGTAATAATGAGTACATACCTTTGAGCCGTACATAGTTTGTGATTTCCATCTCTCAGT	825
DB <td>228 <td>ThrValLysMetSerThrTrpLeuValAlaPheIleIleSerAspPheLysSerValSer</td> <td>247</td> </td>	228 <td>ThrValLysMetSerThrTrpLeuValAlaPheIleIleSerAspPheLysSerValSer</td> <td>247</td>	ThrValLysMetSerThrTrpLeuValAlaPheIleIleSerAspPheLysSerValSer	247
QY <td>826 <td>GGCTTCACTTTCATCAGGGGTCAAGGTGTCCATCTATGATCATCCCGACAGAAACCGAATCAA</td> <td>885</td> </td>	826 <td>GGCTTCACTTTCATCAGGGGTCAAGGTGTCCATCTATGATCATCCCGACAGAAACCGAATCAA</td> <td>885</td>	GGCTTCACTTTCATCAGGGGTCAAGGTGTCCATCTATGATCATCCCGACAGAAACCGAATCAA	885
DB <td>248 <td>LysMetThrLysSerGlyValLysValSerValTyrAlaValProAspLysIleAsnGln</td> <td>267</td> </td>	248 <td>LysMetThrLysSerGlyValLysValSerValTyrAlaValProAspLysIleAsnGln</td> <td>267</td>	LysMetThrLysSerGlyValLysValSerValTyrAlaValProAspLysIleAsnGln	267

GN Name=Arts1; Synonyms=Appils;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC STRAIN=Sprague-Dawley; TISSUE=Pineal gland;
RX MEDLINE=20285344; PubMed=10824104;
RA Schomburg L., Kollmus H., Friedrichsen S., Bauer K.;
RT "Molecular characterization of a puromycin-insensitive leucyl-specific
amino peptidase, PLEU-AP";
RL Eur. J. Biochem. 267:3198-3207(2000).
CC -!- FUNCTION: May play a role in the inactivation of peptide hormones.
CC May be involved in the regulation of blood pressure through the
CC inactivation of angiotensin II and/or the generation of bradykinin
CC in the kidney (By similarity).
CC -!- CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Xaa-|-
CC Xbb-, in which Xaa is preferably Leu, but Met is also acceptable.
CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9J22-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9J22-2; Sequence=VSP_005451, VSP_005452;
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- SIMILARITY: Belongs to the peptidase M1 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF148323; AAF73106.1; .
DR EMBL; AF148324; AAF73107.1; .
DR MEROPS; M01.018; .
DR GO; GO:0005829; C:Cytosol; ISS.
DR GO; GO:0005783; C:endoplasmic reticulum; ISS.
DR GO; GO:0005576; C:extracellular; ISS.
DR GO; GO:0016021; C:integral to membrane; ISS.
DR GO; GO:0005138; F:interleukin-6 receptor binding; ISS.
DR GO; GO:0004178; F:leucyl aminopeptidase activity; ISS.
DR GO; GO:0004239; F:methionyl aminopeptidase activity; ISS.
DR GO; GO:0008270; F:tumor necrosis factor receptor binding; ISS.
DR GO; GO:0004544; P:adipocyte differentiation; ISS.
DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . ; ISS.
DR GO; GO:0006509; P:membrane protein ectodomain proteolysis; ISS.
DR GO; GO:0050714; P:positive regulation of protein secretion; ISS.
DR GO; GO:0008217; P:regulation of blood pressure; ISS.
DR GO; GO:0045088; P:regulation of innate immune response; ISS.
DR InterPro; IPR006025; Rept_M_Zn_BS.
DR InterPro; IPR001930; Peptidase_M1.
DR Pfam; PF01433; Peptidase_M1.
DR PRINTS; PR00756; ALADIPTASE.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Alternative splicing; Aminopeptidase; Glycoprotein; Hydrolase;
KW Metalloprotease; Protease; Signal; Zinc.
FT SIGNAL 1 20 Potential.
FT CHAIN 21 930 Adipocyte-derived leucine aminopeptidase.
FT METAL 342 342 Zinc (catalytic) (By similarity).
FT ACT_SITE 343 343 By similarity.
FT METAL 346 346 Zinc (catalytic) (By similarity).
FT METAL 465 465 Zinc (catalytic) (By similarity).
FT ACT_SITE 427 427 Proton donor (Potential).
FT METAL 59 59 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 143 143 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 403 403 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 655 655 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 749 749 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 890 890 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 883 884 FF -> CM (in isoform 2).
FT VARSPLIC 885 930 /FTID=VSP_005451.
FT VARSPLIC 885 930 Missing (in isoform 2).
FT VARSPLIC 885 930 /FTID=VSP_005452.
SQ SEQUENCE 930 AA; 106418 MW; 928E7143CBD0BE7F CRC64;
Alignment Scores:
Pred. No.: 1,66e-155 Length: 930
Score: 2430.00 Matches: 456
Percent Similarity: 68.90% Conservative: 171
Best Local Similarity: 50.11% Mismatches: 265
Query Match: 48.00% Indels: 18
DB: 1 Gaps: 6
US-10-039-073-3 (1-2883) x ARTI_RAT (1-930)
QY 154 GCTTTCCAGTAGCAGCACTAATGGGAAACGATTTCTTGGCAGGAGCTAAGGCTCCCAAGT 213
DB 26 AlaSerProLysAlaSerAsnGlyAlaSerPheProTyrAsnAsnMetArgLeuProGlu 45
QY 214 GTGGTCATTCTCTCCATTATGACCTCTTTGTCACCCCAATCTACCTCTCTGGACTTT 273
DB 46 TyrIleThrProIleHisTyrAspLeuMetIleHisAlaAsnLeuSerThrLeuThrPhe 65
QY 274 GTTGCATCTGAGAGATCGAAGTCATGCTTGTGTCACCAATGCTACCAGTTTATCATCTTGCAC 333
DB 66 TrpGlyLysThrGluValGluIleThrValSerGlnProThrSerThrIleIleMetHis 85
QY 334 AGCAAGATCTTGAATCAGCAATGCACCTCCCTTCAG-----TCAGAGAGAGATTCACGA 387
DB 86 SerHisGlnLeuGlnIleSerLysAlaThrLeuArgArgGlyAlaGluGlu----- 102
QY 388 TCATGAAACCGAGAAAGAACGTGAAGTTTGTAGTTACCTGCTCATGAACAATGCA 447
DB 103 ---MetLeuProGluGluProLeuLysLeuMetGluTyrSerAlaHisGluGlnValAla 121
QY 448 CTGCTGGTTCCAGAGAAACTTACGCTCACCTGAATATCTATGCTGCTGAGCTTCCAA 507
DB 122 LeuLeuThrAlaGlnProLeuLeuAlaGlySerValTyrThrValIleIleThrTyrAla 141
QY 508 GCCAAGTTAGTGATGGCTTTGAAGGGTTTATAAAGCACATACAGAACTCTTGTGTGT 567
DB 142 AlaAsnLeuSerGluAsnPheHisGlyPheTyrLysSerThrTyrArgThrGlnGluGly 161
QY 568 GAAACAAGAAATCTTGCAGTAACAGATTTTGTAGCCAAACCAGCAGCGATGGCTTCCCT 627
DB 162 GluArgGlyLeuAlaAlaThrGlnPheGluProThrAlaAlaArgMetAlaPhePro 181
QY 628 TCCTTTGTAGAACCGTTGTTCAAGCCAACTTTTCAATCAAGATACAGAGAGAGAGAGAG 687
DB 182 CysPheAspGluProAlaLeuLysAlaSerPheSerIleLysIleLysArgAspProArg 201
QY 688 CATATTGCATCTCCAACTATGCAAGGTTAAGACAACTTCAACTTCAAGAGAGCTTTTGT 747
DB 202 HisLeuAlaIleSerAsnMetProLeuValLysSerValThrValAlaGluGlyLeuIle 221
QY 748 GAAGATCATCTTGAACACTACTGTAAATAAGTAGTACATCTTGTGACCTACATAGTTTGT 807
DB 222 GluAspHisPheAspIleThrValLysMetSerThrTyrLeuValAlaPheIleIleSer 241
QY 808 GATTTCCACTCTCTGAGTGGCTTTCATCTCAGGGGTCAAGGTGCCATCTATGATGCC 867
DB 242 AppPheLysSerValSerLysMetThrLysSerGlyValLysValSerValTyrAlaVal 261
QY 868 CCAGACAAACCGGAATCAACACACATTTATGCTTTGTCAGGCGATCATCAAGCTACTTGT 927
DB 262 ProAspLysIleAsnGlnAlaAspTyrAlaLeuAspAlaAlaValThrLeuLeuGluPhe 281
QY 928 TATGAAAAGTACTTTGATATCTACTATCCACTCTCCAACTGGATTTAATGCTATTCCT 987


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Db 282 TyrGluAspTyrPheSerIleProTyrProLeuProLysGlnAspLeuAlaIlePro 301
Qy 988 GACTTTGCACCTGGAGCCATGAAATATGGGGCTCATATACATATAGGGAGCAGCTCACTG 1047
Db 302 AspPheGlnSerGlyAlaMetGluAsnTrpGlyLeuThrTyrArgGluSerAlaLeu 321
Qy 1048 CTTTTTGGCCCAAGACCTCTCTGCTTCCGATAAAGTGGTGGTCCACAGAGTCATAGCC 1107
Db 322 LeuTyrAspLysGluSerSerAlaSerSerLysLeuGlyIleThrMetThrValSer 341
Qy 1108 CATGAACCTGGCGCACAGCTGTTGGCAACTGGTCAAAATGGAATGGTGGAAATGATATT 1167
Db 342 HisGluLeuAlaHisGlnTrpPheGlyAsnLeuValThrMetGluTrpTrpAsnAspLeu 361
Qy 1168 TGGCTTAAGGAGGGTTTGCAAAATACATACGAACCTTATCGCTGTTAATGCTACATATCCA 1227
Db 362 TrpLeuAsnGluGlyPheAlaLysPheMetGluPheValSerValThrValThrHisPro 381
Qy 1228 GAGCTGCAATTTGATGACTATTTTGAATGTGTGTTTGAAGTAATATACAAAAGATTCA 1287
Db 382 GluLeuLysValGluGluTyrPhePheGlyLysCysPheAsnAlaMetGluValAspAla 401
Qy 1288 TTGAATTCATCCCGCCTATCTCCAAACACGCGGAAACCCGACTCAAAATACAGGAATG 1347
Db 402 LeuAsnSerSerHisProValSerThrProValGluAsnProAlaGlnIleArgGluMet 421
Qy 1348 TTTGATGAAGTTTCTATACAAAGGAGCTTGTATTTTGAATATGCTCAAGGATTTCTGT 1407
Db 422 PheAspGluValSerTyrGluLysGlyAlaCysIleLeuAsnMetLeuArgAspTyrLeu 441
Qy 1408 GGTGAGGAGAAATCCAGAAAGGAATATTCAGTACTTAAAGAGTTCAGTATAGAAAT 1467
Db 442 SerAlaAspThrPheLysArgGlyIleValGlnTyrLeuGlnLysTyrSerTyrLysAsn 461
Qy 1468 GCTAAGATGATGCTGTGGAGCAGCTGTCAAAATAGTGTGTTTGAAGTGAATTTT 1524
Db 462 ThrLysAsnGluAspLeuTrpAsnSerMetMetHisIleCysProThrAspGlyThrGln 481
Qy 1525 ACATCTGCTGGAGTTTGTTCATTCGATCCCAAGATGACCAAGTAAACATGCTCGCTTTCTG 1584
Db 482 ThrMetAspGlyPheCys--SerArgAsnGlnHisSerSerSerThrSerHisTrpArg 500
Qy 1585 GGGGAAATGCAGAGGTCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1644
Db 501 GlnGluValIleAspIleLysSerMetMetAsnThrTrpThrLeuGlnLysGlyPhePro 520
Qy 1645 CTGCTGTGGTTAAACAGACGGTGTTCATCTCCGACTGCAACAGGAGCGTCTCTCCAG 1704
Db 521 LeuIleThrIleThrValArgGlyArgAsnValHisLeuLysGlnGluHisTyrMetLys 540
Qy 1705 GGG-----GTTTCCAGAGAGCCCTGAATGGAGGGCCCTGCAGGAGAGTACTCTGG 1758
Db 541 GlySerGluCysPheProGluThrGlySer-----LeuTrp 552
Qy 1759 CATATCCCATGACTACTCCAGGATTTCTTAATGTGATGCCAGACATCTTAAAA 1818
Db 553 HisValProLeuThrPheIleThrSerLysSerAspSerValGlnArgPheLeuLys 572
Qy 1819 TCAAGACAGATACTCTGGATCTACCTGAAAGACCAAGTGGTGGTGAATTTAATGTGGAC 1878
Db 573 ThrLysThrAspValIleLeuProGluAlaValGluTrpIleLysPheAsnValGly 592
Qy 1879 TCAATGGTTACTACTCGTTCACTATGAGGCTCATGATGGGACCAACTCATTTACACAG 1938
Db 593 MetAsnGlyTyrTyrIleValHisTyrGlyAspAspGlyTrpAlaSerLeuAsnGlyLeu 612
Qy 1939 CTGAATCAGAACACACACTTCTCAGACCTTAAGGACAGAGTAGGTCTGATTCATGATGTG 1998
Db 613 LeuLysGluAlaHisThrThrIleSerSerAsnAspArgAlaSerLeuIleAsnAsnAla 632
Qy 1999 TTTGAGCTAGTTGGTGGAGGAGACTGACCCCTAGACAAAGCTCTTGACATGACTTACTAC 2058
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Db 633 PheGlnLeuValSerIleGlyLysLeuSerIleGluLysAlaLeuAspLeuIleLeuTyr 652
Qy 2059 CTCAACATGAAACAAAGACGCCCTCTTCTCGAAGTCTGAGTTACTTGGAAATCGTTT 2118
Db 653 LeuLysAsnGluThrGluIleMetProIlePheGlnGlyLeuAsnGluLeuProMet 672
Qy 2119 TACCACATGATGGACAGGAATATTTTCAGATATCTCTGAAAACCTCAACGGTTACCTT 2178
Db 673 TyrLysLeuMetGluLysArgAspMetValGluValGluThrGlnPheLysAspPheLeu 692
Qy 2179 CTTCAAGTATTTAAGCCAGGATTCACAGGCAAGCTGGAGTGCACAAAGGCTCAGTCTGG 2238
Db 693 LeuArgLeuLeuLysAspLeuIleAsnLysGlnThrTrpThrAspGluGlySerValSer 712
Qy 2239 GACAGGATGCTCCGCTCGCTCTTGAAGCTGCGCTGTGACCTGAACACCTGCTCTTGC 2298
Db 713 GluArgMetLeuArgSerGlnLeuLeuLeuAlaCysValHisArgTyrGlnLeuCys 732
Qy 2299 ATCCAGAAAGCTGCTGAACCTCTTCTCCAGTGGATGGAAATCCAGTGGAAAATTAATATA 2358
Db 733 ValGlnArgAlaGluArgTyrPheArgGluTrpLysAlaSerAsnGlyAsnMetSerLeu 752
Qy 2359 CCAACAGATGTTTAAAGATTGTGATTCTCTGGTGTCTCAGACAAACAGCAGGATGCAAT 2418
Db 753 ProIleAspValThrLeuAlaValPheAlaValGlyAlaGlnAsnThrGluGlyTrpAsp 772
Qy 2419 TACCTTTTAGAGCAATATGAATGCTCAATGCTCAAGTCTGAACAAACAAATTTCTGTAT 2478
Db 773 PheLeuTyrSerLysTyrGlnSerSerSerSerSerThrGluLysSerGlnIleGluPhe 792
Qy 2479 GCTTTGTCACGACGACATCAGGAAAGTACTGAGTTAATTGAATAGGAAATGGAA 2538
Db 793 SerLeuCysIleSerGlnAspProGluLysLeuGlnTrpLeuLeuAspGlnSerPheLys 812
Qy 2539 GGAAGGTTATCAAGACACAGAACTTGGCAGCTCTCTTCATGCGATTTCGCAGACGTCCA 2598
Db 813 GlyGluIleIleLysThrGlnGluPheProHisIleLeuThrLeuIleGlyArgAsnPro 832
Qy 2599 AAGGGGACGACCACTAGCATGGGATTTTGAAGAAATAATGGACCCATCTTCTCAAAAA 2658
Db 833 ValGlyTyrProLeuAlaTrpLysPheLeuLysGluAsnTrpAsnLysIleValGlnLys 852
Qy 2659 TTTGACTTGGCTCATATGACATGAAGTATCATCTCTGACACAAACAGTCACTTTCT 2718
Db 853 PheGluLeuGlySerSerSerIleAlaHisMetValMetGlyThrThrAsnGlnPheSer 872
Qy 2719 TCAAGGATAGTTGCAAGAGGTGAAACTATTTTCAATCTCTTGAGGCTCAAGGATCA 2778
Db 873 ThrArgAlaArgLeuGluGluValLysGlyPhePheSerSerLeuLysLysAsnGlySer 892
Qy 2779 CATCTGGATATTTTCAAACTGTTGGAACGATACCAAAAAATATAATAATGGCTGGAG 2838
Db 893 GlnLeuArgCysValGlnGlnThrIleGluThrIleGluAsnIleArgTrpMetAsp 912
Qy 2839 AAGAACTTCCGACTCTGAGGACTTGCTA 2868
Db 913 LysAsnPheAspLysIleArgLeuTrpLeu 922
RESULT 9
ID Q6PE23 PRELIMINARY; PRT; 1003 AA.
AC Q6PE23;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein zgc:66103.
GN ORFNames=zgc:66103;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN 1)
```


QY 1534 GGAGTTTGTCTATTCGGATCCCAAGATGACAGTAAACATGCTCGCTTCTCTGGGGGAAAT 1593
Db 580 ----- 580
QY 1594 GCAGAGGTCAAGAGATGATGACTACATGAGTCTCCAGAAAGGAATCCCCCTCTCGGTG 1653
Db 581 LeuAsnValSerGluMetCAsnThrTrpThrValHisLysGlyPheProLeuValThr 600
QY 1654 GTTAAACAGACGGGTGTCTACCGACTCGCAACAGAGCGCTTCTCCACAGGGGGTTTC 1713
Db 601 ValLysArgAsnGlyProGlnValThrLeuSerGlnGluHisPheLeuLeuAsnAla--- 619
QY 1714 CAGGAAGACCTGAATGGAGGGCCCTCGACGAGAGGTACTGTGGCATATCCCAATTGACC 1773
Db 620 -----GluAsnGlyThrAspAspSerLeuTrpHisIleProLeuThr 634
QY 1774 TACTCCACGAGTCTCTTAATGTGATCCACAGA-----CACATTCTAAAA 1818
Db 635 TyrValAsnAspSerCysSerValLeuArgSerCysLysGlnValPheHis---LeuLys 653
QY 1819 TCAAGACAGATACTCTGGATCTACCTGAAAGACCAAGTTGGGTGAAATTTAATGTGGAC 1878
Db 654 AspLysGluAlaThrLeuGlnLeuProGlyGlnValLysTrpLeuLysPheAsnPheArg 673
QY 1879 TCAATGTTACTACATGTTCACTATGAGGTCTATGATGGAGCAACTCATTTACACAG 1938
Db 674 SerAspGlyPheTyrIleValHisTyrAspGluGlnGlyTrpSerAspLeuIleSerAla 693
QY 1939 CTGAATCAGACACACACTCTCAGACCTCAGACAGAGAGTGTGATTCATGATGTG 1998
Db 694 LeuLysValAspValAsnValLeuProSerGluAspLysAlaAlaLeuIleAsnAsnIle 713
QY 1999 TTTCAAGTGTGTTGGTGCAGGAGACTGACCCCTAGACAAAGCTTTGTGACTGACTTACTAC 2058
Db 714 PheAlaLeuSerArgLeuGlyLysValSerPheArgGlnValLeuAsnLeuMetAspTyr 733
QY 2059 CTCACACATGAAACAGACAGCCCGCCTCTTCCGAGGCTGAGTACTTGGAAATCGTTT 2118
Db 734 IleArgAsnGluThrGluThrAlaProLeuThrGluAlaLeuSerGlnLeuGlyGlnIle 753
QY 2119 TACCACATGATGGACAGAGGAATATTTCATATCTCTGAAACCTCAACGGTTTACCTT 2178
Db 754 TyrArgLeuLeuAspLysArgSerAspLeuAsnLeuAlaSerSerMetThrThrTyrIle 773
QY 2179 CTTCAAGTATTTAAGCCAGTATTGACAGAGCAAGCTGGAGTGAAGGGCTCAGTCTGG 2238
Db 774 GluSerHisPheGlySerLeuMetGluSerGlnSerTrpGluValGluThrSerValSer 793
QY 2239 GACAGGATGCTCCGCTCGCTCTTTGAAGTGGCTGTGACCTGAACCAATGCTCCTTGC 2298
Db 794 LysMetThrLeuArgSerAlaLeuLeuGluThrAlaCysAlaLeuAsnArgProAsnCys 813
QY 2299 ATCCAGAAGCTGCTGAACCTCTCCAGTGGATGGATCCAGTGGAAAATTAATATA 2358
Db 814 ThrThrGlnAlaArgArgLeuPheAspGlnTrpLeuAlaSerAsnLysThrLeuGlnIle 833
QY 2359 CCAACAGATGTTTAAAGATTGTATTCTCTGGTGTCTCAGACACAGCAGGAGTGAAT 2418
Db 834 ProSerAspLeuMetArgThrValPheLysValAlaLysThrAspGluGlyTrpSer 853
QY 2419 TACCTTTTACAGCAATATGAATCTGCAATGTCAGTGTGAAACAAAACAAATTTCTGTAT 2478
Db 854 LysLeuLeuGlySerTyrLysHisSerIleTyrAspThrGluLysArgLysMetLeuGlu 873
QY 2479 GCTTTTCAACGACGACATCAGGAAGTTACTGAATTAATGAAGTGAATAGGAATGGAA 2538
Db 874 AlaLeuAlaSerThrGlnAspValArgLysIleIleTrpValLeuGlnLysSerLeuAsp 893
QY 2539 GGAAAGGTTATCAACACACAGAACTTGGCAGCTCTCTTCATGCGATGGCAGACGCCA 2598
Db 894 GlySerGluIleGlnAsnGlnGluPheProLeuValIleHisThrValCysArgAspPhe 913
QY 2599 AAGGGGCAGCAACTAGCATGGGATTTTGTAAAGAGAAAATTGGACCCATCTTCTGAAAAA 2658

Db 914 AlaGlyTyrLeuTyrAlaTrpAspPheMetCysGluAsnTrpGluLysIleThrGlnLys 933
QY 2659 TTTGACTTGGGCTCATATGACATAAGGATCATCTCTGGCACACAGCTCCTCTTCT 2718
Db 934 PheProIleGlySerPheAlaIleGlnSerIleIleThrSerThrThrSerGlnPheSer 953
QY 2719 TCAAGGATAAGTTGCAAGAGGTGAACATATTTTGAATCTCTTGAAGGCTCAAGGATCA 2778
Db 954 ThrLysThrHisLeuAlaGluValGlnAsnPheSerLeuGlyAlaLysGlySer 973
QY 2779 CATCTGGATATTTTCAAACTGTTCTGGAACGATACCAACAAATATATAATGCTGAG 2838
Db 974 GlnMetArgIleValGlnGluAlaIleGluThrIleLysHisAsnMetArgTrpMetGlu 993
QY 2839 AAGAATCTCCGACTCTGAGGACTTGGCTA 2868
Db 994 LysAsnLeuAsnThrLeuGlnSerTrpLeu 1003
RESULT 10
LCAP RAT ID LCAP RAT STANDARD; PRT; 1025 AA.
AC P97629; Q11009;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Leucyl-cystinyl aminopeptidase (EC 3.4.11.3) (Cystinyl aminopeptidase)
DE (Oxytocinase) (Insulin-regulated membrane aminopeptidase)
DE (Insulin-responsive aminopeptidase) (IRAP) (Placental leucine
DE aminopeptidase) (P-LAP) (Vesicle protein of 165 kDa) (Vp165) (GP160).
GN Name=unpep; Synonyms=Irapp, Otase;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=Sprague-Dawley; TISSUE=Adipocyte;
RX MEDLINE=96007507; PubMed=7559527; DOI=10.1074/jbc.270.40.23612;
RA Keller S.R., Scott H.M., Mastick C.C., Abersold R., Lienhard G.E.;
RT "Cloning and characterization of a novel insulin-regulated membrane
RT aminopeptidase from Glut4 vesicles";
RL J. Biol. Chem. 270:23612-23618(1995).
RN [2]
RP SEQUENCE OF 168-176; 387-399; 731-740 AND 893-905.
RX MEDLINE=94164972; PubMed=8119954;
RA Mastick C.C., Abersold R., Lienhard G.E.;
RT "Characterization of a major protein in GLUT4 vesicles. Concentration
RT in the vesicles and insulin-stimulated translocation to the plasma
RT membrane.";
RL J. Biol. Chem. 269:6089-6092(1994).
CC -I- FUNCTION: Release of an N-terminal amino acid, cleave before
CC cysteine, leucine as well as other amino acids. Degrades peptide
CC hormones such as oxytocin, vasopressin and angiotensin III, and
CC plays a role in maintaining homeostasis during pregnancy. May be
CC involved in the inactivation of neuronal peptides in the brain.
CC Cleaves Met-enkephalin and dynorphin. Binds angiotensin IV and may
CC be the angiotensin IV receptor in the brain (By similarity).
CC -I- CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Cys-|-
CC Xaa, in which the half-cysteine residue is involved in a disulfide
CC loop, notably in oxytocin and vasopressin.
CC -I- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -I- SUBUNIT: Homodimer. Binds tankyrases 1 and 2 (By similarity).
CC -I- SUBCELLULAR LOCATION: Type II membrane protein. Localized mainly
CC in intracellular vesicles together with GLUT4. Relocalizes to the
CC plasma membrane in response to insulin. The dileucine
CC internalization motif and/or the interaction with tankyrases may
CC be involved in intracellular sequestration.
CC -I- TISSUE SPECIFICITY: Highly expressed in heart, brain, spleen,
CC lung, kidney and white adipose tissue. Detected at lower levels in
CC skeletal muscle and liver.
CC -I- PTM: N-glycosylated.
CC -I- SIMILARITY: Belongs to the peptidase M1 family.

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EMBL; U76997; AAB19066.1; --
ENBL; U32990; AAB38021.1; --
PIR; I55441; I55441.
MEROPS; M01.011; --
InterPro; IPR001930; Peptidase_M1.
Pfam; PF01433; Peptidase_M1_1.
PRINTS; PR00756; ALADIP7ASE.
PROSITE; PS00142; ZINC_PROTEASE; 1.
AminoPeptidase; Direct protein sequencing; Glycoprotein; Hydrolase;
Metal-binding; Metalloprotease; Protease; Signal-anchor;
Transmembrane; Zinc.
DOMAIN 1 109 Cytoplasmic (Potential).
TRANSMEM 110 131 Signal-anchor for type II membrane
protein (Potential).
DOMAIN 132 1025 Extracellular (Potential).
SITE 53 54 Dileucine internalization motif
(Potential).
SITE 76 77 Dileucine internalization motif
(Potential).
SITE 96 101 Tankyrase binding (By similarity).
METAL 464 464 Zinc (catalytic) (By similarity).
ACT_SITE 465 465 By similarity.
METAL 468 468 Zinc (catalytic) (By similarity).
METAL 487 487 Zinc (catalytic) (By similarity).
CARBOHYD 145 145 N-linked (GlcNAc...) (Potential).
CARBOHYD 184 184 N-linked (GlcNAc...) (Potential).
CARBOHYD 215 215 N-linked (GlcNAc...) (Potential).
CARBOHYD 256 256 N-linked (GlcNAc...) (Potential).
CARBOHYD 266 266 N-linked (GlcNAc...) (Potential).
CARBOHYD 368 368 N-linked (GlcNAc...) (Potential).
CARBOHYD 374 374 N-linked (GlcNAc...) (Potential).
CARBOHYD 447 447 N-linked (GlcNAc...) (Potential).
CARBOHYD 525 525 N-linked (GlcNAc...) (Potential).
CARBOHYD 578 578 N-linked (GlcNAc...) (Potential).
CARBOHYD 664 664 N-linked (GlcNAc...) (Potential).
CARBOHYD 682 682 N-linked (GlcNAc...) (Potential).
CARBOHYD 695 695 N-linked (GlcNAc...) (Potential).
CARBOHYD 758 758 N-linked (GlcNAc...) (Potential).
CARBOHYD 834 834 N-linked (GlcNAc...) (Potential).
CARBOHYD 850 850 N-linked (GlcNAc...) (Potential).
CARBOHYD 989 989 N-linked (GlcNAc...) (Potential).
CONFLICT 909 916 LMKSSSDG -> YGTTQRAW (in Ref. 1;
AAB38021).
FT CONFLICT 916 1025 Missing (in Ref. 1; AAB38021).
SQ SEQUENCE 1025 AA; 117201 MW; 8AD3BA3A446FB5EF CRC64;

Alignment Scores:
Pred. No.: 2,8e-128 Length: 1025
Score: 2027.00 Matches: 402
Percent Similarity: 61.81% Conservative: 158
Best Local Similarity: 44.37% Mismatches: 310
Query Match: 40.04% Indels: 36
DB: 1 Gaps: 5

us-10-039-073-3 (1-2883) x LCAP_RAT (1-1025)
QY 160 CCAGTACCACTAATGGGGAACGATTCCTTGGCAGGAGCTAAGGCTCCCGAGTGGTC 219
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
153 ProileAlaThrAsnGlyLysValPheProTTPAlaGlnIleArgLeuProThrAlaIle 172
QY 220 ATTCTCTCCATATGACCTCTTTGGCCACCCCAATCTCACTCTCTGACCTTTGTGCA 279
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
173 IleProGlnArgTyrGluLeuSerLeuHisProAsnLeuThrSerMetThrPheArgGly 192

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QY 280 TCTGAGAGAGATCGAAGCTCTGGTCAGCAATGCTTACCAGTTTATCATCTTGACAGCAAA 339
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
193 SerValThrIleSerLeuGlnAlaLeuGlnAspThrArgAspIleIleLeuHisSerThr 212
QY 340 GATCTTGAATACAGAAATGCCACCTTCAGTCAGAGGAAGATTCAGATACATGATAACCA 399
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
213 GlyHisAsnIleSerSerValThrPheMetSerAlaValSerSerGln----- 228
QY 400 GGAAGAAGAACTGAAAGTTTGGATTACCTGCTCATGAACAAATTCGACTGCTGGTTC 459
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
229 GluLysGlnValGluIleLeuGluTyrProTyrHisGluGlnIleAlaValAlaPro 248
QY 460 GAGAAATCTTACGCCTCACCTGAAATATGATGGCTATGGACTTCCAAAGTTCAGGT 519
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
249 GluSerLeuLeuThrGlyHisAsnTyrThrLeuLysIleGluTyrSerAlaAsnIleSer 268
QY 520 GATGGCTTTGAAGGGTTTATAAAGACACATACAGAACTCTTGGTGGTGAACAAGATT 579
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
269 AsnSerTyrTyrGlyPheTyrGlyIleThrTyrThrAspLysSerAsnGluLysLysAsn 288
QY 580 CTTCAGTAAACAGATTTTGAGCCCAAGGACGACGATGGCTTCCCTTGGTGTGATGA 639
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
289 PheAlaAlaThrGlnPheGluProLeuAlaAlaArgSerAlaPheProCysPheAspGlu 308
QY 640 CCGTTGTTCCAAAGCCAACTTTCAATCAAGATACGAAGAGAGAGAGAGGATATTGCACTA 699
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
309 ProAlaPheLysAlaThrPheIleIleLysIleThrArgAspGluHisThrAlaLeu 328
QY 700 TCAACATGCCAAAGGTTAAGACAATTGAAGAGGAGGTCTTTTGGAGAGATCACTTT 759
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
329 SerAsnMetProLysLysSerSerValProThrGluGluLeuIleGlnAspGluPhe 348
QY 760 GAACTACTGTAAAATGAGTACATACCTTTAGCCTACATAGTTTGTGATTTCCACTCT 819
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
349 SerGluSerValLysMetSerThrTyrLeuValAlaPheIleValGlyGluMetArgAsn 368
QY 820 CTGAGTGGCTTCACTTTCATCAGGGGTCAAGGTGTCCTATCATGCATCCCGACCAACGG 879
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
369 LeuSerGln---AspValAsnGlyThrLeuValSerValTyrAlaValProGluLysIle 387
QY 880 AATCAAAACACATTATGCTTTGCAGGCATCATCGAAGTACTTGATTTTATGAAAAGTAC 939
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
388 AspGlnValTyrHisAlaLeuAspThrThrValLysLeuLeuGluPheTyrGlnAsnTyr 407
QY 940 TTTGATATCTACTATCCACTCTCCAACTGGATTAATTGCTATTCTCTGACTTTGCACCT 999
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
408 PheGluIleGlnTyrProLysLysLysLeuAspLeuValAlaIleProAspPheGluAla 427
QY 1000 GGAGCCATGGAAAATTTGGGCGCTCATTCATATAGGAGACGCTCACTGCTTTTGGACCC 1059
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
428 GlyAlaMetGluAsnTrpGlyLeuLeuThrPheArgGluGluThrLeuLeuTyrAspAsn 447
QY 1060 AAGACCTCTTCTGCTTCCGATAAATGTGGGTCCACAGAGTCATAGCCCATGAAGTGGCG 1119
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
448 AlaThrSerSerValAlaAlaAspArgLysLeuValThrLysIleIleAlaHisGluLeuAla 467
QY 1120 CACCAAGTGGTTTGGCAACCTGCTCAATGGAATGGTGGAAATGATATTTGGCTTAAGGAG 1179
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
468 HisGlnTrpPheGlyAsnLeuValThrMetGlnTrpTrpAsnAspLeuTrpLeuAsnGlu 487
QY 1180 GGTTTTGGAAAATACATGGAACCTTATCGCTGTTAATGCTACATATCCAGAGCTGCAATTT 1239
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
488 GlyPheAlaThrPheMetGluTyrPheSerValGluLysIlePheLysGluLeuAsnSer 507
QY 1240 GATGACTATTTTGAATGTGTGTTTGAAGTAATATTCACAAAAGATTTCATTGAATTCATCC 1299
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
508 TyrGluAspPheLeuAspAlaArgPheLysThrMetArgLysAspSerLeuAsnSerSer 527
QY 1300 CGCCCTATCTCCAAACAGCGGAAACCCCGACTCAAAATACAGAAATGTTTGTATGAAGTT 1359
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
528 HisProIleSerSerSerValGlnSerSerGluGlnIleGluGluMetPheAspSerLeu 547

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QY 1360 TCCTATAACAAGGAGCTGTATTTTGAATGCTCAAGGATTTTCTGGGTGAGAGAA 1419
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
548 SerTyPheLysGlyAlaSerLeuLeuMetLeuLysSerTyPheLysLeuSerVal 567
QY 1420 TTCAGAAAGGAATAATTCAGTACTTAAGAAGTTTCAGCTATAGAAATGCTAAGAAATGAT 1479
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
568 PheGlnHisAlaIleLeuTyPheLysHisSerTyPheLysAlaIleGlnSerAsp 587
QY 1480 GACTTGTGGAGCAGTCTCTCAAAATAGTTGTTTGAAGATGATTTTACATCTGGTGGAGTT 1539
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
588 AspLeuTyrAspSerPheAsnGlu----- 595
QY 1540 TGTCTATCCGATCCCAAGATGACAAGTAAACATGCTCGCTTCTCTGGGGGGAATAATGCACAG 1599
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
596 -----ValThrGlyLeuThrLeuAsp 602
QY 1600 GTCAGAGAGATGATGACTACATGGAATCTCCAGAAAGGAATCCCTCTCGTGTGTTAAA 1659
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
603 ValLysLysMetLeuLysThrTrpThrLeuGlnLysGlyPheProLeuValThrValGln 622
QY 1660 CAAGACGGGTGTTCATCCGATGCAACAGAGCGCTTCTCCAGGGGGTTCCTCAGGAA 1719
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
623 ArgLysGlyThrGluLeuLeuGlnGlnGluArgPhePheProSerMet----- 639
QY 1720 GACCTGAATGGAGGGCCCTCAGAGAGGTACCTGCGCATATCCCATTCACCTACTCC 1779
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
640 GlnProGluIleGlnAspSerAspThrSerHisLeuTrpHisIleProIleSerTyPheVal 659
QY 1780 ACGAGTTCTTCTAATGTGATCCACAGACAC-----ATTCTAAATCAACACAGAT 1830
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
660 ThrAspGlyArgAsnTyPheSerGluTyrArgSerValSerLeuLeuAspLysSerAsp 679
QY 1831 ACTCTGGATCTACCTGAAACACCAAGTTGGGTGAAATTTAATGTGGACTCAATGGTTAC 1890
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
680 ValIleAsnLeuThrGluGlnValGlnTrpValLysValAsnThrAsnMetThrGlyTyr 699
QY 1891 TACATCGTTCACTATGAGGTGATGGATGGACCACTCATACACAGCTGAATCAGAAC 1950
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
700 TyrIleValHisTyPheAlaHisAspGlyTrpAlaAlaLeuIleAsnGlnLeuLysArgAsn 719
QY 1951 CACACATCTTCAGACCTCAAGACAGAGTAGTCTGATTTCATGATGTTTTCAGTAGTT 2010
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
720 ProTyPheLeuSerAspLysAspArgAlaAsnLeuIleAsnAsnIlePheGluLeuAla 739
QY 2011 GGTGAGGAGGAGACTGACCTCAGACAAAGCTCTTCACATGACTTACTACTCTCAACATGAA 2070
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
740 GlyLeuGlyLysValProLeuGlnMetAlaPheAspLeuIleAspTyPheLysArgAsnGlu 759
QY 2071 ACAAGACCCCGCAGCTCTCGAAGTCTGAGTTACTTGGAAATCGTTTTCACCATGATG 2130
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
760 ThrHisThrAlaProIleThrGluAlaLeuPheGlnThrAspLeuIleTyPheAsnLeuLeu 779
QY 2131 GACAGAGGAATATTTACAGATATCTCTGAAACCTCAAGCGTTACCTTCTTCAGTATTTT 2190
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
780 GluLysLeuGlyHisMetAspLysSerSerArgLeuValThrArgValHisLysLeuLeu 799
QY 2191 AAGCCAGTGATTCAGACAAAGCTGGAGTGACAGGGCTCAGTCTGGGACAGGATGCTC 2250
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
800 GlnAsnGlnIleGlnGlnThrTrpThrAspGluGlyThrProSerMetArgGluLeu 819
QY 2251 CGCTCGGCTCTCTTGAAGCTGCGCTGACCTGAACCATGCTCTTGTGATCCAGAAAGCT 2310
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
820 ArgSerAlaLeuLeuGluPheAlaCysAlaHisSerLeuGluAsnCysThrThrMetAla 839
QY 2311 GCTGAATCTTCTCCAGTGGATGAATCCAGTGGAAAATTAATATATACCAACAGATGTT 2370
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
840 ThrLysLeuPheAspGlyTrpMetAlaSerAsnGlyThrGlnSerLeuProThrAspVal 859
QY 2371 TTAAGATGTTGTATTTCTGTGGTCTCAGACACAGCAGGATGGAATTCCTTTTACAG 2430
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
860 MetThrThrValPheLysValGlyAlaArgThrGluLysGlyTrpLeuPheLeuPheSer 879
QY 2431 CAATATGAATGTCATATGTCAGTCTGAAACAAACAAACAAATTCGTGTATGCTTTGTCAACG 2490
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Db 880 MetTyPheSerSerMetGlySerGluAlaGluLysAspLysIleLeuGluAlaLeuAlaSer 899
QY 2491 AGCAAGCATCAGGAAAAAGTTTCAAGTAAATTTCAACTAGGAATGGAAGGAAAGTTATC 2550
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
900 SerAlaAspAlaHisLysLeuTyPheLeuMetLysSerSerLeuAspGlyAspIleIle 919
QY 2551 AAGACACAGAACTGGGAGCTCTCTTCATGCGGATTCGACAGCTCCAAAGGGGAGCA 2610
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
920 ArgThrGlnLysLeuSerLeuIleArgThrValGlyArgGlnPheProGlyHisLeu 939
QY 2611 CTAGCATGGGATTTTGAAGAGAAATTTGGACCCATCTCTGAAAAAATTTGACTTGGGC 2670
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
940 LeuAlaTrpAspPheValLysGluAsnTrpAsnLysLeuValHisLysPheHisLeuGly 959
QY 2671 TCATATCAGCATTAAGATGATCATCTCTGGCACACACAGCTCACATTTTCTTCCAAAGGATAAG 2730
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
960 SerTyPheThrIleGlnSerIleValAlaGlySerThrHisLeuPheSerThrLysThrHis 979
QY 2731 TTGCAAGAGGTGAACATATTTTGAATCTCTTCAGGCTCAGGATCACATCTCGATATT 2790
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
980 LeuSerGluValGlnGluPhePheGluAsnGlnSerGluAlaThrLeuGlnLeuArgCys 999
QY 2791 TTTCAAACTGTCTGGAAACGATAACCAAAAATATAAAATGGCTGGAGAACTCTCCG 2850
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1000 ValGlnGluAlaPheGluValIleGluLeuAsnIleGlnTrpMetAlaArgAsnLeuLys 1019
QY 2851 ACTCTGAGGACTTGGCTA 2868
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1020 ThrLeuThrLeuTrpLeu 1025 AA.

RESULT 11
Q8C129 ID Q8C129 PRELIMINARY; PRT; 1025 AA.
AC Q8C129;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched
DE library, clone:4732490P18 product:INSULIN-REGULATED MEMBRANE
DE AMINOPEPTIDASE IRAP homolog.
GN Name=Lnpep;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RT The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
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Db      760 AsnHisThrAlaProIleThrGluAlaLeuPheGlnThrAspLeuIleTyrAsnLeuLeu 779
Qy      2131 GACAGAAGGAATATTTTCAGATATCTCTCAAAACCTCAAGCGTTACCTCTTCAGTATTTT 2190
Db      780 GluLysLeuGlyTyrMetAspLeuAlaSerArgLeuValThrArgValPheLysLeuLeu 799
Qy      2191 AAGCCAGTGATTGACAGCAAGAGCTGGAGTGACAAAGGGCTCAGTCTGGGACAGCATGCTC 2250
Db      800 GlnAsnGlnIleGlnGlnThrTrpThrAspGluGlyThrProSerMetArgGluLeu 819
Qy      2251 CGCTCGGCTCTTTGAAGCTGGCTGTGACCTGAACCATGCTCTTCGATCCAGAAAGCT 2310
Db      820 ArgSerAlaLeuLeuGluPheAlaCysThrHisAsnLeuGlyAsnCysSerThrThrAla 839
Qy      2311 GCTGAATCTCTCCAGTGGAATCCAGTCGAGTGGAAATTAATATACCAACAGATGTT 2370
Db      840 MetLysLeuPheAspArgTrpMetAlaSerAsnGlyThrGlnSerLeuProThrAspVal 859
Qy      2371 TTAAGATTGTGTATCTCTGGGTGCTCAGACACAGCAGCATGGAATTACCTTTTAGAG 2430
Db      860 MetThrThrValPheLysValGlyAlaLysThrAspLysGlyTrpSerPheLeuLeuGly 879
Qy      2431 CAATATGAATGTCAATGTCAAGTGTGCAACAAACAAATTCGTATGCTTTGTCAACG 2490
Db      880 LysTyrIleSerIleGlySerGluAlaGluLysAsnLysIleLeuGluAlaLeuAlaSer 899
Qy      2491 AGCAGCATCAGGAAAGTTACTGAAGTTAATTGAACCTAGGATGGAAGGAAGGTTATC 2550
Db      900 SerGluAspValArgLysLeuTyrTrpLeuMetLysSerSerLeuAsnGlyAspAsnPhe 919
Qy      2551 AAGACACAGAACTTGGCAGCTCTCTTCATCGCATTCGACAGCTCCAAAGGGCGACAA 2610
Db      920 ArgThrGlnLysLeuSerPheIleIleArgThrValGlyArgHisPheProGlyHisLeu 939
Qy      2611 CTAGCATGGGATTTTGAAGAAATTTGACCATCTTCTGAAATAATTTGACTTGGGC 2670
Db      940 LeuAlaTrpAspPheValLysGluAsnTrpAsnLysLeuValGlnLysPheProLeuGly 959
Qy      2671 TCATATGACATCAAGCATCATCTCTGGCACACAGCTCCTTTCTTCCAGGATAAG 2730
Db      960 SerTyrThrIleGlnAsnIleValAlaGlySerThrTyrLeuPheSerThrLysThrHis 979
Qy      2731 TTGCAAGAGGTGAACACTATTTTTCATCTCTTGGAGCTCAAGCATCACATCTCGATATT 2790
Db      980 LeuSerGluValGlnAlaPhePheGluAsnGlnSerGluAlaThrPheArgLeuArgCys 999
Qy      2791 TTTCAAATGTTCTGGAAACGATTAACCAAAATATAAATGGCTGGAGAGAAATCTTCCG 2850
Db      1000 ValGlnGluAlaLeuGluValIleGlnLeuAsnIleGlnTrpMetGluLysAsnLeuLys 1019
Qy      2851 ACTCTGAGGACTTGGCTA 2868
Db      1020 SerLeuThrTrpTrpLeu 1025

RESULT 13
Q8C9W5 PRELIMINARY; PRT; 694 AA.
AC Q8C9W5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched
DE library, clone:443008E13 product: type 1 tumor necrosis factor
DE receptor shedding aminopeptidase regulator, full insert sequence.
DE (fragment).
GN Name=Arts1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
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RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA The FANTOM Consortium
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh K., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK040350; BAC30569.1; -.
DR MGD; MGI:1933403; Arts1.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0004178; F:leucyl aminopeptidase activity; IDA.
DR GO; GO:0004239; F:methionyl aminopeptidase activity; IDA.
DR GO; GO:0045766; P:positive regulation of angiogenesis; IMP.
DR InterPro; IPR001930; Peptidase_M1.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF01433; Peptidase_M1; 1.
DR PRINTS; PR00756; ALADIPASE.
DR PROSITE; PS00142; ZINC PROTEASE; UNKNOWN_1.
KW Aminopeptidase; Receptor.
RN NON_TER 1
RP SEQUENCE 694 AA; 80186 MW; B1EA3680BBC60BCB CRC64;
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DB	300	GluHisTyrMetIysGly-----SerGluArgPheProGluThrGly	313
QY	1750	TACCTGGGCATATCCCACTGACCTACTCCACGAGTTCTTCTTAATGTGATCCACAGACAC	1809
DB	314	TyrLeuTrpHisValProLeuThrPheIleThrSerIysSerAspSerValGlnArgPhe	333
QY	1810	ATTCTAAATCAACAGACAGATACTCTCGATCTACCTGAAAAGACCAGTGGGTGGAATTT	1869
DB	334	LeuLeuIysThrIysThrAspValLeuLeuProGluAlaValGlnTrpIleLysPhe	353
QY	1870	AATCTGCATCAAAATGGTTACTACATCGTTCACTATCAGGTCATGATGGACCAACTC	1929
DB	354	AsnValGlyMetAsnGlyTyrTyrIleValHisTyrAlaAspAspGlyTrpAlaSerLeu	373
QY	1930	ATTACAGAGCTGAATCAGAACCAACACACTTCTCAGACCTAAGGACAGAGTAGGTCTGATT	1989
DB	374	SerGlyLeuLeuIysGluAlaHisThrThrIleSerSerAsnAspArgAlaSerLeuIle	393
QY	1990	CATGATGTGTTTACGCTAGTTGGTGAGGAGAGACTGACCTTAGACAAGCTCTTGACATG	2049
DB	394	AsnAsnAlaPheGlnLeuValSerIleGluLysLeuSerIleGluLysAlaLeuAspLeu	413
QY	2050	ACTTACTACTCTCCAAACATGAACCAAGCAGCCCGCACTTCTCGAAGTCTGAGTTACTTG	2109
DB	414	ThrLeuTyrLeuIysAsnGluThrGluIleMetProIlePheGlnAlaLeuAsnGluLeu	433
QY	2110	GAATCGTGTATCCACATGATGGACAGAGGAATATTTTCAGATATCTCTGAAAACCTCAAG	2169
DB	434	IleProMetTyrLysLeuMetGluLysArgAspMetIleGluValGluThrGlnPheLys	453
QY	2170	CGTTACCTTCTTCAGTATTTTAAAGCCTAGTATGACAGGCAAAAGCTCGAGTGCACAGGGC	2229
DB	454	AspPheLeuLeuLysLeuLeuLysAspLeuIleAspLysGlnThrTrpThrAspGluGly	473
QY	2230	TCAGTCTGGGACGAGTCTCCGCTCGCTCTTGAAGCTGCCTCGCTACCTGGAACCAT	2289
DB	474	SerValSerGluArgMetLeuArgSerGlnLeuLeuLeuLeuLysValArgAsnTyr	493
QY	2290	GCTCTTGGCATCCAGAAAGCTGCTGAACTCTTCTCCAGTGGATGGAATCCAGTGGAAAA	2349
DB	494	GlnProCysValGlnArgAlaGluArgTyrPheArgGluTrpLysSerSerAsnGlyAsn	513
QY	2350	TTAATATATACACAGATGTTTTAAAGATTGTGTATTCTCTGGGTGCTCAGACAAACGCA	2409
DB	514	MetSerIleProIleAspValThrLeuAlaValPheAlaValGlyAlaGlnAsnThrGlu	533
QY	2410	GGATGGAATACCTTTTAGAGCAATAGAACTGTCATATGCTCAAGTCTCAAGTGCCTGAACAAACAAA	2469
DB	534	GlyTrpAspPheLeuTyrSerLysTyrGlnSerSerSerSerThrGlnLysLysSerGln	553
QY	2470	ATTCGTATGCTTTGTCAACGAGCAAGCATCAGAAAAGTTTACTGAAAGTTAAATGAACTA	2529
DB	554	IleGluPheSerLeuCysThrSerLysAspProGluLysLeuGlnTrpLeuLeuAspGln	573
QY	2530	GGAAATGGAAGAAAGTTATCAAGACACAGAACTTGGCAGCTCTCCTTCATCGCATGCC	2589
DB	574	SerPheLysGlyGluIleIleLysThrGlnGluPheProHisIleLeuThrLeuIleGly	593
QY	2590	AGAGCTTCAAGGGGACAGCAACTAGCATGGGATTTCTTAAGAGAAATTTGGACCCATCTT	2649
DB	594	ArgAsnProValGlyTyrProLeuAlaTrpLysPheLeuArgGluAsnTrpAsnLysLeu	613
QY	2650	CTGAAAAAATTTGACTTGGGCTCATATGACATAAGGATGATCATCTCTGCACACACAGCT	2709
DB	614	ValGlnLysPheGluLeuLeuGlySerSerSerSerIleAlaHisMetValMetGlyThrThrAsp	633
QY	2710	CACTTTTTCTCCAGGATAAGTTGCAAGAGGTGAAACTATTTTTTGAATCTCTTGAGGCT	2769
DB	634	GlnPheSerThrArgAlaArgLeuGluGluValLysGlyPhePheSerSerLeuLysGlu	653
QY	2770	CAGGATTCATCTGGATATTTTTTCAACTGTCTTGGAAACGATAACCAAAAATATATAA	2829
DB	654	AsnGlySerGlnLeuArgCysValGlnGlnThrIleGluThrIleGluGlnGlnIleArg	673

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QY 2830 TGGCTGAGAGAATCTTCGACTCTGAGGACTTGCTA 2868
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674 TtpMetAspLysAsnPheAspLysIleArgLeuTrpLeu 686
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RESULT 14
Q6PCGS PRELIMINARY; PRT; 997 AA.
AC Q6PCGS;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE MGC69084 protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN _
[1]
RN SEQUENCE FROM N.A.
RC MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Joquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.C., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
[3]
RN SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Klein S., Strausberg R.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC059334; AAH59334.1; -.
DR GO; GO:0004179; F:membrane ananyl aminopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001930; Peptidase_M1.
DR Pfam; PF01433; Peptidase_M1.
DR PRINTS; PR00756; ALADIPTASE.
DR PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.
SQ SEQUENCE 997 AA; 113619 MW; 460E0EC895D2A14 CRC64;

Alignment Scores:
Pred. No.: 4e-116 Length: 997
Score: 1847.00 Matches: 383
Percent Similarity: 59.19% Conservative: 161
Best Local Similarity: 41.68% Mismatches: 287
Query Match: 36.49% Indels: 88
DB: 2 Gaps: 16
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Db 479 LeuTrpLeuAsnGluGlyPheAlaThrTyrMetGluTyrPheSerValSerSerLeuPhe 498
Qy 1225 CCAGAGTCGAATTTGATGACTATTTTGAATGTGTTTGAAGTAATTTACAAAGAT 1284
Db 499 ProGluLeuAsnSerGluAsnSerPheLeuLysMetArgPheMetAlaLeuLysLysAsp 518
Qy 1285 TCATTGAATTCATCCCGCCCTATCTCCAAACCCGGAACCCCGACTCAATACAGAA 1344
Db 519 SerLeuAsnAlaSerHisProIleSerThrAspIleArgSerProGluGlnIleGluGlu 538
Qy 1345 ATGTTTGAATGAGTTTCTTATAACAGGAGCTGTGATTTTGAATATATCTCAAGGATTTT 1404
Db 539 MetPheAsnAspLeuSerTyrIleLysGlyAlaSerIleLeuLeuMetLeuLysThrPhe 558
Qy 1405 CTGGGTGAGGAGAAATTCAGAAAGGAATAATTCAGTACTTAAGAAAGTTCAGCTATAGA 1464
Db 559 LeuSerGluAspMetPheHisLeuSerIleArgSerTyrLeuGlnSerHisGlnTyrGly 578
Qy 1465 AATGCTAAGATGACTCTGGAGCAGCTGTCAATAGTGTGTTTGAAGAGTATTTT 1524
Db 579 SerThrThrSerAspSerLeuTrpAspSerLeuAsn----- 590
Qy 1525 ACATCTGGTGAGTTTGTCAATCGGATCCCAAGATGACAAGTAAACATGCTCGCCTTTCTG 1584
Db 591 -----ValValThr 593
Qy 1585 GGGGAAATCAGAGGTCGAAGAGATGATGACTACATGACTCTCCAGAAAGGAATCCCC 1644
Db 594 LysGluAsnProAsnValLysAsnMetMetLysThrTrpGlnLysAlaGlyTyrPro 613
Qy 1645 CTGCTGGTGGTTAAACAAGAGGGTGTTCATCTCCGACTGCAACAGGAGCGTTCTCCAG 1704
Db 614 LeuValThrAlaLeuArgLysGlyGluGluIleThrValArgGlnGluArgPheLeuArg 633
Qy 1705 GGGGTTTCCAGGAAGACCTGAATGGAGGCGCTCGCAGGAGAGTACTCTGGCATATC 1764
Db 634 SerThr-----LysProAsp---HisAlaThrAsnAlaSerThrValTrpHisIle 649
Qy 1765 CCATGACCTACTCCACGAGTCTTCTAATGTGATCCACAGA-----CAC 1809
Db 650 ProLeuThrTyrValThrLysLysCysAsnGlyValAspProAspCysAspLysValTyr 669
Qy 1810 ATTTAAATCAAGACAGATACTCTGATCTGATCTGAAAGACAGCTTGGTGAATTT 1869
Db 670 LeuLeuLysAlaProThrGlyThrIleAsnValSerSerGluPheProTrpValLysPhe 689
Qy 1870 AATGTGGACTCAAATGGTTTACTACATCTCTACATGAGGTCATGGATGGACCAACTC 1929
Db 690 AsnValAsnMetThrGlyTyrTyrIleValAspTyrGlyAlaAspGlyTyrPaspAlaLeu 709
Qy 1930 ATTACACAGCTGAATCAGAACACACACTTCTCAGACCTTAAGGACAGAGTAGGTCTGATT 1989
Db 710 IleGluGlnLeuHisArgAspHisThrValLeuHisSerSerAspArgAlaAsnLeuIle 729
Qy 1990 CATGATGTTTACGATAGTTGGTCGAGGAGACTGACCTAGACAGCTCTTGACATG 2049
Db 730 HisAspIlePheMetLeuAlaGlyValGlyLysValProLeuAlaLysAlaPheLysLeu 749
Qy 2050 ACTTACTACTCCAAATGAAACAGACCGCCGACCTCTCGAAGGCTCGATTACTGTG 2109
Db 750 LeuGlyTyrLeuValAsnGluThrAspSerAlaProIleIleGlnAla-----Leu 766
Qy 2110 GAATCGTTTTTACCAC-----ATGATGACAGAGGAATATTTACAGATATCTCGAA 2160
Db 767 HisGlnPheTyrHisIleArgGlyIleLeuLeuLysArgGlyLeuAspAspLeuSerAsp 786
Qy 2161 AACCTCAAGCGTTACTCTTTCAGTATTTTAAGCCAGTGATGACGAAAGCTGGAGT 2220
Db 787 LysLeuMetGluArgGlyLeuAspLeuLeuAsnAsnThrLeuIleLysGlnThrTrpLys 806
Qy 2221 GACAGGCTCAGTCTGGACAGGATGCTCGCTCGGCTCTCTTGAAGCTCGCCTGTGAC 2280
Db 807 AspGluGlyThrLeuAlaGluArgGluLeuArgThrSerLeuLeuAspPheAlaCysSer 826

Qy 2281 CTGAAACCATGCTCTTCATCCAGAAAGCTGCTGAACTCTTCTCCAGTCGATGAATCC 2340
Db 827 AsnGlyValLeuAsnCysLysLeuAspArgAlaThrGluLeuPheAsnSerTrp-----Arg 844
Qy 2341 AGTGGAAATTTAAATATACCAACACAGATGTTTAAAGATTTGTGATTCTGTGGGTGCAC 2400
Db 845 PheAsnGluThrArgIleProSerAspValIleAsnIleValPheLysValGlyThrLys 864
Qy 2401 ACAACACAGCATGGAATTTACCTTTTAGACAATATGAATCAATGTCAAGTGTGCTGAA 2460
Db 865 ThrThrGluGlyTrpThrPheLeuArgArgTyrAspSerSerIleTyrGluSerGlu 884
Qy 2461 CAAAACAAAATTCGTATGCTTTGTCAACGACGACATCAGGAAAGTTACTGAAGTTA 2520
Db 885 LysSerLysIleLeuGluAlaLeuAlaSerThrAspAsnAlaLysAspLeuGlnGlyLeu 904
Qy 2521 ATTGAACCTAGGAATGGAAGGAAGTTTATCAAGACACAGAACTTGGCAGCTCTCTTCAT 2580
Db 905 MetGlnGluSerLeuAlaGlyGlySerIleArgSerGlnGluLeuProAsnValIleSer 924
Qy 2581 GCGATTCCGACAGCTCCAAAGGGCAGCAACTAGCAGGATTTTGAAGAGAAAATGG 2640
Db 925 PheIleCysArgArgSerProGlyTyrLeuLeuAlaTrpAsnPheValLysGlnAsnTrp 944
Qy 2641 ACCATCTCTCGAAAATTTGACTTGGGCTCATATGACATAGGATGATCATCTCTGGC 2700
Db 945 AsnLeuIleThrGlnLysLeu----- 951
Qy 2701 ACAACAGCTCACTTT-----TCTTCCAGGATAAGTTGCAAGAGGTGAAACTATTTT 2754
Db 952 -----LeuHisPhePheAsnSerThrLysGluLysSerArgGluValTyrTyrValLys 969
Qy 2755 GAATCTCTTGGGCTCAAGGATCATCATCTGGATATTTTCAAACTGTTCTGGAAACGATA 2814
Db 970 GluAla-----LeuGluThrIle 975
Qy 2815 ACCAAAATATAAATGCTGGAGAGAACTTTCGACTCTGAGGACTGCGCTAATG 2871
Db 976 LysLeuAsnIleLysTrpMetLysAsnAsnLeuAspSerLeuLysThrTrpLeuLeu 994

RESULT 15
Q8WVJ4
ID Q8WVJ4 PRELIMINARY; PRT; 350 AA.
AC Q8WVJ4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE LRAP protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Asavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodríguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RP [2].
RQ SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC017927; AAH17927.1; -.
DR MEROPS; M01.024; -.
DR GO: 0004179; F:membrane alanyl aminopeptidase activity; IEA.
DR GO: 0006508; P:proteolysis and peptidolysis; IEA.
DR PRINTS; PR00756; ALADPTASE.
SQ SEQUENCE 350 AA; 40060 MW; 5234F40276A81253 CRC64;

Alignment Scores:

Pred. No.:	1.29e-105	Length:	350
Score:	1690.00	Matches:	322
Percent Similarity:	99.69%	Conservative:	2
Best Local Similarity:	99.08%	Mismatches:	1
Query Match:	33.39%	Indels:	0
DB:	2	Gaps:	0

US-10-039-073-3 (1-2883) x Q8WVJ4 (1-350)

QY	1	ATGTTCCATTCTTCTGCAATGGTTAATTACACAGAAACCAATGTTTAACATTTCACAGA	60
DB	1	MetPheHisSerAlaMetValAsnSerHisArgLysPrometPheAsnIleHisArg	20
QY	61	GGATTTTACTGCTTAACAGCCACTCTGCCCCAAATATGCATTTGTTCTCAGTTCCTCAGTG	120
DB	21	GlyPheTyrCysLeuThrAlaIleLeuProGlnIleCysIleCysSerGlnPheSerVal	40
QY	121	CCATCTAGTTATCACTTCACTAGGATCTCTGGGCTTTCCAGTAGCCACTAATGGGAA	180
DB	41	ProSerSerTyrHisPheThrGluAspProGlyAlaPheProValAlaThrAsnGlyGlu	60
QY	181	CGATTTCTTGGCAGGAGCTAAGGCTCCCGAGTGTGCTATCTCTCCATTATGACCTC	240
DB	61	ArgPheProIrpGlnGluLeuAsgLeuProSerValValIleProLeuHisTyrAspLeu	80
QY	241	TTGTGTCACCCCAATCTCACTCTCTGGACTTTGTTGCATCTCGAAGAGTCGAAGTCTTG	300
DB	81	PheValHisProAsnLeuThrSerLeuAspPheValAlaSerGluLysIleGluValLeu	100
QY	301	GTACGCAATGCTACCCAGTTTATCATCTTCACAGCAAGAACTCTTGAATCAGCAATGCC	360
DB	101	ValSerAsnAlaThrGlnPheIleIleLeuHisSerLysAspLeuGluIleThrAsnAla	120
QY	361	ACCTTCAGTCAGAGGAAGATTCAAGATACATGAACACGAGAAAGAACTGAAAGTTTG	420
DB	121	ThrLeuGlnSerGluGluAspSerLysTyrMetLysProGlyLysGluLeuLysValLeu	140
QY	421	AGTTACCTGCTCATGAACAAATTCGACTGCTGGTTCAGAGAAACTTAGCCCTCACCTG	480
DB	141	SerTyrProAlaHisGluGlnIleAlaLeuValProGluLysLeuThrProHisLeu	160
QY	481	AAATCTATGTGGCTATGACTTCCAAAGCCAAAGTTAGGTGATGGCTTTGAAGGGTTTAT	540
DB	161	LysTyrTyrValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTyr	180
QY	541	AAAGCACATACAACTCTTGGTGTGAACAGATTCTTCAGTAAACAGATTGAG	600
DB	181	LysSerThrTyrArgThrLeuGlyGlyGluThrArgIleLeuAlaValThrAspPheGlu	200
QY	601	CCAAACCCAGCAGCATGGCTTTCCCTTGCTTGTGATGAACCGTTGTTCAAAGCCAACTTT	660
DB	201	ProThrGlnAlaArgMetAlaPheProCysPheAspGluProLeuPheLysAlaAsnPhe	220
QY	661	TCAATCAAGATACGAAGAGAGCAGGCATATTGCATATCCAAACATGCCAAAGGTTAAG	720
DB	221	SerIleLysIleArgArgGluSerArgHisIleAlaLeuSerAsnMetProLysValLys	240

Search completed: September 26, 2005, 07:44:30
Job time : 537.896 secs

QY	721	ACAAATTGAACCTTGAAGGAGGTCTTTTGGAGATCACTTTGAAACTACTCTGTAATAATGAGT	780
DB	241	ThrIleGluLeuGluGlyGlyLeuLeuGluAspHisPheGluThrThrValLysMetSer	260
QY	781	ACATACCTTGTAGCCTACATAGTTTGTGATTTCCTCACTCTCTGAGTGGCTTCACATCA	840
DB	261	ThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThrSerSer	280
QY	841	GGGTCGAAGGTGTCCATCTATGCATCCCGACACAAACGGAATCAACACATATGCTTG	900
DB	281	GlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyrAlaLeu	300
QY	901	CAGGCATCACTGAAGCTACTTGTATTTTATGAAAAGTACTTTTGATATCTACTATCCACTC	960
DB	301	GlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyrProLeu	320
QY	961	TCCAAACTCGATTTA	975
DB	321	SerLysLeuGlyMet	325

GenCore version 5.1.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 26, 2005, 06:04:35 ; Search time 354.781 Seconds
(without alignments)
6285.736 Million cell updates/sec

Title: US-10-039-073-3

Perfect score: 5062

Sequence: 1 atgttcattcttctgcaat.....ggctaatgggttaactactaa 2883

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-Q=/sgn2_1/USPTO spool_p/US10039073/runat_26092005_070409_21298/app_query.fasta_1.6606
-DB=A_Geneseq -QFMT=fafatan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10039073 @CGN 1 1 933 @runat 26092005_070409_21298 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG-SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: Geneseq16Dec04:*
- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	5052	99.8	960	AAB60299	Human ami
2	5052	99.8	960	AAB60299	Human pro
3	5048	99.7	960	ABP69122	Human pol
4	4141	81.8	785	ABP63022	Human pol
5	3799	75.0	728	ABP63022	Human pol
6	3799	75.0	728	ABP63022	Human pol
7	3770	74.5	722	AAU22399	Novel hum
8	3770	74.5	722	ABP67098	Human pol
9	3770	74.5	722	ABP67098	Human pol
10	3763	74.3	722	ADR41453	Human CD-

11	2516.5	49.7	941	4	AAU07829	Human APT
12	2515.5	49.7	941	5	ABP90347	Human pol
13	2515.5	49.7	941	6	ADA56820	Human sec
14	2515.5	49.7	941	6	ABR47686	Human sec
15	2515.5	49.7	941	6	ABR00040	Human gen
16	2515.5	49.7	941	7	ADB91494	Human sec
17	2515.5	49.7	941	7	ADC74064	Human sec
18	2515.5	49.7	941	7	ADD37852	Human sec
19	2515.5	49.7	941	7	ADD37852	Human col
20	2512.5	49.6	941	3	AAV66736	Membrane-
21	2512.5	49.6	941	3	AAV66736	Membrane-
22	2512.5	49.6	941	3	AAV66736	Membrane-
23	2512.5	49.6	941	3	AAV66736	Membrane-
24	2512.5	49.6	941	3	AAV66736	Membrane-
25	2512.5	49.6	941	3	AAV66736	Membrane-
26	2512.5	49.6	941	3	AAV66736	Membrane-
27	2512.5	49.6	941	3	AAV66736	Membrane-
28	2512.5	49.6	941	3	AAV66736	Membrane-
29	2512.5	49.6	941	3	AAV66736	Membrane-
30	2512.5	49.6	941	3	AAV66736	Membrane-
31	2512.5	49.6	941	3	AAV66736	Membrane-
32	2512.5	49.6	941	3	AAV66736	Membrane-
33	2512.5	49.6	941	3	AAV66736	Membrane-
34	2512.5	49.6	941	3	AAV66736	Membrane-
35	2512.5	49.6	941	3	AAV66736	Membrane-
36	2512.5	49.6	941	3	AAV66736	Membrane-
37	2512.5	49.6	941	3	AAV66736	Membrane-
38	2512.5	49.6	941	3	AAV66736	Membrane-
39	2512.5	49.6	941	3	AAV66736	Membrane-
40	2512.5	49.6	941	3	AAV66736	Membrane-
41	2512.5	49.6	941	3	AAV66736	Membrane-
42	2512.5	49.6	941	3	AAV66736	Membrane-
43	2512.5	49.6	941	3	AAV66736	Membrane-
44	2512.5	49.6	941	3	AAV66736	Membrane-
45	2512.5	49.6	941	3	AAV66736	Membrane-

ALIGNMENTS

RESULT 1

AAB60299

ID AAB60299 standard; protein; 960 AA.

XX

AC AAB60299;

XX

DT 06-APR-2001 (first entry)

XX

DE Human aminopeptidase 17867.

XX

KW Human aminopeptidase 17867; neutral zinc metalloproteinase;

KW zinc-binding region; M1 aminopeptidase family; lung disorder;

KW colon disorder; lung cancer; colon cancer; breast cancer; tumour;

KW squamous cell carcinoma; insulin-related disorder; diabetes;

KW drug screening.

XX

OS Homo sapiens.

XX

PN WO200100811-A2.

XX

PD 04-JAN-2001.

XX

PF 30-JUN-2000; 2000WO-US018250.

XX

PR 30-JUN-1999; 99US-00345650.

XX

PA (MILL-) MILLENNIUM PHARM INC.

XX

PI Kapeller-Libermann R, Williamson M;

XX

DR WPI; 2001-137953/14.

DR N-FSDB; AAF27148.

XX

PT Novel human aminopeptidase polypeptide and polynucleotide useful as

PT target for diagnosis and treatment in aminopeptidase-related disorders
 PT and for identifying modulators of therapeutic use.
 XX Claim 9; Fig 1; 92pp; English.

XX The invention relates to a novel human aminopeptidase, designated
 CC aminopeptidase 17867 (AAB60299) and to cDNA encoding aminopeptidase 17867
 CC (AA227148). Human aminopeptidase 17867 contains a neutral zinc
 CC metalloproteinase zinc-binding region signature motif at residues 367-376,
 CC and an M1 aminopeptidase signature motif at residues 334-338. The
 CC invention also relates to host cells comprising human aminopeptidase
 CC 17867 DNA, the preparation of the protein, an antibody which binds to the
 CC protein, methods of detection of the protein, methods of modulating
 CC activity of the protein, and methods of identifying modulators of protein
 CC activity. Aminopeptidase 17867 proteins and nucleic acids are useful as
 CC targets for diagnosis and treatment in aminopeptidase-related diseases.
 CC Such diseases include a wide variety of lung disorders (e.g., pulmonary
 CC embolism, pulmonary hypertension, emphysema, bronchial asthma) and colon
 CC disorders (e.g., diarrhoea, dysentery, Crohn's disease, ulcerative
 CC colitis). In particular, they may be used in the diagnosis and treatment
 CC of breast and colon carcinoma, lung carcinoma (especially squamous cell
 CC carcinoma), and insulin-related disorders such as diabetes. The
 CC aminopeptidase 17867 proteins are also useful in drug screening methods
 CC to identify modulators of activity, and for raising antibodies for use in
 CC diagnosis and treatment. The present sequence represents human
 CC aminopeptidase 17867

SQ Sequence 960 AA;

Alignment Scores:

Pred. No.: 0 Length: 960
 Score: 5052.00 Matches: 960
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.80% Indels: 0
 DB: 4 Gaps: 0

US-10-039-073-3 (1-2883) x AAB60299 (1-960)

Qy 1 ATGTTCCATCTTCTGCAATGGTTAAATTCACAGAAACCAATGTTTAACTTCACAGA 60
 Db 1 MetPheHisSerSerAlaMetValAsnSerHisArgLysProMetPheAsnIleHisArg 20
 Qy 61 GGATTTTACTCTTAAACAGCCATCTGCCCAATATGTCATTCTCTCAGTCTCTCAGTG 120
 Db 21 GlyPheTyrCysLeuThrAlaIleLeuProGlnIleCysIleCysSerGlnPheSerVal 40
 Qy 121 CCATCTAGTTATCACTTCACTAGGATCTCTGGGCTTTCCAGTAGCCACTTAATGGGAA 180
 Db 41 ProSerSerTyrHisPheThrGluAspProGlyAlaPheProValAlaThrAsnGlyGlu 60
 Qy 181 CGATTTCTTGGCAGGAGCTAAGCTCCCGATGCTGCTCATCTCCATTATGACCTC 240
 Db 61 ArgPheProTrpGlnGluLeuArgLeuProSerValValIleProLeuHisTyrAspLeu 80
 Qy 241 TTTGTCCACCCCAATCTCACCTCTCTGGACTTGTGTCATCTGAGAAGATCGAAGTCTTG 300
 Db 81 PheValHisProAsnLeuThrSerLeuAspPheValIleSerGluIleGluValLeu 100
 Qy 301 GTCAGCAATGCTACCCAGTTTATCATCTTGACAGCAAAAGATCTTGAATCACGAATGCC 360
 Db 101 ValSerAsnAlaThrGlnPheIleLeuHisSerLysAspLeuGluIleThrAsnAla 120
 Qy 361 ACCCTTCAGTCAGAGGAGATTCAAGATACATGATGAACCCAGGAAAGAACTGAAGTTTGT 420
 Db 121 ThrLeuGlnSerGluGluAspSerArgTyrMetLysProGlyLysGluLeuLysValLeu 140
 Qy 421 AGTTACCTCTCATGAACAAATTGCACTGCTGGTTCAGAGAACTTTACCCCTCACCTG 480
 Db 141 SerTyrProAlaHisGluGlnIleAlaLeuLeuValProGluLysLeuThrProHisLeu 160
 Qy 481 AAATACTATGTGGCTATGGACTTCCAGCCCAAGTTAGTGTGATGGCTTTGAAGGTTTAT 540

Db 161 LysTyrTyrValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTyr 180
 Qy 541 AAAAGCACATACAGAACTCTTGGTGTGAAACAGAAATCTTCAGTAAACAGATTTTGTAG 600
 Db 181 LysSerThrTyrArgThrLeuGlyGlyGluThrArgIleLeuAlaValThrAspPheGlu 200
 Qy 601 CCAACCCAGGCACGATGGCTTTCCCTTGTCTTGTATGAACCGTGTGTTCAAAGCCAACTTT 660
 Db 201 ProThrGlnAlaArgMetAlaPheProCysPheAspGluProLeuPheLysAlaAsnPhe 220
 Qy 661 TCAATCAAGATACGAAGAGAGACGAGCATATTTGCATATCCAAACATCCAAAGGTTAAG 720
 Db 221 SerIleLysIleArgArgGluSerArgHisIleAlaLeuSerAsnMetProLysValLys 240
 Qy 721 ACAATTGAATTCGAAGAGGCTCTTTTGGAGATCACTTTGAAACTACTGTAAAAATGAGT 780
 Db 241 ThrIleGluLeuGlyGlyLeuGluAspPheHisPheGluThrThrValLysMetSer 260
 Qy 781 ACATACCTTGTAGCCTACATAGTTTGTGATTTTCCACTCTCTGAGTGGCTTCACTTCATCA 840
 Db 261 ThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThrSerSer 280
 Qy 841 GGGGTCAAGGTGTCCATCTATGATCCCCAGACAAACGGAATCAACACATATGCTTTG 900
 Db 281 GlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyrAlaLeu 300
 Qy 901 CAGGCATCACTGAAGCTACTTGTATTTTATGAAAGTACTTTTCATATCTACTACTCACTC 960
 Db 301 GlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyrProLeu 320
 Qy 961 TCCAAACTGGATTAATTTGCTATTTCTGACTTTTGCACCTGGAGCCATGGAAAAATGGGGC 1020
 Db 321 SerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsnTrpGly 340
 Qy 1021 CTCATTACATATAGGAGAGCTGCTCTTTTGGACCCCAAGACCTCTTCTGCTCCGAT 1080
 Db 341 LeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAlaSerAsp 360
 Qy 1081 AAACCTGGGTCCACAGAGTCATAGCCCATGGAATTCGCGCACCAGTGGTTTGGCAACTG 1140
 Db 361 LysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeu 380
 Qy 1141 GTCACAAATGGAATGGTGAATGATATTTGGCTTTPAAGAGGGTTTGCAAAATACATGGAA 1200
 Db 381 ValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyrMetGlu 400
 Qy 1201 CTTATCGCTGTTAATGCTACATATCCAGAGCTCAATTTGATCACTATTTTTCGATGTG 1260
 Db 401 LeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeuAsnVal 420
 Qy 1261 TGTTCGAAAGTAAATTAACAAAGATTCATTTGAATTCATCCCGCCCTATCTCCAAACCCAGCG 1320
 Db 421 CysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLysProAla 440
 Qy 1321 GAAACCCCGACTCAATACAGGAAATGTTTGTATGAAGTTTCCCTATTAACAAAGGAGCTTGT 1380
 Db 441 GluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGlyAlaCys 460
 Qy 1381 ATTTTGAATATGCTCAAGGATTTTTCGGGTGAGAGAAATTCAGAGAGGAATTAATTCAG 1440
 Db 461 IleLeuAsnMetLeuLysAspPheLeuGlyGluLysPheGlnLysGlyIleIleGln 480
 Qy 1441 TACTTAAAGAAAGTTTCAAGTATGAAATGCTAAGAATGATCACTTGTGGAGCAGTCTCTCA 1500
 Db 481 TyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspAspLeuTrpSerSerLeuSer 500
 Qy 1501 AATAGTTGTTTACAAAAGTATTTTACATCTGGTGGAGTTTGTTCATTCGGATCCCAAGATG 1560
 Db 501 AsnSerCysLeuGluSerAspPheThrSerGlyGlyValCysHisSerAspProLysMet 520
 Qy 1561 ACAAGTAAACATGCTCGCTTCTTCTGGGGGAAATTCAGAGGCTCAAGAGATGATCACTACA 1620
 Db 521 ThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGluValLysGluMetMetThrThr 540

QY 1621 TGGACTCTCCAGAAAGGAATCCCTCGTGTGGTGTAAACAAGACGGGTGTTCACTCCGA 1680
DB 541 TrpThrLeuGlnLysGlyLeuProLeuValValLysGlnAspGlyCysSerLeuArg 560
QY 1681 CTGCAACAGGAGCGCTTCTCCAGAGGGGTTTTCCAGGAAGACCCCTGAAATGGAGGCCCTCG 1740
DB 561 LeuGlnGlnLysGlyPheLeuGlnGlyValPheGlnGluAspProGluTrpArgAlaLeu 580
QY 1741 CAGGAGAGGTACTCTGTGGCATATCCCATTTAGCACTACTCCACGAGTTCTTAAATGTGATC 1800
DB 581 GlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerThrSerSerAsnValIle 600
QY 1801 CACAGACACATTCTAAATCAAGAAGACAGATCTCTGGATCTACCTGAAAGACAGCTGG 1860
DB 601 HisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThrSerTrp 620
QY 1861 GTGAAATTAATGTGGACTCAATCGTTACTACATCGTTTCACTATGAGGGTCATGGTGG 1920
DB 621 ValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHisGlyTrp 640
QY 1921 GACCAACTCATTACACAGCTGAATCAGAACACACACACTTCTCAGACCTAAAGACAGAGTA 1980
DB 641 AspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAspArgVal 660
QY 1981 GGTCTGATTCATGATGTGTTTCACTAGTTGTGTGAGGAGACTGACCTCTAGACAAAGCT 2040
DB 661 GlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAspLysAla 680
QY 2041 CTTGACATGACTTACTCTCAACATGAAACAGCAGCCCGCACTTCTCGAAGGTCTG 2100
DB 681 LeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProAlaLeuLeuGluGlyLeu 700
QY 2101 AGTTACTTGGAAATCGTTTACCACATGATGAGCAGAGAATATTTACAGATATCTCGAA 2160
DB 701 SerTyrLeuGluSerPheTyrHisMetMetAspArgArgenIleSerAspIleSerGlu 720
QY 2161 AACCTCAAGCGTTACTCTTCACTGATTTTAAAGCAGTGATGACAGCAAGCTGGAGT 2220
DB 721 AsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSerTrpSer 740
QY 2221 GACAGGGCTCAGCTGGACAGGATGCTCGCTGGCTCTCTGAACTGGCGCTGAC 2280
DB 741 AspyLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAlaCysAsp 760
QY 2281 CTGAACCATGCTCTTGCATCCAGAAAGCTGCTGAACTCTTCTCCAGTGGATGGAATCC 2340
DB 761 LeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMetGluSer 780
QY 2341 AGTGAAATTAATATATACCAACAGATGTTTTAAAGATGTGTATTTCTGTGGTCTCAG 2400
DB 781 SerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrSerValGlyAlaGln 800
QY 2401 ACAACAGCGAGTGGATTTACCTTTTAGCAATATGAATGCTCAATGCTCAAGTCTGAA 2460
DB 801 ThrThrAlaGlyTrpAsnTyrLeuLeuGluGlnTyrGluLeuSerMetSerSerAlaGlu 820
QY 2461 CAAACAAATTTCTGTATGCTTTGTCAACAGCAAGCATCAGAAAAGTTACTGAAGTTA 2520
DB 821 GlnAsnLysIleLeuTyrAlaLeuSerThrSerLysHisGlnGluLysLeuLeuLysLeu 840
QY 2521 ATTGAACAGTAATGGAAGGAAGTTATCAAGACACAGAACTTCGCAGCTCTCTTCAT 2580
DB 841 IleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaAlaLeuLeuHis 860
QY 2581 GCGATTGCCAGCTCCAAAGGGGAGCACTAGCATGGATTTTGTGAAGAAAATGG 2640
DB 861 AlaIleAlaArgArgProLysGlyGlnGlnLeuAlaTrpAspPheValArgGluAsnTrp 880
QY 2641 ACCCATCTTCTGAAAAATTTTCACTTGGGCTCATATGACATAGGATGATCATCTCTGGC 2700
DB 881 ThrHisLeuLeuLysLysPheAspLeuGlySerTyrAspIleArgMetIleIleSerGly 900

QY 2701 ACAACAGCTCACTTTTCTTCCAGGATAAAGTTGCAAGAGGTGAACATAATTTTGAATCT 2760
DB 901 ThrThrAlaHisPheSerSerLysAspLysLeuGlnGluValLysLeuPhePheGluSer 920
QY 2761 CTTGAGGCTCAAGGATCACATCTCGATATTTTCAAACCTGTTCTGGAAACGATAACCAA 2820
DB 921 LeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIleThrLys 940
QY 2821 AATATAAATGGCTGGAGAGAATCTTCCGACTCTGAGGACTTGGCTTAATGTTAATACT 2880
DB 941 AsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeuMetValAsnThr 960
RESULT 2
ID AAE04879 standard; protein; 960 AA.
XX AAE04879;
XX 10-SEP-2001 (first entry)
XX Human protease protein-6 (PRTS-6).
DE Human; protease protein-6; PRTS-6; cytostatic; hypotensive; gene therapy;
KW gastrointestinal disorder; anorexia; dysphagia; cardiovascular disorder;
KW atherosclerosis; vasculitis; autoimmune disorder; inflammatory disorder;
KW Alzheimer's disease; cell proliferative disorder; dermatitis; cirrhosis;
KW acquired immune deficiency syndrome; AIDS; neurological disorder; asthma;
KW developmental disorder; epithelial disorder; eczema; dementia; neoplastic;
KW neurological disorder; reproductive disorder; infertility; teratogenesis;
KW immunosuppressive; drug screening; actinic keratosis; cardiac; epilepsy;
KW anaemia; antitumour; antiviral; antibacterial.
XX Homo sapiens.
OS Homo sapiens.
XX Key Location/Qualifiers
FH Peptide 1..35
FT /label= Signal_peptide
FT Protein 36..960
FT /note= "Mature human PRTS-6"
FT Binding-site 367..377
FT /label= Zinc_binding_region
FT Binding-site 367..376
FT /label= Zinc_binding_region
XX WO200146443-A2.
XX 28-JUN-2001.
XX 19-DEC-2000; 2000WO-US034811.
XX 23-DEC-1999; 99US-0172055P.
XX 21-JAN-2000; 2000US-0177334P.
XX 28-JAN-2000; 2000US-0178884P.
XX 02-FEB-2000; 2000US-0179903P.
XX (INCY-) INCYTE GENOMICS INC.
XX Yang J, Baughn MR, Burford N, Au-Young J, Lu DAM, Raddy R;
PI Yue H, Nguyen DB, Tang VT, Yao MG, Lal P;
XX WPI; 2001-418080/44.
DR N-PSDB; AAD09543.
XX Novel human protease proteins (PRTS) useful for diagnosing, treating,
PT preventing gastrointestinal, cardiovascular, autoimmune/inflammatory,
PT cell proliferative disorders associated with abnormal expression of PRTS.
XX Claim 1; Page 110-112; 129pp; English.
XX The present sequence is human protease protein (PRTS-6). Human PRTS and
CC its nucleic acid molecule are useful for the diagnosis, treatment and
CC prevention of disorders associated with increased or decreased expression
CC of PRTS. Examples of such disorders include, gastrointestinal disorder

CC such as anorexia, dysphagia; cardiovascular disorder such as
CC atherosclerosis, vasculitis; autoimmune/inflammatory disorder such as
CC acquired immune deficiency syndrome (AIDS), asthma; cell proliferative
CC disorder such as actinic keratosis, cirrhosis; developmental disorder
CC such as epilepsy, anaemia; epithelial disorder such as allergic contact
CC dermatitis, eczema; neurological disorder such as Alzheimer's disease,
CC dementia and reproductive disorder such as infertility and teratogenesis.
CC PRTS DNA is useful for creating 'knockin' humanised animals (pigs) or
CC transgenic animals (mice or rats) to model human disease. PRTS DNA is
CC also in use for gene therapy. PRTS and its immunogenic fragments are
CC useful for screening libraries of compounds in several drug screening
CC assays. PRTS is useful for analysing the proteome of a tissue or cell
CC type

XX
SQ Sequence 960 AA;

Alignment Scores:

Pred. No.: 0 Length: 960
Score: 5052.00 Matches: 960
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.80% Indels: 0
DB: 4 Gaps: 0

US-10-039-073-3 (1-2883) x AAE04879 (1-960)

QY 1 ATGTTCCATCTCTGCAATGGTTAAATTCACACAGAAAAACCAATGTTTAAACATTCACAGA 60
DB 1 MetPheHisSerSerAlaMetValAsnSerHisArgLysProMetPheAsnIleHisArg 20
QY 61 GGATTTTACTGCTTAAACAGCCATCTTGCCCAATATGCAATTTGTTCTCAGTCTCAGTG 120
DB 21 GlyPheTyrCysLeuThrAlaIleLeuProGlnIleCysIleCysSerGlnPheSerVal 40
QY 121 CCATCTAGTTATCACTCACTGAGATCCCTGGGCTTCCAGTAGCCACTAATGGGAA 180
DB 41 ProSerSerTyrHisPheThrGluAspProGlyAlaPheProValAlaThrAsnGlyGlu 60
QY 181 CGATTTCTTGGCAGGAGCTAAGGCTCCCAAGTGTGGTCAATCTCTCCATATGACCTC 240
DB 61 ArgPheProTyrGlnGluLeuArgLeuProSerValValIleProLeuHisTyrAspLeu 80
QY 241 TTTGTCCACCCCAATCTCACCTCTCTGACCTTCTTGCACTCTGAGAGATCGAAGCTTGT 300
DB 81 PheValHisProAsnLeuThrSerLeuAspPheValAlaSerGluLysIleGluValLeu 100
QY 301 GTCAGCATGCTACCCAGTTATCATCTTCACAGCAAGATCTTGAATCACGAATGCC 360
DB 101 ValSerAsnAlaThrGlnPheIleLeuHisSerLysAspLeuGluIleThrAsnAla 120
QY 361 ACCCTTCAGTCAGAGGAAGATTCAAGATACATGAACACAGMAAAGAACTGAAAGTTTGT 420
DB 121 ThrLeuGlnSerGluGluAspSerArgTyrMetLysProGlyLysGluLeuLysValLeu 140
QY 421 AGTTACCTGCTCATGAACAAATTCGACTGCTGTTCCAGAGAACTTACCCCTCACCTG 480
DB 141 SerTyrProAlaHisGluGlnIleAlaLeuLeuValProGluLysLeuThrProHisLeu 160
QY 481 AAATACTATGGCTATGGACTTCCAGCCCAAGTAGTGTAGTGGCTTTGAAGGGTTTAT 540
DB 161 LysTyrTyrValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTyr 180
QY 541 AAAAGACATACAGAACTCTTGGTGGTGAACAAAGAAATCTTGCAGTAACAGATTTTGTAG 600
DB 181 LysSerThrTyrArgThrLeuGlyGlyGluThrArgIleLeuAlaValThrAspPheGlu 200
QY 601 CCAACCCAGGCACCGATGGCTTCCCTTGGCTTTGATGAACCGTGTGTTCAAAGCCAACTTT 660
DB 201 ProThrGlnAlaArgMetAlaPheProCysPheAspGluProLeuPheLysAlaAsnPhe 220
QY 661 TCATCAAGATACGAAGAGAGAGCAGGCATATTCACATATCCACATGCGCAAGAGTTAAG 720
DB 221 SerIleLysIleArgArgGluSerArgHisIleAlaLeuSerAsnMetProLysValLys 240

QY 721 ACAATTCAACTGAAGAGAGTCTTTTGGAGATCACTTTGAAACTACTGTAAAAATGAGT 780
DB 241 ThrIleGluLeuGluGlyLeuLeuGluAspHisPheGluThrThrValLysMetSer 260
QY 781 ACATACCTTGTAGCCCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACTTCATCA 840
DB 261 ThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThrSerSer 280
QY 841 GGSGTCAAGGTGTCATCTATGATCCACAGACAAAACGGAATCAAAACACATATGCTTTCG 900
DB 281 GlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyrAlaLeu 300
QY 901 CAGGCATCACTGAAGCTACTTGAATTTTATGAAAGTACTTTTCATCTACTATCCACTC 960
DB 301 GlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyrProLeu 320
QY 961 TCCAAACTGGATTTAATGCTATTCCTGACCTTTCGACCTGGAGCCATGGAAAAATGGGGC 1020
DB 321 SerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsnTyrGly 340
QY 1021 CTCATTTACATATAGGAGAGCTCAGCTGCTTTTGGACCCCAAGACCTCTCTGCTCCGAT 1080
DB 341 LeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerAlaSerAsp 360
QY 1081 AAACCTGGGTCAACAGAGTCATAGCCCATGAACCTGGCGCACCGAGTGGTTTGGCAACCTG 1140
DB 361 LysLeuTyrValThrArgValIleAlaHisGluLeuAlaHisGlnTyrPheGlyAsnLeu 380
QY 1141 GTCACAAATGGAATGGTGGAAATGATATTTGGCTTAAAGAGGGTTTTCGAAAAATCATGGAA 1200
DB 381 ValThrMetGluTyrTrpAsnAspIleTyrLeuLysGluGlyPheAlaLysTyrMetGlu 400
QY 1201 CTTATCGCTGTTAAATCTACATATCCAGAGCTGCAATTTGACACTATTTTGAATGTG 1260
DB 401 LeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeuAsnVal 420
QY 1261 TGTTTTGAAGTAAATTAACAAAGATTCATTTCAATTCATCCCGCCCTATCTCCAAACACAGCG 1320
DB 421 CysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLysProAla 440
QY 1321 GAAACCCCGACTCAAAATACAGGAATGTTTGTATGAAGTTTCTTATTAACAGGGAGCTTGT 1380
DB 441 GluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGlyAlaCys 460
QY 1381 ATTTTCAATATGCTCAAGGATTTTCTGGGTGAGGAGAAATCCAGAAAGAAATAATTCAG 1440
DB 461 IleLeuAsnMetLeuLysAspPheLeuGlyGluGluLysPheGlnLysGlyIleIleGln 480
QY 1441 TACTTAAAGAAAGTTCAAGCTATAGAAATGCTAAGAATGATGACTTGTGGAGCAGCTCTGTCA 1500
DB 481 TyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspAspLeuTyrPsrSerLeuSer 500
QY 1501 ATAGTTGTTTGAAGAGTGATTTTACATCTGGTGGAGTTTGTTCATTCGAGATCCCAAGATG 1560
DB 501 AsnSerCysLeuGluSerAspPheThrSerGlyGlyValCysHisSerAspProLysMet 520
QY 1561 ACAAGTAAACATGCTCCCTTCTGGGGGAAATTCAGAGAGTCAAGAGATGATGACTACA 1620
DB 521 ThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGluValLysGluMetMetThrThr 540
QY 1621 TGACCTCTCCAGAAAGAAATCCCTTCTGCTGGTGGTGTAAACAAAGACGGGTGTTTCACTCCGA 1680
DB 541 TrpThrLeuGlnLysGlyIleProLeuLeuValValLysGlnAspGlyCysSerLeuArg 560
QY 1681 CTGCAACAGAGAGCGCTTCTCCAGGGGGTTTTCAGGAAAGACCTCGAATGGAGGGCCCTG 1740
DB 561 LeuGlnGlnGluArgPheLeuGlnGlyValPheGlnGluAspProGluTyrArgAlaLeu 580
QY 1741 CAGGAGAGTACTGCTGGCATATCCCATTCAGCTACTCCACGAGTTCTTCTAATGTGATC 1800
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QY 1801 CACAGACACATCTCTAAATCAAGACAGACAGATCTCTGGATCTACCTGAAAAGACGATGG 1860
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QY 1861 GTGAATTTAATGTGGATCAATCGTTACTACATCGTTCACTATGAGGTCATGATGG 1920
Db 621 VAllySPheAsnValAspSerAsnGlyTyrrIleValHisLysrGluGlyHisGlyTrp 640
QY 1921 GACCAACTCATTACACAGCTGAATCAGAACACACACACTTCTCAGACCTTAAGGACAGAGTA 1980
Db 641 AspGlnLeuLeuThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAspArgVal 660
QY 1981 GGTCTGATTCATGATGTTTTCAGCTAGTGTGTGAGGAGACTGACCTCAGACAAAGCT 2040
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QY 2101 AGTTACTTTGGAAATCGTTTACCACATGATGACAGAGGAATATTTTCAGATATCTCTGAA 2160
Db 701 SerTyrrLeuGluSerPheTyrrHisMetMetAspArgAsnIleSerAspIleSerGlu 720
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Db 721 AsnLeuLysArgTyrrLeuLeuGlnTyrrPheLysProValIleAspArgGlnSerTrpSer 740
QY 2221 GACAGGGCTCAGTCTGGACAGGATGCTCCGCTCGGCTCTCTGAAAGCTGGCTGTGAC 2280
Db 741 AspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAlaCysAsp 760
QY 2281 CTGAACCATGCTCTTGTGATCCAGAAAGCTGCTGAACTCTTCTCCAGTGTGATGAATCC 2340
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QY 2341 AGTGAAAATTAATATATACCAACAGATGTTTTAAAGATTGTGTATTTCTGGTGGCTCAG 2400
Db 781 SerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrrSerValGlyAlaGln 800
QY 2401 ACACAGCAGGATGAATACCTTTTACGCAATATGAACTGCTCAATCTCAAGTCTGAA 2460
Db 801 ThrThrAlaGlyTrpAsnTyrrLeuLeuGluGlnTyrrGluLeuSerMetSerAlaGlu 820
QY 2461 CAAACAAAATCTGTATGCTTTGTCAACAGCAGCATCAGAAAAGTTACTGAAGTTA 2520
Db 821 GlnAsnLysIleLeuTyrrAlaLeuSerThrSerLysHisGlnGluLysLeuLeuLysLeu 840
QY 2521 ATTGAAGTGGATGGAAGGAAAGTTATCAAGACACAGAACTTGGCAGCTCTCTTCAT 2580
Db 841 IleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaLeuLeuHis 860
QY 2581 GCGATTGCCAGCTCCAAAGGGGAGCACTAGCATGGATTTTGTAAAGAAAATGG 2640
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QY 2641 ACCCATCTCTGAAAAATTTGACTTGGCTCATATGATGATCAATGAAGATGATCTCTGGC 2700
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QY 2701 ACAACAGCTCACTTTTCTTCCAGGATGAAGTTGCAAGGTTGAACATACTATTTTGAATCT 2760
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QY 2761 CTTGAGGCTCAGGATCAGATCTGATATTTTCAACTGTCTCGAAGCAACCAACAAA 2820
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QY 2821 AATATAAATGCTCGAGAGAAATCTTCGACTCTGAGGACTTGGCTAATGGTTAATACT 2880
Db 941 AsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeuMetValAsnThr 960
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RESULT 3

```
ABP69122
ID ABP69122 standard; protein; 960 AA.
XX
AC ABP69122;
XX
DT 20-JAN-2003 (first entry)
XX
DE Human polypeptide SEQ ID NO 1169.
XX
KW Human; genome mapping; gene therapy; food supplement; virus; fungus;
cell-proliferative disorder; neurodegenerative disease; bacterial;
Parkinson's disease; Alzheimer's disease; autoimmune disease;
multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
arthritis; cytostatic; immunomodulator; neotropic; neuroprotective;
antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;
antiarthritic.
XX
OS Homo sapiens.
XX
PN WO200270539-A2.
XX
PD 12-SEP-2002.
XX
PF 05-MAR-2002; 2002WO-US005095.
XX
PR 05-MAR-2001; 2001US-00799451.
XX
(PYSE-) HYSEQ INC.
XX
PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
PI Wehrman T, Wang J, Wang D, Drmanac RT;
XX
DR WPI; 2002-759812/82.
DR N-ESDB; ABZ11339.
XX
New polynucleotides comprising sequences assembled from expressed
sequence tags (ESTs), useful for treating cell-proliferative,
neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
or coagulation disorders.
XX
Claim 9; SEQ ID NO 1169; 1012pp + Sequence Listing; English.
XX
The invention relates to an isolated polynucleotide (I) comprising a
nucleotide sequence selected from any of 948 sequences (ABZ11119-
ABZ12066) or their mature protein coding portion, active domain coding
protein or complementary sequences. The polynucleotides are useful for
identifying expressed genes or for physical mapping of human genome. The
encoded polypeptides (ABP6902-ABP6949) are useful as molecular weight
markers, as a food supplement, for generating antibodies, in medical
imaging, screening and diagnostic assays and for treating cell-
proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
platelet or coagulation disorders, wound, burns, incision, ulcers, liver
or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
arthritis, etc. Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic format
directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 960 AA;
Alignment Scores:
Pred. No.: 0 Length: 960
Score: 5048.00 Matches: 959
Percent Similarity: 100.00% Conservativeness: 1
Best Local Similarity: 99.90% Mismatches: 0
Query Match: 99.72% Indels: 0
DB: 5 Gaps: 0
US-10-039-073-3 (1-2883) x ABP69122 (1-960)
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Db 1 MetPheHisSerSerAlaMetValAsnSerHisArgLysProMetPheAsnIleHisArg 20
QY 61 GGATTTTACTGCTTAAACAGCCATCTTGCCCAATATGTCATTGCTTCAGTTCCTCAGTG 120
Db 21 GlyPheTyrCysLeuThrAlaIleuProGlnIleCysIleCysSerGlnPheSerVal 40
QY 121 CCATCTAGTTATCACTTCACAGAGATCCTGGGCTTTCCAGTAGCCACTAAATGGGGAA 180
Db 41 ProSerSerTyrHisPheThrGluAspProGlyAlaPheProValAlaThrAsnGlyGlu 60
QY 181 CGATTTCTTGGCAGGAGCTAAGGCTCCCAAGTGTGTCATTCTCTCCATTATGACCTC 240
Db 61 ArgPheProTrpGlnGluLeuArgLeuProSerValValIleProLeuHisTyrAspLeu 80
QY 241 TTTGTCCACCCCAATCTCACCTCTCTGACCTTCTGCATCTGAGAGATCGAAGTCTTG 300
Db 81 PheValHisProAsnLeuThrSerLeuAspPheValAlaSerGluIleGluValLeu 100
QY 301 GTCAGCAATGTCACCCAGTTTATCATCTTGCAACAGCAAGATCTTGAATCACCAGATGCC 360
Db 101 ValSerAsnAlaThrGlnPheIleIleuHisSerLysAspLeuGluIleThrAsnAla 120
QY 361 ACCCTTCAGTCAGAGGAAGATTCAGATACATGAAACCCAGGAAAAGAACTGAAAGTTTG 420
Db 121 ThrLeuGlnSerGluGluAspSerArgTyrMetLysProGlyLysGluLeuLysValLeu 140
QY 421 AGTTACCTGCTCATGAACAATTCGACTGCTGCTCCAGAGAACTTACGCTCACCTG 480
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QY 481 AAATACTATGTGGCTATGGACTTCCAAAGCCCAAGTTAGTGTATGGCTTTGAAGGGTTTAT 540
Db 161 LysTyrTyrValAlaMetAspPheGluAlaLysLeuGlyAspGlyPheGluGlyPheTyr 180
QY 541 AAAAGCACAACAGAACTCTTTGGTGGTGAACAAAGAAATCTTGCAGTAACAGATTTTGAG 600
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QY 601 CCRACCAGGCACATCGCTTCCCTTCTGCTTTCATGAACCGTGTTCAAAGCCAACTTT 660
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QY 661 TCAATCAAGATACGAAGAGAGAGCAGGCATATTCGACTTCCAAACATGCCAAAGGTTAAG 720
Db 221 SerIleLysIleArgArgGluSerArgHisIleAlaLeuSerAsnMetProLysValLys 240
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QY 781 ACATACCTTGTAGCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACCTTCATCA 840
Db 261 ThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThrSerSer 280
QY 841 GGGGTCAAGGTGTCATCTATGCATCCCAACAAACCGAATCAACACATTAATGCTTTG 900
Db 281 GlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyrAlaLeu 300
QY 901 CAGGCATCACATGAAGCTACTTGTATTTTATGAAGAAGTACTTTGTATATCTACTATCCACTC 960
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QY 1081 AAACGTGGGTCAACAGAGTCATACCCCATGAACCTGGCGCACCAAGTGGTTTGGCAACCTG 1140

Db 361 LysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeu 380
QY 1141 GTCACAATGGAATGGTGGAAATGATATTGGCTTAAAGAGGGTTTTCAAAATAACATCGAA 1200
Db 381 ValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyrMetGlu 400
QY 1201 CTTTATCGCTGTTAATGCTACATATCCAGAGCTGCAATTTTGATGACTATTTTGAATGTG 1260
Db 401 LeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspPhePheLeuAsnVal 420
QY 1261 TGTTTTGAAGTAATTAACAAAGATTCAATGAATTATCCCGCCCTATCTCCAAACACAGCG 1320
Db 421 CysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLysProAla 440
QY 1321 GAAACCCCGACTCAAAATACAGGAAATGTTTGATGAAGTTTCCCTATACAAAGGAGCTTGT 1380
Db 441 GluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGlyAlaCys 460
QY 1381 ATTTTGAATATGCTCAAGGATTTTCTGGGTGAGGAGAAATTCAGAAAAGGAATAATTTCAG 1440
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QY 1441 TACTTAAAGAGTTCACTATAGAAATGCTAAGAAATGATGACTTGTGGAGCAGTCTGTCA 1500
Db 481 TyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspLeuTrpSerSerLeuSer 500
QY 1501 AATAGTTGTTTACAAAAGTGAATTTTACATCTGGTGGAGTTTGTTCATTCGGATCCCAAGATG 1560
Db 501 AsnSerCysLeuGlnSerAspPheThrSerGlyGlyValCysHisSerAspProLysMet 520
QY 1561 ACAAGTAACATGCTCCGCTTCTGGGGGAAAAATGCAGAGGTCAAGAGATGATGACTACA 1620
Db 521 ThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGluValLysGluMetMetThrThr 540
QY 1621 TGGACTCTCCAGAAAGAAATCCCCCTGCTGGTGGTTAAACAAGACCGGTGTTCACTCCGA 1680
Db 541 TrpThrLeuGlnLysGlyIleProLeuLeuValLysGlnAspGlyCysSerLeuArg 560
QY 1681 CTGCAACAGGAGCGCTTCTCCAGGGGTTTTCAGGAAAGACCTCAATGGAGGGCCCTG 1740
Db 561 LeuGlnGlnGluArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArgAlaLeu 580
QY 1741 CAGGAGAGGTACCTGTGGCATATCCCATTCACCTACTCCACAGTTCCTTCTAATGTATC 1800
Db 581 GlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerThrSerSerSerAsnValIle 600
QY 1801 CACAGACACATCTTAAATCAAAAGACAGATACTCTGGATCTACCTGAAAGACAGTTGG 1860
Db 601 HisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThrSerTrp 620
QY 1861 GTGAAATTTAATGTGACTCAAAATGGTTACTACATCGTTTCACTATCAGGCTCATGGATGG 1920
Db 621 ValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHisGlyTrp 640
QY 1921 GACCAACTCATTTACACAGCTGAATCAGAACCCACACACTTCTCAGACCTTAAGGACAGAGTA 1980
Db 641 AspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAspArgVal 660
QY 1981 GGTCTCATTCATGATGTGTTTTCAGCTAGTGGTGGAGGAGACTGACCTTAGACAAAGCT 2040
Db 661 GlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAspLysAla 680
QY 2041 CTTGACATCACTTACTACCTCCAAACATGAACAAGCAGCCCGCACTTCTCGAAGTCTG 2100
Db 681 LeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProAlaLeuLeuGluGlyLeu 700
QY 2101 AGTTACTTGGAAATCGTTTTTACCACATGATGAGCAGAGGAATAATTTTTCAGATATCTCGAA 2160
Db 701 SerTyrLeuGluSerPheTyrHisMetMetAspArgArgAsnIleSerAspIleSerGlu 720
QY 2161 AACCTCAAGGTTACCTTCTTCAGTATTTTAAAGCCAGTGATTCACAGGCAACCTGGAGT 2220

Db 721 AsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSerTrpSer 740

QY 2221 GACAAAGGCTCAGTCTGGACAGGATGCTCCGCTCGCTCTCTTGAAGCTGCGCTGTGAC 2280

Db 741 AspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAlaCysAsp 760

QY 2281 CTGAACCATGCTCCTTGGATCCAGAAAGCTGCTGAACCTCTTCTCCAGTGGATGCAATCC 2340

Db 761 LeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMetGluSer 780

QY 2341 AGTGAAATTAATAATACCAACAGATGTTTTAAAGATTGTATTCTGTGGTCTCAG 2400

Db 781 SerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrSerValGlyAlaGln 800

QY 2401 ACAACAGCAGGATGGAATTTACCTTTTAGACCAATATGAACCTGTCAATCTCAAGTCTGAA 2460

Db 801 ThrThrAlaGlyTrpAsnTyrLeuLeuGluGlnTyrGluLeuSerMetSerSerAlaGlu 820

QY 2461 CAAACAAATTTCTGTATGCTTTGTCAAGCAGCAAGCATCAGGAAAGTTACTGAAGTTA 2520

Db 821 GlnAsnLysIleLeuTyrAlaLeuSerThrSerLysHisGlnGluLysLeuLysLeu 840

QY 2521 ATTGAACCTAGGAATCGAAGGAAGTATTCAAGACACAGAACTTGGCAGCTCTCTTCAT 2580

Db 841 IleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaLeuLysHis 860

QY 2581 GCGATTGCCAGCGTCCAAAGGGCAGCAACTAGCATGGGATTTTGTAAAGAGAAATGG 2640

Db 861 AlaIleAlaArgArgProLysGlyGlnGlnLeuAlaTrpAspPheValArgGluAsnTrp 880

QY 2641 ACCCATCTTCGAAAAATTTGACTTGGCTCATATGACATATGACATATGATCATCTCTGGC 2700

Db 881 ThrHisLeuLeuLysLysPheAspLeuGlySerTyrAspIleArgMetIleIleSerGly 900

QY 2701 ACAACAGCTCACTTTCTTCCAGGATTAAGTTCAGAGGTGAACACTATTTTGAATCT 2760

Db 901 ThrThrAlaHisPheSerSerLysAspLysLeuGlnGluValLysLeuPhePheGluSer 920

QY 2761 CTTGAGGCTCAAGGATCACTGATATTTTCAAACTGTTCTGAAACGATTAACCAA 2820

Db 921 LeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIleThrLys 940

QY 2821 AATATAAATGGCTGGAGGAATCTTCGACTCTGAGGACTTGCTGCTTAATGTTAATCT 2880

Db 941 AsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeuMetValAsnThr 960

RESULT 4

ABP63022 standard; protein; 785 AA.

AC ABP63022;

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DE 14-OCT-2002 (first entry)

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XX

XX

XX

Human polypeptide SEQ ID NO 459.

XX

XX

Human; vulnery; dermatological; neuroprotective; nootropic; cancer;

KW antiparkinsonian; immunostimulant; cytostatic; immunosuppressive;

KW antidiabetic; antiallergic; gene therapy; wound healing; tissue repair;

KW burn; central nervous system disorder; Alzheimer's disease;

KW Parkinson's disease; Huntington's disease; immune disorder;

KW autoimmune disorder; multiple sclerosis; diabetes; allergy.

XX

OS Homo sapiens.

XX

XX

PN WO200218424-A2.

XX

XX

PD 07-MAR-2002.

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PF 31-AUG-2001; 2001WO-US027093.

XX

XX

PR 01-SEP-2000; 2000US-00654935.

XX

(HYSE-) HYSEQ INC.

Tang YT, Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;

PI Zhao QA, Wang D, Liu C, Drmanac RT, Wehrman T;

XX

DR WPI: 2002-583321/62.

XX N-PSDB; ABQ93501.

XX

PT New polynucleotide and polypeptides, useful for treatment and diagnosis

PT of Alzheimer's, Parkinson's, Huntington's, amyotrophic lateral

PT sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple

PT sclerosis, diabetes and allergies.

XX

PS Claim 20; SEQ ID NO 459; 284pp + Sequence Listing; English.

XX

CC The invention relates to an isolated polynucleotide (I) comprising one of

CC 245 sequences (ABQ93288-ABQ93532). Treating a condition comprising

CC administering to a mammalian subject a composition comprising the protein

CC (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II).

CC (I), (II) and (III) are useful for diagnostic evaluation of disorders.

CC (I) is useful for gene therapy of diseases and (II) can be used for

CC therapeutic treatment. Diseases that may be treated include wound healing

CC and tissue repair, burns, central nervous system disorders (e.g.

CC Alzheimer's, Parkinson's, Huntington's and amyotrophic lateral

CC sclerosis), immune deficiencies, cancer, autoimmune disorders, multiple

CC sclerosis, diabetes and allergies. Note: The sequence data for this

CC patent did not form part of the printed specification, but was obtained

CC in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 785 AA;

Alignment Scores:

Pred. No.: 0 Length: 785

Score: 4141.00 Matches: 782

Percent Similarity: 99.74% Conservatve: 0

Best Local Similarity: 99.74% Mismatches: 2

Query Match: 81.81% Indels: 0

DB: 5 Gaps: 0

US-10-039-073-3 (1-2883) x ABP63022 (1-785)

QY 1 ATGTTTCATCTTCTGCAATGGTTAATTCACACAGAAACCAATGTTTAACTTACACAGA 60

Db 1 MetPheHisSerSerAlaMetValAsnSerHisArgLysProMetPheAsnIleHisArg 20

QY 61 GGATTTTACTGCTTAAACAGCCATCTTCCCCCAATATGATCTTCTTCTCAGTCTCAGTG 120

Db 21 GlyPheTyrCysLeuThrAlaIleLeuProGlnIleCysIleCysSerGlnPheSerVal 40

QY 121 CCATCTAGTTATCACTTCACTGAGGATCTGGGGCTTTCCAGTAGCCACTAATGGGAA 180

Db 41 ProSerSerTyrHisPheThrGluAspProGlyAlaPheProValAlaThrAsnGlyGlu 60

QY 181 CGATTTCTTGGCAGGAGCTTAAGGCTCCCAGTGTGTCATTTCTCTCCATATGACCTC 240

Db 61 ArgPheProTrpGlnGluLeuArgLeuProSerValValIleProLeuHisTyrAspLeu 80

QY 241 TTGTCCACCCCAATCTCACTCTCTGACCTTTGTCATCTGAGAGATCGAAGTCTTG 300

Db 81 PheValHisProAsnLeuThrSerLeuAspPheValAlaSerGluLysIleGluValLeu 100

QY 301 GTCAGCAATGCTACCCAGTTTATCATCTTGACAGCAAGATCTTGAATCACCAGTCC 360

Db 101 ValSerAsnAlaThrGlnPheIleIleLeuHisSerLysAspLeuGluIleThrAsnAla 120

QY 361 ACCCTTCAGTCAGAGGAAGATTCAAGATACATGAACACAGAGAAAGAACTGAAAGTTTG 420

Db 121 ThrLeuGlnSerGluGluAspSerArgTyrMetLysProGlyLysGluLeuLysValLeu 140

QY 421 AGTTACCTGCTCATGAACAAATGTCAGTCTGCTGCTCCAGAGAACTTACGCTCACCCTG 480

Db 141 SerTyrProAlaHisGluGlnIleAlaLeuLeuValProGluLysLeuThrProHisLeu 160

QY	481	AAATACATATGGCTATGGACTTCCAAAGCCCAAGTTAGTGATGGCTTTGAAGGTTTAT	540
Db	161	LysTyrTyrValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTyr	180
QY	541	AAAGACATACAGAACTCTGGTGGTGAACAGAAATCTTGCAGTAAACAGATTTTGAG	600
Db	181	LysSerThrTyrArgThrLeuGlyGlyGluThrArgIleLeuAlaValThrAspPheGlu	200
QY	601	CCAAACCCAGGCACATCGCTTCCCTTGGCTTTCATGAACCGTGTTCAAAGCCCAACTTT	660
Db	201	ProThrGlnAlaArgMetAlaPheProCysPheAspGluProLeuPheLysAlaAsnPhe	220
QY	661	TCAATCAAGATACGAAGAGAGAGCAGCATATCCACTATCCAAATGCCAAAGGTTAAG	720
Db	221	SerIleLysIleArgArgGluSerArgHisIleAlaLeuSerAsnMetProLysValLys	240
QY	721	ACAATTGAACCTGAAGAGGTCCTTTTGGAGATCACCTTTGAACTACTGTAAAAATGAGT	780
Db	241	ThrIleGluLeuGluGlyGlyLeuLeuGluAspHisPheGluThrValLysMetSer	260
QY	781	ACATACCTTGTAGCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACTTCATCA	840
Db	261	ThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThrSerSer	280
QY	841	GGGTCAAGGTGTCCATCTATGCATCCCCACGAAACGGAATCAAAACACATTTATGCTTTG	900
Db	281	GlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyrAlaLeu	300
QY	901	CAGGCATCACTGAAGCTACTGATTTTATGAAAGTACTTTGATATCTACTATCCACTC	960
Db	301	GlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyrProLeu	320
QY	961	TCCAAATCGGATTTAAATTCCTGACTTTCACCTGGAGCCATGGAAATTTGGGGC	1020
Db	321	SerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsnTrpGly	340
QY	1021	CTCATATCATATAGGAGAGCTACTGCTTTTTCACCCCAAGACCTCTTCTGCTCCGAT	1080
Db	341	LeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAlaSerAsp	360
QY	1081	AACTGTGGTCCACAGATCATAGCCCATGCACTGGCCACCGACTGGTTGGCAACCTG	1140
Db	361	LysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeu	380
QY	1141	GTCAAAATGGAATGGTGAATGATATTGGCTTAAGGAGGCTTTGCAAAATACATCGAA	1200
Db	381	ValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyrMetGlu	400
QY	1201	CTTATCGCTGTTAATGCTACATATCCAGAGCTGCAATTTGATGACTATTTTGAATGTG	1260
Db	401	LeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeuAsnVal	420
QY	1261	TGTTTTGAAGTAATTACAAAGATTCATTGATTCATCCCGCCCTATCTCCAAACACGCG	1320
Db	421	CysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLysProAla	440
QY	1321	GAACCCCGACTCAAAATACAGAAATGTTTGATCAAGTTTCCCTATAACAGGGAGCTTGT	1380
Db	441	GluThrProThrGlnIleGlnLysPheAspGluValSerTyrAsnLysGlyAlaCys	460
QY	1381	ATTTTGAATATGCTCAAGGATTTTCTCGGTGAGAGAAATTCAGAAAGGAATTAATTCAG	1440
Db	461	IleLeuAsnMetLeuLysAspPheLeuGlyGluGlyLysPheGlnLysGlyIleIleGln	480
QY	1441	TACTTAAAGATTCACGTATAGAAATCTTAAGATGATGATCTGTGGAGCAGTCTGTCA	1500
Db	481	TyrLeuLysLysPheSerTyrArgAsnAlaAsnAsnAspAspLeuTrpSerSerLeuSer	500
QY	1501	AATAGTTGTTTAAAGAGTATTTTACATCTCGTGGAGTTGTCTCATTCGGATCCCAAGATG	1560
Db	501	AsnSerCysLeuGluSerAspPheThrSerGlyValCysHisSerAspProLysMet	520

QY	1561	ACAGTAAACATGCTCCCTTTCTGGGGGAAAATGCAGAGGTCAAGAGATGATGACTACA	1620
Db	521	ThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGluValLysGluMetMetThrThr	540
QY	1621	TGGACTCTCCAGAAAGAAATCCCCCTGCTGGTGTAAACCAACACGGGTGTTCACTCCGA	1680
Db	541	TrpThrLeuGlnLysGlyIleProLeuLeuValLysGlnAspGlyCysSerLeuArg	560
QY	1681	CTGCAACAGGAGCGCTCTCTCCAGGGGGTTTTCAGAAAGACCCCTGAATGGAGGGCCCTG	1740
Db	561	LeuGlnGlnArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArgAlaLeu	580
QY	1741	CAGGAGAGTACTGTGGCATATCCCATCTGACCTACTCCACGAGTCTTCTTAATGTGATC	1800
Db	581	GlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerThrSerSerSerAsnValIle	600
QY	1801	CACAGACACATCTCAAATCAAAGACAGATACCTCTGATCTACTCTGAAAGACAGTTGG	1860
Db	601	HisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThrSerTrp	620
QY	1861	GTGAAATTTAATGTGACTCAAAATGGTTACTACATCGTTTCACTATGAGGTCATGGATGG	1920
Db	621	ValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHisGlyTrp	640
QY	1921	GACCACTCATTRACACAGCTGAATCAGAACACACACTTCTCAGACCTTAAGCAGAGTA	1980
Db	641	AspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAspArgVal	660
QY	1981	GGTCTCATTCATGCTGTCTTTCAGCTAGTTGGTGAGGGAGACTGACCTTAGACAAAGCT	2040
Db	661	GlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAspLysAla	680
QY	2041	CTTGACATGACTTACCTCCAAATGAACAAAGCAGCCCGCACCTTCTCGAAGGTCTG	2100
Db	681	LeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProAlaLeuLeuGluGlyLeu	700
QY	2101	AGTTACTTGGAAATCGTTTTACCATGATGGCAGAGGAATATTTTCAGATATCTCTGAA	2160
Db	701	SerTyrLeuGluSerPheTyrHisMetMetAspArgArgAsnIleSerAspIleSerGlu	720
QY	2161	AACTCAAGGTTTACCTTCTCAGTATTTTAAAGCCAGTATTTCAGACAGGCAAGCTGGAGT	2220
Db	721	AsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSerTrpSer	740
QY	2221	GACAGGGCTCAGTCTGGACAGGATGCTCCGCTCCGCTCTCTTGAAGCTGGCTGTGAC	2280
Db	741	AspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAlaCysAsp	760
QY	2281	CTGAACCATGCTCTTGCATCCAGAAAGCTGTGAACTCTTCTCCAGTGGATGGAATCC	2340
Db	761	LeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheGlnTrpMetGluSer	780
QY	2341	AGTGGAAATTA 2352	
Db	781	SerGlyLysLeu 784	
RESULT 5			
ABBI0338			
ID	ABB10338	standard; protein; 728 AA.	
XX	ABB10338;		
DT	10-JAN-2002	(first entry)	
XX			
XX		Human cDNA SEQ ID NO: 646.	
XX		Human; gene therapy; neural disorder; immune system disorder;	
KW		muscular disorder; reproductive disorder; gastrointestinal disorder;	
KW		pulmonary disorder; cardiovascular disorder; renal disorder;	
KW		proliferative disorder; inflammation.	
OS		Homo sapiens.	

PN WO200154474-A2.
XX 02-AUG-2001.
PD 17-JAN-2001; 2001WO-US001349.
PF 31-JAN-2000; 2000US-0179065P.
PF 04-FEB-2000; 2000US-0180628P.
XX 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
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PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
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PR 17-NOV-2000; 2000US-0249244P.
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PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
PI

XX WPI; 2001-476161/51.
DR N-PSDB; ABA06560.
XX
PT Isolated nucleic acid molecule encoding an inflammation-associated
PT polypeptide is used in preventing, treating or ameliorating a medical
XX condition.
XX
PS Claim 11; SEQ ID NO 646; 859pp + Sequence Listing; English.
XX
XX The present invention provides human cDNAs, proteins and related genomic
CC DNAs. These can be used in the treatment of neural, immune system,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal and proliferative disorders and inflammation. The present sequence
CC is a protein of the invention
XX
XX
SQ Sequence 728 AA;

Alignment Scores:
Pred. No.: 0 Length: 728
Score: 3799.00 Matches: 722
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 75.05% Indels: 0
DB: 4 Gaps: 0

US-10-039-073-3 (1-2883) x ABB10338 (1-728)

QY 715 GTTAAGCAATTTGAAGAGGCTCTTTTGAAGATCACCTTTGAAACTACTGTAAAA 774
DB 7 ValysThrIleGluLeuGluGlyGlyLeuLeuGluAspHisPheGluThrThrValys 26

QY 775 ATGAGTACATACCTTGAGCCTACATAGTTGTGATTTCCACTCTCTGAGTGGCTTCAC 834
DB 27 MetSerThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThr 46

QY 835 TCATCAGGGGTCAAGGTGTCCATCTATGCATCCCCAGACAAACGGAATCAAAACACATTAT 894
DB 47 SerSerGlyValysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyr 66

QY 895 GCTTTGAGGATCACCTGAGCTACTGATTTTATGAAAGTACTTTGTATCTACTAT 954
DB 67 AlaLeuGlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyr 86

QY 955 CCACCTCTCCAACTGGGATTTAATGTCTATTCTGACCTTTCACCTGGAGCCATGGAAAAAT 1014
DB 87 ProLeuSerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsn 106

QY 1015 TGGGGCTCATTTACATATAGGGAGACGTCACTGCTTTTTCACCCCAAGACCTCTCTGCT 1074
DB 107 TrpGlyLeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAla 126

QY 1075 TCCGATAAAGCTGGGTCCAGAGTCATAGCCCATGAAGTGGGCGACAGTGGTTGGC 1134
DB 127 SerAspLysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGly 146

QY 1135 AACCTGTGTCAATAGGAATGGTGAATGATATTGGCTTAAGGAGGGTTTTGCAAAATAC 1194
DB 147 AsnLeuValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyr 166

QY 1195 ATGGAACCTTATCGCTGTTAATGTCTACATATCCAGAGCTGCAATTTGTATGATATTTTGG 1254
DB 167 MetGluLeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeu 186

QY 1255 AATGTGTGTTTGAAGTAATTAACAAAGATTCATTGAATTCATCCCGCCCTATCTCCAAA 1314
DB 187 AsnValCysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLys 206

QY 1315 CCAGCGAAACCCCGACTCAAAATACAGAAATGTTTCATCAAGTTCCTTATACAGGGA 1374
DB 207 ProIleGluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGly 226

QY 1375 GCTTGTATTTTGAATATGCTCAAGGATTTTCTGGGTGAGGAGAAATTTCCAGAAAGGAATA 1434

DB 227 AlaCysIleLeuAsnMetLeuLysAspPheLeuGlyGluGluLysPheGlnLysGlyIle 246
QY 1435 ATTCACTACTTAAGAAGTTCACTATAGAAATGCTAAGAAATGATGATCTTGTGAGCAGT 1494
DB 247 IleGlnTyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspLeuTrpSerSer 266
QY 1495 CTGTCAAAATAGTTGTTTAGAAAGTGATTTTACATCTGGTGGAGTCTTGTCTCATTCGGATCCC 1554
DB 267 LeuSerAsnSerCysLeuGluSerAspPheThrSerGlyValCysHisSerAspPro 286
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DB 287 LysMetThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGluValLysGluMetMet 306
QY 1615 ACTACATGACTCTCCAGAAAGGAATCCCGCTGCTGGTGGTTAAACAAGACGGGTGTCA 1674
DB 307 ThrThrTrpThrLeuGlnLysGlyIleProLeuLeuValLysGlnAspGlyCysSer 326
QY 1675 CTCGAGCTGCAACAGGAGCGCTTCTCTCCAGGGGGTTTTCCAGGAAGACCTGTAATGAGG 1734
DB 327 LeuArgLeuGlnGlnGluArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArg 346
QY 1735 GCCCTCCAGGAGAGGTACCTGTGGCATATCCCATTCACCTACTCCACGAGTCTCTTAAT 1794
DB 347 AlaLeuGlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerThrSerSerAsn 366
QY 1795 GTGATCCACAGACACATCTTAATAATCAAGACAGATACTCTGGATCTACTGAAAAGACC 1854
DB 367 ValIleHisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThr 386
QY 1855 AGTTGGGTGAAATTTAATGTGGACTCAAATGGTTACTACATCTTCACTATAGGGTTCAT 1914
DB 387 SerTrpValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHis 406
QY 1915 GGATGGGACCAACTCATATTACACAGCTGAATCAGAACACACACTTCTCAGACCTTAAGGAC 1974
DB 407 GlyTrpAspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAsp 426
QY 1975 AGNATGCTCTGATTCATGATGTGTTTACAGTAGTTGGTCAGGGAGACTGACCTAGAC 2034
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DB 447 LysAlaLeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProAlaLeuLeuGlu 466
QY 2095 GGTCTGAGTTACTTGAATCGTTTTTACCACATGATGGACAGAAAGGAATATTTCCAGATATC 2154
DB 467 GlyLeuSerTyrLeuGluSerPheTyrHisMetMetAspArgArgAsnIleSerAspIle 486
QY 2155 TCTGAAAACCTCAAGCGTTACCTTCTTCAGTATTTTAAAGCCAGTGTTCACAGGCAAGC 2214
DB 487 SerGluAsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSer 506
QY 2215 TGGAGTGAACAAGGCTCAGTCTGGGACAGATGCTCCGCTCGGCTCTCTTGAAGCTGGCC 2274
DB 507 TrpSerAspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAla 526
QY 2275 TGTGACCTGAACCATGCTCTTGCATCCAGAAAGCTGCTGAACCTCTTCTCCAGTGGATG 2334
DB 527 CysAspLeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMet 546
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QY 2395 GCTCACACAACAGCAGGATGGAATTAACCTTTTAGAGCAATATGAACCTGCAATGTCAAGT 2454
DB 567 AlaGlnThrThrAlaGlyTrpAsnTyrLeuLeuGluGlnTyrGluLeuSerMetSerSer 586
QY 2455 GCTGAACAAAAACAAATTCGTATGCTTGTGTCAACGACGACGATCAGGAAAGATTACTG 2514

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Qy 2515 AAGTTAATTGAAGTAGGAATGAAGAAAGTTATCAAGACACAGAACTTGGCAGCTCTC 2574
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Qy 2575 CTTGATGGATGCCAGACGTCCAAAGGGGAGCAGCACTAGCATGGGATTTTGTAAAGAA 2634
Db 627 LeuHisAlaIleAlaAArgProLysGlyGlnGlnLeuAlaTrpAepPheValArgGlu 646
Qy 2635 AATTGGACCCATCTTCTCAAAAAATTTGACTTGGGCTCATATGACATAAGGATGATCATC 2694
Db 647 AsnTrpThrHisLeuLeuLysLysPheAspLeuGlySerTyAspIleArgMetIleIle 666
Qy 2695 TCTGCAACAAGCTCACTTTTCTTCCAAAGGATGAAGTTGCAAGAGTGAAGAACTATTTT 2754
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Qy 2755 GAATCTCTGAGGCTCAAGGATCACATCTGATATTTTCAACTGTTCTCGAAGCAGTA 2814
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Qy 2875 AATACT 2880
Db 727 AsnThr 728
RESULT 6
ABP66925
ID ABP66925 standard; protein; 728 AA.
XX
AC ABP66925;
XX
DT 09-DEC-2002 (first entry)
XX
DE Human polypeptide SEQ ID NO 646.
XX
KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparkinsonian; antispasmodic; antianaemic; antiarthritic; cancer;
KW antirheumatic; hepatotrophic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
PN US2002090672-A1.
XX
PD 11-JUL-2002.
XX
PF 17-JAN-2001; 2001US-00764853.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180629P.
PR 28-JUN-2000; 2000US-0214886P.
PR 07-JUL-2000; 2000US-0216647P.
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PR 14-AUG-2000; 2000US-0225757P.

PR 14-AUG-2000; 2000US-0225758P.
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PR 02-OCT-2000; 2000US-0236802P.
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PR 01-NOV-2000; 2000US-0244617P.
PR 17-NOV-2000; 2000US-0249299P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
XX
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
XX
PI Rosen CA, Ruben SM, Barash SC;
XX
WPI: 2002-681727/73.
XX N-PSDB, ABV83897.
XX
DR Novel polypeptide useful for diagnosis, prognosis, prevention, and
XX treatment of immune, hyperproliferative, renal, respiratory,
PT cardiovascular, reproductive, endocrine, gastrointestinal and
PT neurological disorders.
XX
FS Claim 11; SEQ ID NO 646; 369pp + Sequence Listing; English.
XX
CC The invention relates to novel genes (ABV83682-ABV84101) and proteins
CC (ABP66710-ABP67129) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 728 AA;
Alignment Scores:
Pred. No.: 0 Length: 728
Score: 3799.00 Matches: 722

Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	75.05%	Indels:	0
DB:	5	Gaps:	0
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Dd	7	VallysthrileGluLeuGluGlyGlyLeuLeuGluAspHisPheGluThrValLys	26
Qy	775	ATGAGTACATACCTTGTAGCCTACATAGTTTGTGATTTCACATCTCTGAGTGGCTTCACT	834
Dd	27	MetSerThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThr	46
Qy	835	TCATCAGGGGTCAAGGTGTCATCTATGCATCCGCCAGACAAACCGAATCAACACATTAT	894
Dd	47	SerSerGlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyr	66
Qy	895	GCTTTGCAGGCATCACTGAACTACTTGAATTTTATGAAAAGTACTTTTGATATCTACTAT	954
Dd	67	AlaLeuGlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyr	86
Qy	955	CCACTCTCCAAACTGGATTAAATTGCTATTCTCTGACTTTTGCCACCTGGAGCCATGGAAAT	1014
Dd	87	ProLeuSerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsn	106
Qy	1015	TGGGGCCTCATATACATATAGGAGACGTCACTGCTTTTGGACCCCAAGACTCTCTCGCT	1074
Dd	107	TrpGlyLeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAla	126
Qy	1075	TCCGATAAACTGTGGGTCAACAGAGTCATAGCCCATGAACCTGGCGCACCAAGTGTGTGGC	1134
Dd	127	SerAspLysLeuThrValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGly	146
Qy	1135	AACCTGTGTCAATPGGAATGGTGAATCATATTTTGGCTTAAAGGAGGTTTTGCAAAATAC	1194
Dd	147	AsnLeuValThrMetGluThrTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyr	166
Qy	1195	ATGGAACATTATCGCTGTGAATGCTACATATCCAGAGCTGCATTTGATGACTATTTTGG	1254
Dd	167	MetGluLeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeu	186
Qy	1255	AATGTGTGTTTGAAGTAATTACAAAAGATTCAATTGAATTCAATCCGCCCTCATCTCCAAA	1314
Dd	187	AsnValCysPheGluValIleThrLysAspSerLeuAsnSerSerArgProLysSerLys	206
Qy	1315	CCAGCGAAACCCCGACTCAATACAGGAAATGTTTGAAGTTTCCCTATAACAAGGGA	1374
Dd	207	ProAlaGluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGly	226
Qy	1375	GCTTGATTTTGAATATGCTCAAGGATTTTCTGGGTGAGGAGAAATTCAGAAAGGNATA	1434
Dd	227	AlaCysIleLeuAsnMetLeuLysAspPheLeuGlyGluGlyLysPheGlnLysGlyIle	246
Qy	1435	ATTCAAGTACTTAAAGAAAGTTCAAGTATAGAAATGCTAAGAAATGATGACTTGTGAGCAGT	1494
Dd	247	IleGlnTyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspAspLeuTrpSerSer	266
Qy	1495	CTGTCAAATAGTTTGTAGAAAGTGATTTTACATCTCGTGGAGTTTGTCAATTCGGATCCC	1554
Dd	267	LeuSerAsnSerCysLeuGluSerAspPheThrSerGlyGlyValCysHisSerAspPro	286
Qy	1555	AAGATGACAGTACATGCTCGCTTCTTGGGGGAAAATTCAGAGGTCAAGAGATGATG	1614
Dd	287	LysMetThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGluValLysGluMetMet	306
Qy	1615	ACTACATGGACTCTCCAGAAAGGAATCCCTCGCTGGTGGTTAAACAAGACGGGTGTCA	1674
Dd	307	ThrThrTrpThrLeuGlnLysGlyIleProLeuLeuValLysGlnAspGlyCysSer	326
Qy	1675	CTCCGACTGCACAGGAGCGCTTCTCCTCAGGGGTTTTCCAGGAAGACCTCGAATGAGG	1734

Dd	327	LeuArgLeuGlnGlnGluArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArg	346
Qy	1735	GCCCTCAGAGAGGTACCTGTGGCATATCCCAATTGACCTACTCCAGGAGTTCTTCTAAT	1794
Dd	347	AlaLeuGlnGluArgTyrIleuTrpHisIleProLeuThrTyrSerThrSerSerAsn	366
Qy	1795	GTGATCCACAGACACATCTTAAATCAAAGACAGATACTCTGGATCTCTACCTGAAAAGACC	1854
Dd	367	ValIleHisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThr	386
Qy	1855	AGTTGGGTGAAATTTAATGTGGACTCAAATGGTTACTACATCTTCACTATGAGGTCAT	1914
Dd	387	SerTrpValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHis	406
Qy	1915	GGATGGGACCACTCAATACACAGCTGAATCAGAACACACACTTCTCAGACCTAAGGAC	1974
Dd	407	GlyTrpAspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAsp	426
Qy	1975	AGAGTAGGTCTGATTCATGATGTGTTTCAGCTAGTTGGTGCAGGAGACTGACCCCTAGAC	2034
Dd	427	ArgValGlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAsp	446
Qy	2035	AAAGCTCTTGACATGACTTACTACCTCCAACATGAACAAGCAGCCCCGCACTTCTCGAA	2094
Dd	447	LysAlaLeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProAlaLeuLeuGlu	466
Qy	2095	GGTCTCAGTTACTTGAATCGTTTACCACATGATGACAGAGGAATATTTCCAGATATC	2154
Dd	467	GlyLeuSerTyrLeuGluSerPheTyrHisMetMetAspArgAsnIleSerAspIle	486
Qy	2155	TCTGAAAACTCAAGCGTTTACCTTCTTCAGTATTTTAAAGCCAGTATTGACAGGCCAAAGC	2214
Dd	487	SerGluAsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSer	506
Qy	2215	TGAGGTGACAAAGGCTCAGTCTGGGACAGGATGCTCCGCTCGGCTCTCTTGAAGCTGGCC	2274
Dd	507	TrpSerAspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAla	526
Qy	2275	TGTGACCTCAACCATCTCTTCATCCAGAAAGCTGTGMACTCTTCCCAAGTGGATG	2334
Dd	527	CysAspLeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMet	546
Qy	2335	GAATCAGTGGAAAAATAATATACCAACAGATGTTTTAAAGATTGTGTTCTGTGGGT	2394
Dd	547	GluSerSerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrSerValGly	566
Qy	2395	GCTCAGAACACAGCAGGATGGAATTTACCTTTTAGACAAATATGAACCTGCAATGTCAAGT	2454
Dd	567	AlaGlnThrThrAlaGlyTrpAsnTyrLeuLeuGluGlnTyrGluLeuSerMetSerSer	586
Qy	2455	GCTGAAACAAACAAATTTCTGTATGCTTTGTCAACGAGCAAGCATCAGGAAAGTTACTG	2514
Dd	587	AlaGluGlnAsnLysIleLeuTyrAlaLeuSerThrSerLysHisGlnGluLysLeuLeu	606
Qy	2515	AAGTTAATTGAACATAGGAATGGAAGGAAAGTTTATCAAGACACAGAACTTGGCAGCTCTC	2574
Dd	607	LysLeuIleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaLeu	626
Qy	2575	CTTCATGCGATTGCCAGAGCTCCAAAGGGCGAGCAACTAGCATGGGATTTTGTAAAGAA	2634
Dd	627	LeuHisAlaIleAlaArgArgProLysGlyGlnGlnLeuAlaTrpAspPheValArgGlu	646
Qy	2635	AATTGACCCATCTCTCGAAAAAATTTGACTTGGGCTCATATGACATATAGGATGATCATC	2694
Dd	647	AsnTrpThrHisLeuLeuLysLysPheAspLeuGlySerTyrAspIleArgMetIleIle	666
Qy	2695	TCTGGCACACAGCTCACTTTTCTTCCAAAGGATAAGTTTCAAGAGGTGAAACTATTTTTT	2754
Dd	667	SerGlyThrThrAlaHisPheSerSerLysAspLysLeuGlnGluValLysLeuPhePhe	686
Qy	2755	GAATCTCTTGAGGCTCAAGATCACATCTGGATATTTTTTCAAACTGTTCTGGAAACGATA	2814
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QY 2815 ACCAAATATATAATGGCTGGAGAGAAATCTTCGACTCTGAGACTTGGCTAATGGTT 2874
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Db 707 ThrLysAenIleLysTrpLeuGluLysAenLeuProThrLeuArgThrTrpLeuMetVal 726
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QY 2875 AATACT 2880
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Db 727 AsnThr 728
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RESULT 7
AAU22999
ID AAU22999 standard; protein; 722 AA.
XX
AC AAU22999;
XX
XX
DT 18-DEC-2001 (first entry)
XX
DE Novel human enzyme polypeptide #85.
XX
XX Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
KW ligase; hyperproliferative disorder; immunodeficiency disorder;
KW autoimmune disorder; neurological disorder; metabolic disorder;
KW inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW blood-related disorder; infectious disorder; cytostatic; anti arthritic;
KW nephrotropic; anticoagulant.
XX
OS Homo sapiens.
XX
XX WO200155301-A2.
FN
XX
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001239.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
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 PR 05-JAN-2001; 2001US-0259678P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.

XX
 XX Rosen CA, Baraesh SC, Ruben SM;
 XX
 XX WPI; 2001-465566/50.
 DR N-PSDB; AAS40869.

XX
 XX Novel polypeptides and polynucleotides useful for diagnosing, preventing,

PT treating neural, immune system, muscular, reproductive, pulmonary,
 PT cardiovascular, renal, proliferative disorders and cancerous diseases.
 XX

PS Claim 11; SEQ ID NO 995; 1180pp; English.

XX The present invention relates to the isolation of novel human enzyme
 CC polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences
 CC encoding them. The enzyme polypeptides of the invention may comprise the
 CC functional classes of oxidoreductases, transferases, hydrolases, lyases,
 CC isomerases or ligases. The sequences of the invention are useful in the
 CC diagnosis, treatment, prevention and/or prognosis of a wide range of
 CC disorders including hyperproliferative disorders (e.g. cancer),
 CC immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g.
 CC arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic
 CC disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma),
 CC cardiovascular disorders (e.g. atherosclerosis), blood-related disorders
 CC (e.g. haemophilia), reproductive disorders (e.g. infertility) and
 CC infectious disorders (e.g. Influenza). The polynucleotides of the
 CC invention can also be used in gene therapy. AAU22915-AAU23814 represent
 CC the novel human enzyme polypeptides of the invention. Note: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 722 AA;

Alignment Scores:
 Pred. No.: 0 Length: 722
 Score: 3770.00 Matches: 717
 Percent Similarity: 99.31% Conservative: 0
 Best Local Similarity: 99.31% Mismatches: 5
 Query Match: 74.48% Indels: 0
 DB: 4 Gaps: 0

US-10-039-073-3 (1-2883) x AAU22999 (1-722)

QY 715 GTTAAGACAAATGAACCTGAAGGAGGTCTTTGGAGACTCACTTTGAACTACTGTAAAA 774
 DB 1 VallysThrIleGluLeuGluGlyGlyLeuLeuGluAspHisPheGluThrVallys 20

QY 775 ATGAGTACATACCTGTAGCCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACT 834
 DB 21 MetSerThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThr 40
 QY 835 TCATCAGGGGTCAAGGTGTCCTATCTATGCATCCCCAGACAAACGGGAATCAACACATTAT 894
 DB 41 SerSerGlyVallysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyr 60
 QY 895 GCTTTTCAGGCATCCTGGAAGCTACTTGTATTTTATGAAAGTACTTTTGATATCTACTAT 954
 DB 61 AlaLeuGlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyr 80
 QY 955 CCACTCTCCAACTGGATTAAATTGCTATTCTGACTTTTGCACCTTGGAGCATCGGAAAT 1014
 DB 81 ProLeuSerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsn 100
 QY 1015 TGGGGCTCATATCATATATAGGAGAGCTCATCTGCTTTTGGACCCCAAGACCTCTCTGCT 1074
 DB 101 TrpGlyLeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAla 120
 QY 1075 TCCGATAAAGCTGTGGGTCCACGAGTCATAGCCCATGAACTGGCGCACCATGCTTGGC 1134
 DB 121 SerAspLysLeuThrValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGly 140
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Qy 1975 AGAGTAGCTCGATTTCATGATGTGTTTCAGCTAGTGTGTGAGGAGACTGACCTAGAC 2034
Db 421 ArgValGlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAsp 440
Qy 2035 AAAGCTCTTGACATGACTTACTTACCTCCAAACATGAACAAGCAGCCCGCACTTCTCGAA 2094
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Qy 2095 GGTCTGAGTTACTTGGAAATCGTTTTTACCACATGATGAGAGAAGAAATATTTCAGATATC 2154
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Qy 2155 TCTGAAAACCTCAAGCGTTACTTCTTCAGTATTTTAAAGCCAGTGATGACAGGCAAGC 2214
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Db 501 TrpSerAspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAla 520
Qy 2275 TGTGACCTGAACCATGCTCCTTGTGATCAGAAAGCTGCTGAACCTTCTCCAGTGGATG 2334
Db 521 CysAspLeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMet 540
Qy 2335 GAATCCAGTGAAATTAATAATACCAACAGATGTTTTAAAGATGTGTATTCGTGGGT 2394
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Qy 2395 GCTCAGACACAGCAGGATGGAATTTACCTTTAGAGCAATATGACTGCTCAATGTCAGT 2454
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Qy 2515 AAGTTAATGAACCTAGGAATGAAGAAAGTTATCAAGACACAGAACTTGGCAGCTCTC 2574
Db 601 LysLeuIleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaAlaLeu 620
Qy 2575 CTTCATGCGATTGCCAGCTCCCAAGGGGAGCACTAGCATGGATTTTGTAAAGAA 2634
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Qy 2635 AATTGGACCCATCTTCTGAAAAAATTTGACCTTGGGCTCATATGACATAAGGATGATCATC 2694
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Db 661 SerGlyThrThrAlaHisPheSerSerLysAspLysLeuGlnGluValLysLeuPhePhe 680
Qy 2755 GAATCTCTTGGCTCAGGATCAGATCTGATATTTTCAACTGTTCTCGGAACGATA 2814
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Qy 2875 AATACT 2880
Db 721 ***Thr 722

ID XX ABB10511 standard; protein; 722 AA.
AC XX ABB10511;
XX 10-JAN-2002 (first entry)
XX Human cDNA SEQ ID NO: 819.
DE XX
XX Human; gene therapy; neural disorder; immune system disorder;
KW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; cardiovascular disorder; renal disorder;
KW proliferative disorder; inflammation.
XX Homo sapiens.
XX WO200154474-A2.
XX 02-AUG-2001.
XX 17-JAN-2001; 2001WO-US001349.
PF 31-JAN-2000; 2000US-0179065P.
XX 04-FEB-2000; 2000US-0180628P.
XX 24-FEB-2000; 2000US-0184664P.
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PR 01-DEC-2000; 2000US-0250391P.

PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
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PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-476161/51.
XX N-PSDB; ABA06733.
DR
DR Isolated nucleic acid molecule encoding an inflammation-associated
PT polypeptide is used in preventing, treating or ameliorating a medical
PT condition.
XX
XX Claim 11; SEQ ID NO 819; 859pp + Sequence Listing; English.
XX
XX The present invention provides human cDNAs, proteins and related genomic
CC DNAs. These can be used in the treatment of neural, immune system,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal and proliferative disorders and inflammation. The present sequence
CC is a protein of the invention
XX
XX SQ Sequence 722 AA;

Alignment Scores:
Pred. No.: 0 Length: 722
Score: 3770.00 Matches: 717
Percent Similarity: 99.31% Conservative: 0
Best Local Similarity: 99.31% Mismatches: 5
Query Match: 74.48% Indels: 0
DB: 4 Gaps: 0

US-10-039-073-3 (1-2883) x ABB10511 (1-722)

Qy 715 GTTAAGCAATGAAGTGAAGAGGTCTTTTGAAGATCACCTTGAAGTACTGTAAAA 774
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Qy 775 ATGAGTACATACCTTGTAGCCTACATAGTTTGTGATTTCACCTCTCTGAGTGGCTTCAC 834
Db 21 MetSerThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThr 40

Qy 835 TCATCAGGGGTCAAGGTGCTCCATCTATGCATCCCGACAGAAAGGATCAACACATTAT 894
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Qy 895 GCTTTTCAGGCATCACTGAAGCTACTTGTATTTTATGAAAAGTACTTTGATATCTACTAT 954
Db 61 AlaLeuGlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyr 80

Qy 955 CCACTCTCCAACTGGATTAAATTGCTATTCTCTGACTTTTGACCTGGAGCCATGGAAAT 1014
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Qy 1015 TGGGGCTCATATACATATAGGGAGAGCTCACTGCTTTTTCAGCCCAAGACCTCTTCGCT 1074
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Qy 1075 TCCGATAAACTGTGGGTCCACAGAGTCATAGCCCATGAACTGGCGCACCAAGTGGTTGGC 1134
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Db 161 MetGluLeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeu 180
QY 1255 AATGTGCTTTTGAAGTAATTACAAAGATTCAATTCATTCATCCGGCCCTATCTCCAAA 1314
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Db 301 ThrThrTrpThrLeuGlnLysGlyIleProLeuLeuValValLysGlnAspGlyCysSer 320
QY 1675 CTCGACATGCAACAGAGCGCTTCTCCAGGGGGTTTCCAGGAGAGCCCTGAATGGAGG 1734
Db 321 LeuArgLeuGlnGlnLysPheLeuGlnGlyValPheGlnGlnAspProGluTrpArg 340
QY 1735 GCCCTGACGAGAGGTACTCTGTGGCATATCCCATGACCTACTCCACAGATTTCTTCTAAT 1794
Db 341 AlaLeuGlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerSerSerAsn 360
QY 1795 GTGATCCACAGACACATTTAAATCAAAAGACAGATCTCTGGATCTACCTGAAAGACC 1854
Db 361 ValIleHisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThr 380
QY 1855 AGTTGGGTGAATTTAATGTGACCTCAATGCTTACTCATCGTTTCACTATGAGGGTCAAT 1914
Db 381 SerTrpValLysPheAsnValAspSerAsnGlyTyrIleValIleHisIleGlyHis 400
QY 1915 GGATGGGACCACTCATTACAGCTGAATCAGAACCAACACACTTCTCAGACCTAAGGAC 1974
Db 401 GlyTrpAspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAsp 420
QY 1975 AGAGTAGTCTGATTCATGATGTTTTCAGTGTGTTGAGTGTGAGGAGACTGACCTTAGAC 2034
Db 421 ArgValGlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAsp 440
QY 2035 AAAGCTCTTGACACTACTTACTCTCAACATGAACAAAGCAGCCCGCACTTCTCCAA 2094
Db 441 LysAlaLeuAspMetThrTyrTyrLeuGlnHisIleGluThrSerSerProAlaLeuLeuGlu 460
QY 2095 GGTCTGAGTTACTTGGAAATCGTTTTTACCACATGATGGAGAGAAATATTTACAGATATC 2154
Db 461 GlyLeuSerTyrLeuGluSerPheTyrHisMetMetAspArgArgAsnIleSerAspIle 480
QY 2155 TCTGAAACCTCAAGGGTTACTTCTTTCAGTATTTTAAAGCCAGTGTGACAGGCAAGC 2214
Db 481 SerGluAsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSer 500
QY 2215 TGGAGTGACAGGGCTAGCTGGGACAGGATGCTCCGCTCGGCTCTCTGAAGTCGCC 2274
Db 501 TrpSerAspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAla 520

QY 2275 TGTGACCTGAACCATGCTCTCTTGCAATCCAGAAAGCTGCTGAACCTCTTCTCCAGTGGATG 2334
Db 521 CysAspLeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMet 540
QY 2335 GAATCCAGTGGAAATTTAAATATATATACCAACAGATGTTTTTAAAGATTGTGTATTCTGTGGGT 2394
Db 541 GluSerSerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrSerValGly 560
QY 2395 GCTCAGACAAACAGCAGGATGGAATTTACCTTTTACAGCAATATGAATCTGCTCAATGTCAAGT 2454
Db 561 AlaGlnThrThrAlaGlyTrpAsnTyrLeuLeuGluGlnTyrGluLeuSerMetSerSer 580
QY 2455 GCTGAAACAAACAAATTTCTGTATGCTTTGTCAACGAGCAAGCATCAGGAAAAAGTTACTG 2514
Db 581 AlaGluGlnAsnLysIleLeuTyrAlaLeuSerThrSerLysHisGlnGluLysLeuLeu 600
QY 2515 AAGTTAATTGAACCTAGCAATGGAAGGAAAGTTATCAAGACACAGAACTTCGCAGCTCTC 2574
Db 601 LysLeuIleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaAlaLeu 620
QY 2575 CTTTCATCGATTGCGACAGCTCCAAAGGGGCGAGCACTAGCATGGGATTTTGTAAAGAGAA 2634
Db 621 LeuHisAlaIleAlaArgProLysGlyGlnGlnLeuAlaTrpAspPheValArgGlu 640
QY 2635 AATTGGACCCATCTTCTGAAAAAATTTGACCTTGGGCTCATATGACATAAGGATGATCATC 2694
Db 641 AsnTrpThrHisLeuLeuLysLysPheAspLeuGlySerTyrAspIleArgMetIleIle 660
QY 2695 TCTGGCAACACAGCTCACTTTCTTCCAAAGGATAAGTTGCAAGAGGTGAACTATTTT 2754
Db 661 SerGlyThrThrAlaHisPheSerSerLysAspLysLeuGlnGluValLysLeuPhePhe 680
QY 2755 GAATCTCTTGAAGCTCAAGGATCACATCTGGATATTTTCAAACTGTTCTCGAAACGATA 2814
Db 681 GluSerLeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIle 700
QY 2815 ACCAAAAATATAAATGGCTGGAGAAAGATCTTCCGACTCTGAGGACTTGGCTTAATGGTT 2874
Db 701 ThrLysAsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeu***** 720
QY 2875 AATACT 2880
Db 721 ***Thr 722
RESULT 9
ABP67098
ID ABP67098 standard; protein; 722 AA.
XX AC ABP67098;
XX 09-DEC-2002 (first entry)
XX Human polypeptide SEQ ID NO 819.
XX Human; nootropic; neuroprotective; cytostatic; dermatologic; virucide;
XX immunosuppressive; anti-inflammatory; anti-HIV; antibacterial; vulnerary;
XX antiparkinsonian; antischlicking; antianaemic; antiarthritic; cancer;
XX antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
XX antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
XX antiparasitic; cardiant; immune disorder; cardiovascular disorder;
XX neurological disease; infection; nephrotropic; gene therapy; vaccine.
XX Homo sapiens.
XX OS
XX PN US2002090672-A1.
XX PD 11-JUL-2002.
XX PF 17-JAN-2001; 2001US-00764853.
XX PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.

PR 28-JUN-2000; 2000US-0214886P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 07-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 11-JUL-2000; 2000US-0217496P.
 PR 14-JUL-2000; 2000US-0218239P.
 PR 26-JUL-2000; 2000US-0220963P.
 PR 26-JUL-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225267P.
 PR 14-AUG-2000; 2000US-0225268P.
 PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225577P.
 PR 22-AUG-2000; 2000US-0225758P.
 PR 22-AUG-2000; 2000US-0226868P.
 PR 30-AUG-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229344P.
 PR 01-SEP-2000; 2000US-0229345P.
 PR 05-SEP-2000; 2000US-0229509P.
 PR 05-SEP-2000; 2000US-0229513P.
 PR 08-SEP-2000; 2000US-0231413P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234274P.
 PR 25-SEP-2000; 2000US-0234997P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239935P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 XX (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 XX
 PI Rosen CA, Ruben SM, Barash SC;
 XX
 DR WPI; 2002-681727/73.
 DR N-PSDB; ABV84070.
 XX
 PT Novel polypeptide useful for diagnosis, prognosis, prevention, and
 PT treatment of immune, hyperproliferative, renal, respiratory,
 PT cardiovascular, reproductive, endocrine, gastrointestinal and
 PT neurological disorders.
 XX
 XX Claim 11; SEQ ID NO 819; 369pp + Sequence Listing; English.
 PS
 PS The invention relates to novel genes (ABV83682-ABV84101) and proteins
 CC (ABP6710-ABP67129) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune

CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
 CC infectious diseases such as viral, bacterial, fungal and parasitic
 CC infections. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pt_sequences
 XX
 SQ Sequence 722 AA;

Alignment Scores:

Pred. No.: 0 Length: 722
 Score: 3770.00 Matches: 717
 Percent Similarity: 99.31% Conservative: 0
 Best Local Similarity: 99.31% Mismatches: 5
 Query Match: 74.48% Indels: 0
 DB: 5 Gaps: 0

US-10-039-073-3 (1-2883) x ABP67098 (1-722)

QY 715 GTTAAGACAATTGAACCTGAAGAGGTCTTTGGGAAGATCACCTTGAACACTACTGTAAAA 774
 Db 1 ValLysThrIleGluLeuGluGlyLeuLeuGluAspHisPheGluThrValLys 20
 QY 775 ATGAGTACATACCTCTGTAGCCTACATAGTTTGATTTCACACTCTCTGAGTGGCTTCACT 834
 Db 21 MetSerThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThr 40
 QY 835 TCATCAGGGGTCAAGGTGTCCATCTATGCATCCCCAGACAAACGGAATCAAAACACATTAT 894
 Db 41 SerSerGlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyr 60
 QY 895 GCTTTCAGGCATCACTGAAGCTACTTGATTTTATGAAAAGTACTTTGATATCTACTAT 954
 Db 61 AlaLeuGlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyr 80
 QY 955 CCACTCTCCAAACTGGATTAAATTGCTATTCTGACTTTGCACCTTCGAGCCATGGAAAAT 1014
 Db 81 ProLeuSerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsn 100
 QY 1015 TGGGGCTCATATACATATAGGAGAGCTCACTGCTTTTGGACCCCAAGACCTCTCTGCT 1074
 Db 101 TrpGlyLeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAla 120
 QY 1075 TCCGATAAACTGTGGGTCAACAGATCATAGCCCATGAACCTGCGCACACAGTGGTTGGC 1134
 Db 121 SerAspLysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGly 140
 QY 1135 AACCTGGTCACAATGGAATGGTGAATGATATTGGCTTAAGGAGGGTTTTCGAAAATAC 1194
 Db 141 AsnLeuValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyr 160
 QY 1195 ATGGAACTTATCGCTGTTAATGCTACATATCCAGAGCTCAATTTGATGACTATTTTTTG 1254
 Db 161 MetGluLeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeu 180
 QY 1255 AATGTGTGTTTGAAGTAATTACAAAGATTCAATGGAATTCATCCCGCCCTATCTCAAA 1314
 Db 181 AsnValCysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLys 200
 QY 1315 CCAGCGGAAACCCCGACTCAAAATACAGGAAATGTTTGTAGTAAGTTCCTATATCAAGGGA 1374
 Db 201 ProAlaGluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGly 220
 QY 1375 GCTTGTTATTTGAATATGCTCAAGGATTTCCTGGGTGAGGAGAAATTCAGAGAAGAATA 1434
 Db 221 AlaCysIleLeuAsnMetLeuLysAspPheLeuGlyGluGluLysPhe***LysGlyIle 240
 QY 1435 ATTCACTACTTAAAGAGTTTCAGCTATAGAAATGCTAAGAATGATGACTCTGTGGACAGT 1494
 Db 241 IleGlnTyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspAspLeuTrpSerSer 260

QY 1495 CTGTCATAGTGTGTTAGAAAGTGAATTTTACATCTGGTGGAGTTTGTCTATCTCGATCCC 1554
Db 261 LeuSerAsnSerCysLeuGluSerAspPheThrSerGlyGlyValCysHisSerAspPro 280
QY 1555 AAGATGACAAAGTAACATGCTCGCCCTTCTGGGGGAAATGCAGAGGTCAAAAGAGATGATG 1614
Db 281 LysMetThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGlu***LysGluMetMet 300
QY 1615 ACTACATGGACTCTCCAGAAAGAAATCCCCCTGCTGGTGGTTAAACAAGACGGGTTCAT 1674
Db 301 ThrThrTrpThrLeuGlnLysGlyLeuProLeuLeuValValLysGlnAspGlyCysSer 320
QY 1675 CTCCGACTGCAACAGAGCGCTTCTCCAGGGGGTTTCCAGGAAGACCTGAAATGGAGG 1734
Db 321 LeuArgLeuGlnGlnArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArg 340
QY 1735 GCCTGTCAGGAGAGGTACTCTGGGCATATCCATTGACCTACTCCACAGTTCCTCTAAT 1794
Db 341 AlaLeuGlnGluArgTrpLeuTrpHisLeuProLeuThrTyrrSerSerSerSerAsn 360
QY 1795 GTGATCCACAGACACATTTAAAATCAAGACAGATCTCTGGATCTACCTGAAAGACC 1854
Db 361 ValIleHisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThr 380
QY 1855 AGTGGGTGAATTTAATGTGACTCAAAATGGTTACTACATCGTTCACTATGAGGGTCAT 1914
Db 381 SerTrpValLysPheAsnValAspSerAsnGlyTyrrTyrrIleValHisTyrrGluGlyHis 400
QY 1915 GGATGGGACCAACTCATTTACACAGCTGAATCAGACACACACTTCTCAGACCTTAAGGAC 1974
Db 401 GlyTrpAspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAsp 420
QY 1975 AGAGTAGTCTGATTCATGATGTTTTCAGCTAGTTGGTGCAGGAGACTGACCCCTAGAC 2034
Db 421 ArgValGlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAsp 440
QY 2035 AAAGCTTTGACATGACTTACTCTCAACATGAAACAAGCAGCCCGCCTTCTCGAA 2094
Db 441 LysAlaLeuAspMetThrTyrrTyrrLeuGlnHisGluThrSerSerProAlaLeuLeuGlu 460
QY 2095 GGTCTGAGTCTACTTGGAAATCGTTTACCACATGATGGACAGAGAAATTTTCAGATATC 2154
Db 461 GlyLeuSerTyrrLeuGluSerPheTyrrHisMetMetAspArgAsnIleSerAspIle 480
QY 2155 TCTGAAAACCTCAAGCGTTACTCTTTCAGTATTTTAAGCCAGTGATTCAGACGCAAGC 2214
Db 481 SerGluAsnLeuLysArgTyrrLeuLeuGlnTyrrPheLysProValIleAspArgGlnSer 500
QY 2215 TGGAGTGACAGGGCTCAGTCTGGACAGGATGCTCCGCTCGCTCTCTTGAAGCTGGCC 2274
Db 501 TrpSerAspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAla 520
QY 2275 TGTGACCTGAACCACTGCTTGCATCCAGAAAGCTGCTGAACCTTCTCCAGTGGATG 2334
Db 521 CysAspLeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMet 540
QY 2335 GAATCCAGTGGAAAATTAATATACCAACAGATGTTTAAAGATTGTATTCTGTGGGT 2394
Db 541 GluSerSerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrrSerValGly 560
QY 2395 GCTCAGACACAGCAGGATGGAATTAATCTTTTAGAGCAATATGAATCTCAATGTCAAGT 2454
Db 561 AlaGlnThrThrAlaGlyTrpAsnTyrrLeuLeuGluGlnTyrrGluLeuSerMetSerSer 580
QY 2455 GCTGAACAAAACAATTTCTGTATGCTTGTTCACAGCAGCAAGCATTCAGAAAGTTACTG 2514
Db 581 AlaGlnGlnAsnLysIleLeuTyrrAlaLeuSerThrSerLysHisGlnGluLysLeuLeu 600
QY 2515 AAGTTAAATTGAAGTGAAGAAAGGTTATCAAGACACAGAACTTGGCAGCTCTC 2574
Db 601 LysLeuIleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaAlaLeu 620

QY 2575 CTTTCATGGATTGCCAGACGTCCTCAAGGGGCGAGCAACTAGCATGGATTTTGTAGAGAA 2634
Db 621 LeuHisAlaIleAlaArgArgProLysGlyGlnGlnLeuAlaTrpAspPheValArgGlu 640
QY 2635 AATTGGACCCATCTTCTGMAAAATTTGACTTGGGCTCATATGACATAAGGATGATCATC 2694
Db 641 AsnTrpThrHisLeuLeuLysLysPheAspLeuGlySerTyrrAspIleArgMetIleIle 660
QY 2695 TCTGCGCAACAGCTCACTTTTCTTCCAGGATTAAGTTGCAAGGGTGAATCTATTTTTT 2754
Db 661 SerGlyThrThrAlaHisPheSerSerLysAspLysLeuGlnGluValLysLeuPhePhe 680
QY 2755 GAATCTCTTGGGCTCAAGGATCAGATCAGATCTGGATATTTTCAAACTGTTCTCGAACGATA 2814
Db 681 GluSerLeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIle 700
QY 2815 ACCAAAAATATAAATGGCTGGAGAAGAAATCTTCCGACTCTGAGGACTTGGCTAATGGTT 2874
Db 701 ThrLysAsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeu***** 720
QY 2875 AATACT 2880
Db 721 ***Thr 722
RESULT 10
ID ADR41453 standard; protein; 722 AA.
XX ADR41453;
XX AC ADR41453;
XX DT 07-OCT-2004 (first entry)
XX DE Human CD-like molecule HAIDK30, SEQ ID NO:252.
XX KW Human; CD-like molecule; cluster of differentiation; diagnosis;
KW prevention; immune disorder; immunodeficiency; autoimmune disorder;
KW blood-related disorder; haematological disorder; haemostatic disorder;
KW thrombolytic disorder; hyperproliferative disorder; cancer; tumour;
KW apoptotic disorder; cardiovascular disorder; respiratory disorder;
KW angiogenic disorder; neovascularisation; neurological disorder;
KW endocrine disorder; reproductive system disorder; infectious disease;
KW gastrointestinal disorder; drug screening; tissue regeneration;
KW chemotaxis; gene therapy; antibody therapy; drug targeting;
KW chromosome mapping; forensic analysis; immunophenotyping; cytostatic;
KW haemostatic; tranquiliser; vulnery; anti-inflammatory; nephrotropic;
KW cardiant; antiallergic; anti-HIV; antineumatic; antiarthritic;
KW antipsoriatic; immunosuppressive; vasotropic; nootropic; neuroprotective;
KW antithyroid; thyromimetic; gynaecological; virucide; hepatotropic;
KW antibacterial; dermatological; chromosome 16.
XX OS Homo sapiens.
XX OS WO200226930-A2.
XX PN 04-APR-2002.
XX FD 25-SEP-2001; 2001WO-US029838.
XX PF 26-SEP-2000; 2000US-0235484P.
XX PR (HUMA-) HUMAN GENOME SCI INC.
XX PA Rosen CA, Birse CE;
XX PT WPI: 2002-405050/43.
XX DR N-PSDB; ADR41277.
XX DR Novel polynucleotides and polypeptides useful for treating, preventing or
XX ameliorating cardiovascular, renal, neurovascular, and autoimmune
XX disorders.
XX PS Claim 11; SEQ ID NO 252; 1243pp; English.

CC The invention relates to 167 novel human CD (cluster of differentiation)-
CC like molecules (ADR41388-ADR41563) and to cDNAs encoding them (seqid:11)-
XX
SQ Sequence 722 AA;

Alignment Scores:

Pred. No.: 0 Length: 722
Score: 3763.00 Matches: 717
Percent Similarity: 99.31% Conservative: 5
Best Local Similarity: 99.31% Mismatches: 0
Query Match: 74.34% Indels: 0
DB: 5 Gaps: 0

US-10-039-073-3 (1-2883) x ADR41453 (1-722)

QY	715	GTTAAGCAATTGAACCTTGAGGAGCTCTTTTGGAGATCACCTTGGAACTACTGTAAAA	774
Db	1	VallysThrIleGluLeuGluGlyGlyLeuLeuGluAspHisPheGluThrThrVallys	20
QY	775	ATGAGTACATACCTTGTAGCCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCAC	834
Db	21	MetSerThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThr	40
QY	835	TCATCAGGGTCAAGGTGTCATCTATGCAATCCAGACAAACGGAATCAAAACACATTAT	894
Db	41	SerSerGlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyr	60
QY	895	GCTTTGCAGGCATCACATGAGCTACTTGTATTTTATGAAAGTACTTTGTATCTACTAT	954
Db	61	AlaLeuGlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyr	80
QY	955	CCACTCTCCAACTGGATTTAAATTGCTATTCTGACTTTTGCACTGGAGCCATGGAAAAAT	1014
Db	81	ProLeuSerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsn	100
QY	1015	TGGGGCTCATATCATATAGGAGAGCTCACTGCTGTTTTGACCCCAAGACTCTCTCGCT	1074
Db	101	TrpGlyLeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAla	120
QY	1075	TCCGATAAAGCTGGGTCACAGAGTCATAGCCCATCAAGCTGGCGCACAGTGGTTGGC	1134
Db	121	SerAspLysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGly	140
QY	1135	AACCTGTGTCAATAGGAATGGTGAATCATATTTGGCTTAAGAGGGTTTTGCAAAATAC	1194
Db	141	AsnLeuValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyr	160
QY	1195	ATGGAACCTTATCGCTGTTAATGCTACATATCCAGAGCTGCAATTTGTATGATCTATTTTG	1254
Db	161	MetGluLeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeu	180
QY	1255	AATGTGTGTTTGAAGTAATTACAAAAGATTTCATTGAATTCATCCCGCCCTATCTCCAA	1314
Db	181	AsnValCysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLys	200
QY	1315	CCAGCGAAACCCGACTCAAAATACAGAAATGTTTTCATGAAGTTTCTTATAACAAGGGA	1374
Db	201	ProAlaGluThrProThrGlnIleGlnGluMet***AspGluValSerTyrAsnLysGly	220
QY	1375	GCTTGATATTTGAATATGCTCAAGGATTTTCTGGGTGAGGAGAAATTCAGAAAGGAATA	1434
Db	221	AlaCysIleLeuAsnMetLeuLysAspPheLeuGlyGluGluLysPheGlnLysGlyIle	240
QY	1435	ATTCAAGTACTTAAGAAGTTCAGCTATAGAAATGCTAAGATGATGACTTGTGGAGCGT	1494
Db	241	IleGlnTyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspAspLeuTrpSerSer	260
QY	1495	CTGTCAATATAGTTCTTTAGAAAGTGATTTTACATCTGGTGGAGTTTGTCTATCGGATCCC	1554
Db	261	LeuSerAsnSer***LeuGluSerAspPheThrSerGlyValCysHisSerAspPro	280
QY	1555	AAGATGACAGTAACTGCTGCTTCTGCGGGGAAAAATGCAGAGTCAAAAGATGATG	1614

Db	281	LysMetThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGluValLysGluMetMet	300
QY	1615	ACTACATGAGCTCTCCAGAAAGGAATCCCCCTGCTGCTGTTAAACAAGACGGGTGTCA	1674
Db	301	ThrThrTrpThrLeuGlnLysGlyIleProLeuLeuValLysGlnAspGlyCysSer	320
QY	1675	CTCCGACTGCACAGGAGCGCTTCTCCAGGGGGTTTCCAGGAAGACCCCTGTAATGAGG	1734
Db	321	LeuArgLeuGlnGlnGluArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArg	340
QY	1735	GCCCTCCAGAGAGGTACCTGTGGCATATCCCATTTGACCTACTCCACGAGTCTTCTTAAT	1794
Db	341	AlaLeuGlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerThrSerSerAsn	360
QY	1795	GTGATCCACAGACACATCTAAATCAAAAGACAGATACTCTGATCTACTGAAAAGACC	1854
Db	361	ValIleHisIleGlnHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThr	380
QY	1855	AGTTGGGTGAAATTTTAAATGTGGACTCAAAATGGTTTACTACATCGTTACATGAGGGTCA	1914
Db	381	SerTrpValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHis	400
QY	1915	GGATGGGACCAACTCATACACAGCTGAATCAGAACACACACTTCTCAGACCTAAGGAC	1974
Db	401	GlyTrpAspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAsp	420
QY	1975	AGAGTAGGTCTGATTCATGATGTTTTCAGCTAGTTGGTGCGGGAGACTGACCTAGAC	2034
Db	421	ArgValGlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAsp	440
QY	2035	AAAGCTCTTTGACATGACTTACTACTCTCAACATGAAACAAGCAGCCCCCCTTCTCGAA	2094
Db	441	LysAlaLeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProAlaLeuLeuGlu	460
QY	2095	GGTCTGAGTTACTTGAATCGTTTTACACATGATCGACAGAGGAATATTTTCAGATATC	2154
Db	461	GlyLeuSerTyrLeuGluSerPheTyrHisMetMetAspArgAsnIleSerAspIle	480
QY	2155	TCTGAAAACTCAAGGTTTACCTTCTTCAGTATTTTAAAGCCAGTGTATGACAGGCAAGC	2214
Db	481	SerGluAsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSer	500
QY	2215	TGGAGTGAACAAGGGCTCAGTCTGGGACAGGATGCTCCGCTCGGCTCTTTGAAGCTGGCC	2274
Db	501	TrpSerAspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAla	520
QY	2275	TGTGACCTGAACCATCTCTCTTCATCCAGAAAGCTGCTGAACTCTTCCCGAGTGGATG	2334
Db	521	CysAspLeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMet	540
QY	2335	GAATCCAGTGGAAAAATTAATATATACCAACAGATGTTTTTAAAGATTCTGTATTCTGTGGGT	2394
Db	541	GluSerSerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrSerValGly	560
QY	2395	GCTCAGACAACAGCAGGATGGAATTAACCTTTTAGAGCAATATGAACGTGTCATGTCAAGT	2454
Db	561	AlaGlnThrThrAlaGlyTrpAsnTyrLeuLeuGluGlnTyrGluLeuSerMetSerSer	580
QY	2455	GCTGAACAAAAACAAATTTCTGTATGTTGTCACAGCAGCAGCATCAGGAAAGTTACTG	2514
Db	581	AlaGluGlnAsnLysIleLeuTyrAlaLeuSerThrSerLysHisGlnGluLysLeuLeu	600
QY	2515	AAATTAATTTGAATAGGAATGGAAGGAAAGGTTTATCAAGACACAGAACTTGGCAGCTCTC	2574
Db	601	LysLeuIleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaLeu	620
QY	2575	CTTTCATGCGATTGCCAGACGTCCAAAGGGCGCAGCAACTAGCATGGGATTTTGTAAAGAA	2634
Db	621	LeuHisAlaIleAlaArgProLysGlyGlnGlnLeuAlaTrpAspPheValArgGlu	640
QY	2635	AATTGACCCATCTTCTGAAAAATTTGACTTGGGCTCATATGACATAGGATGATCATC	2694
Db	641	AsnTrpThrHisLeuLeuLysLysPheAspLeuGlySerTyrAspIleArgMetIleIle	660

QY 2695 TCTGCCACACAGCTCATTCTTCCAGGATAGTTGCGAGGTGAACATATTTTT 2754
 Db |||||||
 QY 661 SerGlyThrAlaHisPheSerSerLysAspLysLeuGlnGluValLysLeuPhePhe 680
 Db |||||||
 QY 2755 GAATCTCTTGAGGCTCAAGGATCACATCTGGATATTTTCAAACCTGTTCTCGAAACGATA 2814
 Db |||||||
 QY 691 GluSerLeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIle 700
 Db |||||||
 QY 2815 ACCAAAAATATAAATGGCTGGAGAGAAATCTTCCGACTCTGAGGACTTGGCTAATGTT 2874
 Db |||||||
 QY 701 ThrLysAsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeu***** 720
 QY 2875 AATACT 2880
 Db |||||
 Db 721 ***Thr 722
 RESULT 11
 AAU07829
 ID AAU07829 standard; protein; 941 AA.
 AC AAU07829;
 XX
 XX 04-DEC-2001 (first entry)
 XX Human ARTS-1 polypeptide.
 DE Human; aminopeptidase regulator of type I; cytokine signalling; ARTS-1;
 KW tumour necrosis factor receptor ectodomain shedding; interleukin-1;
 KW interleukin-6; immune disorder; TNF-mediated immune disease;
 KW inflammatory disorder; anti arthritic; vasotropic; immunomodulator;
 KW immunosuppressive; antibacterial; gene therapy.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Domain 350..361
 FT /label= Zinc_binding domain
 FT Domain 353..376
 FT /label= Zinc_metalloproteinase_catalytic_motif
 FT Domain 372..379
 FT /label= Zinc_binding_catalytic_site
 XX
 FN WO200164856-A2.
 XX
 XX 07-SEP-2001.
 XX
 XX 28-FEB-2001; 2001WO-US006464.
 XX
 XX 28-FEB-2000; 2000US-0185586P.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX Levine S;
 XX
 DR WPI; 2001-550175/61.
 DR N-PSDB; AAS09227.
 XX
 XX Novel polypeptide useful for the regulation of ectodomain shedding of
 PT type I, tumor necrosis factor receptor and other cytokine receptors and
 PT for treating disorders and diseases of the immune system.
 XX
 XX Claim 2; Fig 1; 139pp; English.
 XX
 CC The present invention relates to the isolation of a novel human
 CC polypeptide, defined as aminopeptidase regulator of type I, 55 kDa tumour
 CC necrosis factor (TNF) receptor ectodomain shedding (ARTS-1), and the
 CC polynucleotide sequence encoding for ARTS-1. The invention describes
 CC compositions and methods for the regulation of cytokine signalling
 CC through the TNF pathway. The ARTS-1 polypeptide and antibodies that bind
 CC ARTS-1 are useful for regulating the shedding of the extracellular domain
 CC of a cytokine receptor such as type-I tumour necrosis factor receptor,
 CC type I or II interleukin-1 cytokine receptor and interleukin-6 cytokine

CC receptor alpha-chain gp80, by delivering the molecules to a tissue
 CC comprising one or more cells expressing the cytokine receptor or their
 CC plasma membrane extracellular surface. The ARTS-1 sequences are
 CC useful for treating a subject, preferably human, displaying, suspected
 CC of, or at risk of displaying a pathology resulting from abnormal cytokine
 CC activity, such as tumour necrosis factor alpha, interleukin-lalpha, lbeta
 CC or interleukin-6. A vector comprising the polynucleotide encoding ARTS-1
 CC is useful in gene therapy. The ARTS-1 sequences are useful in diagnostic
 CC and therapeutic regimens in treating immune disorders (e.g. TNF-mediated
 CC immune diseases) and inflammatory disorders (e.g. rheumatoid arthritis).
 CC The present sequence represents human ARTS-1 polypeptide
 XX
 SQ Sequence 941 AA;

Alignment Scores:
 Pred. No.: 2e-246 Length: 941
 Score: 2516.50 Matches: 478
 Percent Similarity: 69.34% Conservative: 171
 Best Local Similarity: 51.07% Mismatches: 268
 Query Match: 49.71% Indels: 19
 DB: 4 Gaps: 7

US-10-039-073-3 (1-2883) x AAU07829 (1-941)

QY 67 TACTGCTTAACAGCCATCTTGGCCCAATATGCATTGTTCTCAGTTCAGTGCCATCT 126
 Db :: |||||
 Db 15 PheLeuLeuSerSerLeuLeuAlaLeuLeuThrVal-----SerThrProSer 30
 QY 127 AGTTATCACTCACTGAGGATCCTGGGCTTCCAGTAGCCACTAATGGGAACGATTT 186
 Db |||||
 Db 31 TrpCysGlnSerThrGlu-----AlaSerProLysArgSerAspGlyThrProPhe 47
 QY 187 CTTGGCAGGAGCTAAGCTCCCGAGTGTGCTCTCTCCATTATGACCTCTTTGTC 246
 Db |||||
 Db 48 ProTrpAsnLysIleArgLeuProGluTy-ValIleProValHisTyAspLeuLeu 67
 QY 247 CACCCCAATCTCACTCTCGGACTTTGTCATCTCAGAGATCGAGTCTTGTCAGC 306
 Db |||||
 Db 68 HisAlaAsnLeuThrThrLeuThrPheTrpGlyThrThrLysValGluIleThrAlaSer 87
 QY 307 AATGCTACCCAGTTTATCATCTTGACAGCAAGATCTTGAAATCAGCAATGCCACCTT 366
 Db |||||
 Db 88 GlnProThrSerThrIleIleLeuHisSerHisLeuGlnIleSerArgAlaThrLeu 107
 QY 367 CAGTCAGAGGAAGATTCAAGATACATGAAACACGAGAAAGAACTGAAGTTTTCAGTTAC 426
 Db |||||
 Db 108 ArgLysGlyAlaGlyGluArgLeuSerGlu-----GluProLeuGlnValLeuGluHis 125
 QY 427 CTTGCTCATGAACAAATTGCATGCTGTTCCAGAGAAACTTACGCTCACCTGAATAC 486
 Db |||||
 Db 126 ProArgGlnGluGlnIleAlaLeuLeuAlaProGluProLeuLeuValGlyLeuProTyr 145
 QY 487 TATGTGGCTATGGACTTCCAAAGCCAAAGTATAGGTAGTGGCTTTGAAGGTTTATAAAGC 546
 Db |||||
 Db 146 ThrValValIleHisTyAlaGlyAsnLeuSerGluThrPheHisGlyPheTyLysSer 165
 QY 547 ACATACAGAACTCTTGGTGGTGAACAAAGAATTCTTCAGTAAACAGATTTTGAGCCAAAC 606
 Db |||||
 Db 166 ThrTyArgThrLysGluGlyGluLeuArgIleLeuAlaSerThrGlnPheGluProThr 185
 QY 607 CAGCAGCATGCTTCCCTTGTGTTGATGAACCGTTGTTCAAGGCAACTTTTCAATC 666
 Db |||||
 Db 186 AlaAlaArgMetAlaPheProCysPheAspGluProAlaPheLysAlaSerPheSerIle 205
 QY 667 AAGATACGAAGAGAGACGAGCATATTGCACTATCCAAACATGCCAAAGGTTAAGACAATT 726
 Db |||||
 Db 206 LysIleArgGluProArgHisLeuAlaIleSerAsnMetProLeuValLysSerVal 225
 QY 727 GAATCTGAAGAGAGTCTTTTGGAGAGATCACTTTGAAACTACTGTAAATAATGAGTACATAC 786
 Db |||||
 Db 226 ThrValAlaGluGlyLeuIleGluAspHisPheAspValThrValLysMetSerThrTyr 245
 QY 787 CTTGTAGCCCTACATAGTTTGTGATTCCCACTCTCTGAGTGGCTTCACTTCAATCAGGGTC 846

Db 246 LeuValAlaPheIleIleSerAspPheGluSerValSerLysIleThrLysSerGlyVal 265
QY 847 AAGGTGTCATCATGCCAGACAAACGGNAATCAACACATATATGCTTTGCAGGCA 906
Db 266 LysValSerValTyrAlaValProAspLysIleAsnGlnAlaAspTyrAlaLeuAspAla 285
QY 907 TCACCTGAAGCTACTGTGATTTTATGAAAGTACTTTTGATATCTACTATCCACTCTCCAAA 966
Db 286 AlaValThrLeuLeuGluPheTyrGluAspTyrPheSerIleProTyrProLeuProLys 305
QY 967 CTGGATTAAATGCTATTCTCGACTTTGCACTGGAGCCATGGAATAATGGGCGCTCAT 1026
Db 306 GlnAspLeuAlaIleProAspPheGlnSerGlyAlaMetGluAsnTrpGlyLeuThr 325
QY 1027 ACATATAGGAGAGCTCAGCTGCTTTTGGACCCCAAGACCTCTCTGCTCCGATAACTG 1086
Db 326 ThrTyrArgGluSerAlaLeuLeuPheAspAlaGluLysSerSerAlaSerSerLysLeu 345
QY 1087 TGGGTCAACGAGTCATAGCCCATGAACCTGGCGCACAGTGGTTTGGCAACCTGGTCACA 1146
Db 346 GlyIleThrMetThrValAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeuValThr 365
QY 1147 ATGGAATGGTGAATGATATTTGGCTTAAGAGGGTTTTCGAAAATACATGGAACCTTATC 1206
Db 366 MetGluTrpTrpAsnAspLeuTrpLeuAsnGluGlyPheAlaLysPheMetGluPheVal 385
QY 1207 GCTGTTAATGCTACATATCCAGAGCTCAATTTGATGACATATTTTGAATGTGTGTTT 1266
Db 386 SerValSerValThrHisProGluLeuLysValGlyAspTyrPhePheGlyLysCysPhe 405
QY 1267 GAAGTAATTCAMAAGATTTCATGAATTCATCCCGCTCTATCCAAACCCAGCGGAACC 1326
Db 406 AspAlaMetGluValAspAlaLeuAsnSerSerHisProValSerThrProValGluAsn 425
QY 1327 CCGACTCAATACAGGAAATGTTTGATGAAATTTCTTATACAAAGGAGCTGTGATTTTG 1386
Db 426 ProAlaGlnIleArgGluMetPheAspValSerTyrAspLysGlyAlaCysIleLeu 445
QY 1387 AATATGCTCAAGGATTTCTGGGTGAGGAGAAATCCAGAAAGGATAATTCAGTACTTA 1446
Db 446 AsnMetLeuArgGluTyrLeuSerAlaAspAlaPheLysSerGlyIleValGlnTyrLeu 465
QY 1447 AAGAAATTCAGCTATAGAAATGCTAAGAATGATGACTTTGGAGCAGCTGTCAAATAGT 1506
Db 466 GlnLysHisSerTyrLysAsnThrLysAsnGluAspLeuTrpAspSerMetAlaSerIle 485
QY 1507 TGTTTAGAAAGTATTTTACATCTGGT-----GGAGTTTGTCTATCGGATCCCAAGATG 1560
Db 486 Cys---ProThrAspGlyValLysGlyMetAspGlyPheCys---SerArgSerGlnHis 503
QY 1561 ACAAGTAACATGCTCGCTTCTGGGGGAAATGCAGAGCTCAAGAGATGATGACTACA 1620
Db 504 SerSerSerSerHisTrpHisGlnGluGlyValAspValLysThrMetMetAsnThr 523
QY 1621 TGGACTCTCAGAAAGAAATCCCGCTCTGTGGTTTAAACAAGACGGGTGTCACTCCGA 1680
Db 524 TrpThrLeuGlnLysGlyPheProLeuIleThrIleThrValargGlyArgAsnValHis 543
QY 1681 CTGCAACAGGAGCGCTTCTCCAGGGGGTTTTCAGGAAGACCCCTGAAATCGAGGGCCCTG 1740
Db 544 MetLysGlnGluHisTyrMetLysGly-----SerAspGlyAlaPro 557
QY 1741 CAGGAGAGTACCTGTGGCATATCCCATTTGACCTACTCCAGAGTCTTCTAATGTGATC 1800
Db 558 AspThrGlyTyrLeuTrpHisValProLeuThrPheIleThrSerLysSerAspMetVal 577
QY 1801 CACAGACACATTCATAAATCAAGACAGATACTCTGGATCTCTACCTGAAAAGACCGATTGG 1860
Db 578 HisArgPheLeuLeuLysThrLysThrAspValLeuLeuLeuProGluGluValGluTrp 597
QY 1861 GTGAAATTTAATGTGGACTCAAATGGTTTACTACATCGTTTCACTATGAGGCTCATGGATGG 1920
:::|||||

Db 598 IleLysPheAsnValGlyMetAsnGlyTyrTyrIleValHisTyrGluAspAspGlyTrp 617
QY 1921 GACCAACTCATATACACAGCTGAATCAGAACCCACACACTTCTCAGACTTAAGGACAGATA 1980
Db 618 AspSerLeuThrGlyLeuLeuLysGlyThrHisThrAlaValSerSerAsnAspArgAla 637
QY 1981 GGTCTCATTCATGATGTGTTTTCAGCTAGTTGGTGCGAGGAGACTGACCCCTAGACAAAGCT 2040
Db 638 SerLeuIleAsnAsnAlaPheGlnLeuValSerIleGlyLysLeuSerIleGluLysAla 657
QY 2041 CTTGACATGACTTACTTACCTCCAAATGAAACAGCAGCCCGCCACTTCTCGAAGTCTG 2100
Db 658 LeuAspLeuSerLysLeuLysHisGluThrGluIleMetProValPheGlnGlyLeu 677
QY 2101 AGTTACTTCGGAATCGTTTACCACATGATGGACAGAGGAATATTTTCAGATATCTCTGAA 2160
Db 678 AsnGluLeuIleProMetTyrLysLeuMetGluLysArgAspMetAsnGluValGluThr 697
QY 2161 AACCTCAAGCGTTTACCCTTCTTTCAGTATTTTAAACCCAGTATTGACAGGCAAGCTCGAGT 2220
Db 698 GlnPheLysAlaPheLeuIleArgLeuLeuAArgAspLeuIleAspLysGlnThrTrpThr 717
QY 2221 GACAAGGCTCAGTCTGGGACAGAGTCTCCGCTCGGCTCTCTGGAAGCTGGCTGTGAC 2280
Db 718 AspGluGlySerValSerGluArgMetLeuArgSerGlnLeuLeuLeuAlaCysVal 737
QY 2281 CTGAACCATGCTCTTGCATCCAGAAAGCTGCTGAATCTTCTCCAGTGGATGGAATCC 2340
Db 738 HisAsnTyrGlnProCysValGlnArgAlaGluGlyTyrPheArgLysTrpLysGluSer 757
QY 2341 AGTGGAAAAATTAATATACCAACAGATGTTTAAAGATTGTGTATTCTGTGGTGTCTCAG 2400
Db 758 AsnGlyAsnLeuSerLeuProValAspValThrLeuAlaValPheAlaValGlyAlaGln 777
QY 2401 ACAACAGCAGATGGAATTAACCTTTTAGAGCAATATGAATGCTCAATGTCAAGTCTGAA 2460
Db 778 SerThrGluGlyTrpAspPheLeuTyrSerLysTyrGlnPheSerLeuSerSerThrGlu 797
QY 2461 CAAAACAAATCTGTATGCTTTTGTCAACGAGCAAGCATCAGGAAAGTTTACTGAAGTTA 2520
Db 798 LysSerGlnIleGluPheAlaLeuCysArgThrGlnAsnLysGluLysLeuGlnTrpLeu 817
QY 2521 ATTGAATAGGAATGGAAGAAAGGTTTCAAGACACAGAACTTGGCAGCTCTCTTCAT 2580
Db 818 LeuAspGluSerPheLysGlyAspLysIleLysThrGlnGluPheProGlnIleLeuThr 837
QY 2581 GCGATTGCCAGAGCTCCAAAGGGCGAGCAACTAGCATGGGATTTGTAGAGAAATGCG 2640
Db 838 LeuIleGlyArgAsnProValGlyTyrProLeuAlaTrpGlnPheLeuArgLysAsnTrp 857
QY 2641 ACCCATCTTCTGAAAATTTGACTTTGGGCTCATATGACATAGGATGATCATCTCTGGC 2700
Db 858 AsnLysLeuValGlnLysPheGluLeuGlySerSerIleAlaHisMetValMetGly 877
QY 2701 ACAACAGCTCAGCTTTTCTCCAAGGATAAGTTGCAAGAGGTGAAACTATTTTGAATCT 2760
Db 878 ThrThrAsnGlnPheSerThrArgThrArgLeuGluGluValLysGlyPhePheSerSer 897
QY 2761 CTTGAGGCTCAGGATCAGATCTGGATATTTTCAAACTGTTCTGGAACGATAACCAA 2820
Db 898 LeuLysGluAsnGlySerGlnLeuArgCysValGlnGlnThrIleGluThrIleGluGlu 917
QY 2821 AATATAAATGCTGGAGAAAGAAATCTTCGAGCTCTGAGGACTTGGCTA 2868
Db 918 AsnIleGlyTrpMetAspLysAsnPheAspLysIleArgValTrpLeu 933
RESULT 12
ABB90347
ID ABB90347 standard; protein; 941 AA.
XX ABB90347;
AC ABB90347;
DT 24-MAY-2002 (first entry)

QY	1327	CCGACTCAAATACAGGAAATGTTTGATGAAGATTTCTTATAACAAGGAGGACTTGTGATTTTG	1386
Db	426	ProAlaGlnIleArgGluMetPheAspAspValSerTyrAspIysGlyAlaCysIleLeu	445
QY	1387	AATATGCTCAAGGATTTTCTGGGTGAGGAGANAATTCAGAAAGGAATAATTCAGTACTTA	1446
Db	446	AsnMetLeuArgGluTyrLeuSerAlaAspAlaPheIysSerGlyIleValGlnTyrLeu	465
QY	1447	AAGAAGTTACGATACAGAAATGCTAAGAAATGATGACTTGTGGAGCACTGTCACAAATAGT	1506
Db	466	GlnIysHisSerTyrIlysAsnThrLysAsnGlnAspLeuItrPheSerMetAlaSerIle	485
QY	1507	TGTTTGAAGAAGTGATTTTACATCTGGT-----GGAGTTTGTCTTCGGATCCCAAGATG	1560
Db	486	Cys--ProThrAspGlyValLysGlyMetAspGlyPheCys---SerArgSerGlnHis	503
QY	1561	ACAAGTAAACATCTCGCGCTTCTGGGGGAAAAATGCACAGAGTCAAAGAGATGATGACTACA	1620
Db	504	SerSerSerSerHisTrpHisGlnGluGlyValAspValLysThrMetMetAsnThr	523
QY	1621	TGACTCTCCAGAAAGAAATCCCTCTCGTGTGTTAAACAAGACGGGTCTTCACCTCCGA	1680
Db	524	TrpThrLeuGlnArgGlyPheProLeuIleThrIleThrValArgGlyArgAsnValHis	543
QY	1681	CTGCAACAGGAGCGCTTCTCCACGGGGGTTTTCCAGGAAGACCTCAATCGAGGGCGCTG	1740
Db	544	MetLysGlnGluHisTyrMetLysGly-----SerAspGlyAlaPro	557
QY	1741	CAGGAGAGGTACTGTGCGCATATCCCATGTACCTACTCCACGAGTCTTCTTAAATGTGATC	1800
Db	558	AspThrGlyTyrLeuTrpHisValProLeuThrPheIleThrSerLysSerAspMetVal	577
QY	1801	CACAGACACATTTCTAAATCAAGACAGATACTCTGGATCTACTCTGAAAGACCACTTGG	1860
Db	578	HisArgPheLeuLeuLysThrLysThrAspValLeuLeuLeuProGluGluValGluItrp	597
QY	1861	GTCAAAATTTAATGTGGACTCAAAATGGTATTACATCGTTCACACTATGAGGTCTGATGG	1920
Db	598	IleLysPheAsnValGlyMetAsnGlyTyrTyrIleValHisTyrGluAspAspGlyTyrp	617
QY	1921	GACCAACTCATTACACAGCTGAATCAGAACACACACACTTCTCAGACTTAAGGACAGATG	1980
Db	618	AspSerLeuThrGlyLeuLeuLysGlyThrHisThrAlaValSerSerAsnAspArgAla	637
QY	1981	GGTCTGATTCATGATGTGTTTCAGCTAGTTGGTCAGGGAGACTGACCCCTAGACAAAGCT	2040
Db	638	SerLeuIleAsnAsnAlaPheGlnLeuValSerIleGlyLysLeuSerIleGluLysAla	657
QY	2041	CTTGACATGACTTACTACCTCCAACATGAACAAGCAGCCCGCACCTTCTCGAAGGCTCG	2100
Db	658	LeuAspLeuSerLeuTyrLeuLysHisGluThrGluIleMetProValPheGlnGlyLeu	677
QY	2101	AGTTACTTGAATCGTTTATACCATGATGGACAGAGGAATATTTCCAGATATCTCTGAA	2160
Db	678	AsnGluLeuIleProMetTyrLysLeuMetGluLysArgAspMetAsnGluValGluThr	697
QY	2161	AACCTCAAGGTTACCTTCTTCAGTATTTAAGCCAGTGATTCACAGGCAAACTGGAGT	2220
Db	698	GlnPheLysAlaPheLeuIleArgLeuLeuArgAspLeuIleAspLysGlnThrTrpThr	717
QY	2221	GACAAGGGCTCAGTCTGGGACAGATCTCCGCTCGGCTCTTCTGAAGCTGGCCTGTGAC	2280
Db	718	AspGluGlySerValSerGluArgMetLeuArgSerGluLeuLeuLeuLeuAlaCysVal	737
QY	2281	CTGAACCATGCTCCTTCATCCACAAAGCTGCTGAACCTTCTCCAGTCGGATCGAATCC	2340
Db	738	HisAsnTyrGlnProCysValGlnArgAlaGluGlyTyrPheArgLysTrpLysGluSer	757
QY	2341	AGTGGAAAAATTAATATACCAACAGATGTTTTAAAGATTCTGTATTCTGTGGGTCTCAG	2400
Db	758	AsnGlyAsnLeuSerLeuProValAspValThrLeuAlaValPheAlaValGlyAlaGln	777

Qy	2401	ACAACAGCAGGATGGAATTAACCTTTTAGACGATATAGAACTGTCAATGTCAAGTGCTGAA	2460
Db	778	SerThrGluGlyTrpAspPheLeuSerLysTyrglnPheSerLeuSerSerThrGlu	797
Qy	2461	CAAAACAAAATCTGTATGCTTTGTCAACAGCAAGCATCAGAGAAAGTTACTGAAGTTA	2520
Db	798	LysSerGlnIleGluPheAlaLeuCysArgThrGlnAsnLysGluLysLeuGlnTrpLeu	817
Qy	2521	ATTGAACTAGGAATGGAAGGAAAAGGTTATCAAGACACAGAACTTGGCAGCTCTCCTTCAT	2580
Db	818	LeuAspGluSerPheLysGlyAspLysIleLysThrGlnGluPheProGlnIleLeuThr	837
Qy	2581	CGGATTCACAGACGTCCTCAAGGGGCGACAACTAGCATGGGATTTGTAAAGAGAAAATTGG	2640
Db	838	LeuIleGlyArgAsnProValGlyTyrProLeuAlaTrpGlnPheLeuAlaGlyAsnTrp	857
Qy	2641	ACCATCTCTGAAAATAATTTGACTTGGGCTCATATGACATAGGATGATCATCTCTGGC	2700
Db	858	AsnLysLeuValGlnLysPheGluLeuGlySerSerSerIleAlaHisMetValMetGly	877
Qy	2701	ACAACAGCTCACATTTCTTCCAAGGATAAGTCCAAAGAGGTGAAACTATTTTTTGAATCT	2760
Db	878	ThrThrAsnGlnPheSerThrArgThrArgLeuGluGluValLysGlyPhePheSerSer	897
Qy	2761	CTTGAGGCTCAAGGATCACATCTGGATATTTTCAAACATGTTCTCGAAACGATAACCAA	2820
Db	898	LeuLysGluAsnGlySerGlnLeuArgCysValGlnGlnThrIleGluThrIleGluGlu	917
Qy	2821	AATATAAATGGCTGGAGAGAACTCTCCGACTCTGAGGACTTGGCTA	2868
Db	918	AsnIleGlyTrpMetAspLysAsnPheAspLysIleArgValTrpLeu	933
RESULT	13		
ADAS6820			
ID	ADAS6820	standard; protein; 941 AA.	
XX	ADA56820;		
XX	AC		
XX	AC		
DT	20-NOV-2003	(first entry)	
XX			
DE	Human secreted protein #103.		
XX			
Kw	immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;		
Kw	cytostatic; cerebroprotective; neuroprotective; nootropic;		
Kw	cardiovascular; antiarteriosclerotic; gene therapy;		
Kw	human secreted protein; immune disorder; inflammation;		
Kw	respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;		
Kw	inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;		
Kw	multiple sclerosis; ischemic brain injury; Parkinson's disease;		
Kw	Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;		
XX	triple helix formation; antisense gene therapy; forensic biology.		
OS	Homo sapiens.		
XX			
FN	WO2002102994-A2.		
XX			
PD	27-DEC-2002.		
XX			
PF	19-MAR-2002; 2002WO-US008278.		
XX			
XX	21-MAR-2001; 2001US-0277340P.		
PR	19-JUL-2001; 2001US-0306171P.		
PR	13-NOV-2001; 2001US-0331287P.		
XX			
FA	(HUMA-) HUMAN GENOME SCI INC.		
XX			
PI	Rosen CA, Ruben SM;		
XX			
DR	WPI; 2003-167512/16.		
DR	N-PSDB; ADA55924.		
XX			
PT	New human secreted polypeptides and polynucleotides, useful for		
PT	diagnosing, treating or preventing e.g. immune disorders, inflammatory		


```
Db      778 SerThrGluGlyTrpAspPheLeuTyrSerLysTyrGlnPheSerLeuSerSerThrGlu 797
Qy      2461 CAAACAAAAATCTGTATGCTTGTCAACGAGCAAGCATCAGGAAAAGTTACTGAAGTTA 2520
      ::::||||| ::::||||| ::::||||| ::::||||| ::::|||||
Db      798 LysSerGlnIleGluPheAlaLeuCysArgThrGlnAsnLysGluLysLeuGlnTrpLeu 817
      ::::||||| ::::||||| ::::||||| ::::||||| ::::|||||
Qy      2521 ATTGAAC TAGAATGGAAGAAAGGTTATCAAGACACAGAACTTGGCAGCTCTCCTTCAT 2580
      ::::||||| ::::||||| ::::||||| ::::||||| ::::|||||
Db      818 LeuAspGluSerPheLysGlyAspLysIleLysThrGlnGluPheProGlnIleLeuThr 837
      ::::||||| ::::||||| ::::||||| ::::||||| ::::|||||
Qy      2581 GCGATTGCCAGACGTCCAAAGGGCAGCAACTAGCATGGGATTTGTAAAGAGAAATGG 2640
      ::::||||| ::::||||| ::::||||| ::::||||| ::::|||||
Db      838 LeuIleGlyArgAsnProValGlyTyrProLeuAlaTrpGlnPheLeuArgLysAsnTrp 857
      ::::||||| ::::||||| ::::||||| ::::||||| ::::|||||
Qy      2641 ACCCATCTTCTGAAAAAATTGACTTGGGCTCATATGACATAAGGATGATCATCTCTGGC 2700
      ::::||||| ::::||||| ::::||||| ::::||||| ::::|||||
Db      858 AsnLysLeuValGlnLysPheGluLeuGlySerSerSerIleAlaHisMetValMetGly 877
      ::::||||| ::::||||| ::::||||| ::::||||| ::::|||||
Qy      2701 ACAACAGCTCACTTTTCTTCCAGGATAAGTTGCAAGGTGAAACTATTTTGTGAATCT 2760
      ::::||||| ::::||||| ::::||||| ::::||||| ::::|||||
Db      878 ThrThrAsnGlnPheSerThrArgThrArgLeuGluGluValLysGlyPhePheSerSer 897
      ::::||||| ::::||||| ::::||||| ::::||||| ::::|||||
Qy      2761 CTTGAGGCTCAAGGATCACATCTGGATATTTTCAAACTGTTCTGGAAACGATAACCAA 2820
      ::::||||| ::::||||| ::::||||| ::::||||| ::::|||||
Db      898 LeuLysGluAsnGlySerGlnLeuArgCysValGlnGlnThrIleGluThrIleGluGlu 917
      ::::||||| ::::||||| ::::||||| ::::||||| ::::|||||
Qy      2821 AATATAAAATGGCTGGAGAGAAGATCTTCCGACTCTGAGGACTTGGCTA 2868
      ::::||||| ::::||||| ::::||||| ::::||||| ::::|||||
Db      918 AsnIleGlyTrpMetAspLysAsnPheAspLysIleArgValTrpLeu 933
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Search completed: September 26, 2005, 07:11:45
Job time : 443.781 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model
Run on: September 26, 2005, 06:43:03 ; Search time 369.314 Seconds
(without alignments)
6354.782 Million cell updates/sec

Title: US-10-039-073-3
Perfect score: 5062
Sequence: 1 atgttcattcttctgcaat.....ggctaagtgttaactactaa 2883

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1826554 seqs, 407025358 residues
Total number of hits satisfying chosen parameters: 3653108

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool_p/US10039073/runat_26092005_070411_21348/app_query.fasta_1.6606
-DB=PublishedApplications_AA -QMTS=fatcat -SUFFIX=rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptco -NORM=ext -HEAPSZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10039073@cgn 1.1 921 @runat_26092005_070411_21348
-NCPU=6 -ICPU=3 -NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA:
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3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PTCUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5052	99.8	960	13	US-10-039-073-1 Sequence 1, Appli
2	5052	99.8	960	14	US-10-168-425-6 Sequence 6, Appli
3	4141	81.8	785	15	US-10-363-616-459 Sequence 459, App
4	3799	75.0	728	9	US-09-764-853-646 Sequence 646, App
5	3770	74.5	722	9	US-09-764-853-819 Sequence 819, App
6	2516.5	49.7	941	15	US-10-220-443-2 Sequence 2, Appli
7	2515.5	49.7	941	15	US-10-364-237-2723 Sequence 2723, Ap
8	2515.5	49.7	941	18	US-10-472-533-329 Sequence 329, App
9	2515.5	49.7	944	14	US-10-106-698-6381 Sequence 6381, Ap
10	2512.5	49.6	941	9	US-09-989-722-353 Sequence 353, App
11	2512.5	49.6	941	9	US-09-989-723-353 Sequence 353, App
12	2512.5	49.6	941	9	US-09-989-279-353 Sequence 353, App
13	2512.5	49.6	941	9	US-09-989-727-353 Sequence 353, App
14	2512.5	49.6	941	9	US-09-989-731-353 Sequence 353, App
15	2512.5	49.6	941	9	US-09-989-732-353 Sequence 353, App
16	2512.5	49.6	941	9	US-09-991-073-353 Sequence 353, App
17	2512.5	49.6	941	9	US-09-990-442-353 Sequence 353, App
18	2512.5	49.6	941	9	US-09-991-163-353 Sequence 353, App
19	2512.5	49.6	941	9	US-09-993-604-353 Sequence 353, App
20	2512.5	49.6	941	9	US-09-990-456-353 Sequence 353, App
21	2512.5	49.6	941	9	US-09-989-721-353 Sequence 353, App
22	2512.5	49.6	941	9	US-09-992-598-353 Sequence 353, App
23	2512.5	49.6	941	9	US-09-989-293A-353 Sequence 353, App
24	2512.5	49.6	941	9	US-09-989-735-353 Sequence 353, App
25	2512.5	49.6	941	9	US-09-990-444-353 Sequence 353, App
26	2512.5	49.6	941	9	US-09-991-181-353 Sequence 353, App
27	2512.5	49.6	941	9	US-09-989-730-353 Sequence 353, App
28	2512.5	49.6	941	9	US-09-990-436-353 Sequence 353, App
29	2512.5	49.6	941	9	US-09-993-687-353 Sequence 353, App
30	2512.5	49.6	941	10	US-09-989-734-353 Sequence 353, App
31	2512.5	49.6	941	10	US-09-997-653-353 Sequence 353, App
32	2512.5	49.6	941	10	US-09-989-724-353 Sequence 353, App
33	2512.5	49.6	941	10	US-09-989-728-353 Sequence 353, App
34	2512.5	49.6	941	10	US-09-990-441-353 Sequence 353, App
35	2512.5	49.6	941	10	US-09-993-667-353 Sequence 353, App
36	2512.5	49.6	941	10	US-09-997-428-353 Sequence 353, App
37	2512.5	49.6	941	10	US-09-997-666-353 Sequence 353, App
38	2512.5	49.6	941	10	US-09-990-438-353 Sequence 353, App
39	2512.5	49.6	941	10	US-09-990-562-353 Sequence 353, App
40	2512.5	49.6	941	10	US-09-990-711-353 Sequence 353, App
41	2512.5	49.6	941	10	US-09-989-726-353 Sequence 353, App
42	2512.5	49.6	941	10	US-09-998-156-353 Sequence 353, App
43	2512.5	49.6	941	10	US-09-990-437-353 Sequence 353, App
44	2512.5	49.6	941	10	US-09-991-157-353 Sequence 353, App
45	2512.5	49.6	941	10	US-09-997-514-353 Sequence 353, App

ALIGNMENTS

RESULT 1
US-10-039-073-1
; Sequence 1, Application US/10039073
; Publication No. US20020098177A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: 17867, A No. US20020098177A1e1 Human Amino-peptidase
; FILE REFERENCE: 35800/240749(5800-36
; CURRENT APPLICATION NUMBER: US/10/039.073
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 09/345,650
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 960
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-073-1

Alignment Scores:

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Score: 5052.00 Matches: 960
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.80% Indels: 0
DB: 13 Gaps: 0

US-10-039-073-3 (1-2883) x US-10-039-073-1 (1-960)

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DB 21 GlyPheTyrCysLeuThrAlaIleLeuProGlnIleCysIleCysSerGlnPheSerVal 40
QY 121 CCATCTAGTTATCACTTCAGTCAGGATCCTGGGGCTTTCCAGTAGCCACTTAATGGGGAA 180
DB 41 ProSerSerTyrHisPheThrGluAspProGlyAlaPheProValAlaThrAsnGlyGlu 60
QY 181 CGATTTCTTGCGCAGGAGCTAAAGCTCCCGCAGTGTGTCATTCTCTCCATTATGACCTC 240
DB 61 ArgPheProTrpGlnGluLeuArgLeuProSerValValIleProLeuHisTyrAspLeu 80
QY 241 TTTGTCCACCCCAATCTCACTCTCTGACCTTGTGCACTTGTGCACTGGAAGATCGAAGCTTG 300
DB 81 PheValHisProAsnLeuThrSerLeuAspPheValAlaSerGluLysIleGluValLeu 100
QY 301 GTCAGCAATGCTACCCAGTTTATCATCTTGACAGCAAGATCTTGAAATCACGAATGCC 360
DB 101 ValSerAsnAlaThrGlnPheIleIleLeuHisSerLysAspLeuGluIleThrAsnAla 120
QY 361 ACCCTTCAGTCAGGAGAGATTCAAGATACATGAACCAAGCAAGAAAGAACTGAAAGTTTGT 420
DB 121 ThrLeuGlnSerGluGluAspSerArgTyrMetLysProGlyLysGluLeuLysValLeu 140
QY 421 AGTTACCTGCTCATGAACAAATTCGACTGCTGTTCCAGAGAACTTAGCCCTCACCTG 480
DB 141 SerTyrProAlaHisGluGlnIleAlaLeuLeuValProGluLysLeuThrProHisLeu 160
QY 481 AAATACTATGTGGCTATGGACTTCCAAAGCCAAAGTTAGTGTGATGGCTTTGAAGGTTTAT 540
DB 161 LysTyrTyrValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTyr 180
QY 541 AAAAGCACATACAGAACTCTTGGTGGTGAACCAAGAAATTCCTGCAGTAAACAGATTTTGAG 600
DB 181 LysSerThrTyrArgThrLeuGlyGlyGluThrArgIleLeuAlaValThrAspPheGlu 200
QY 601 CCAACCCAGGCAGCATGGCTTTCCCTTCTGTTGATGAACGGTTGTTCAAAGCCAACTTT 660
DB 201 ProThrGlnAlaArgMetAlaPheProCysPheAspGluProLeuPheLysAlaAsnPhe 220
QY 661 TCAATCAAGATACCAAGAGAGAGCAGCATATTCCTACTATCCACATGCCAAAGGTTAAG 720
DB 221 SerIleLysIleArgArgGluSerArgHisIleAlaLeuSerAsnMetProLysValLys 240
QY 721 ACAATTGAATCTGAAGGAGGTCTTTTGGAAAGATCACCTTTGAAACTACTGTAAAAATGAGT 780
DB 241 ThrIleGluLeuGluGlyGlyLeuLeuGluAspHisPheGluThrThrValLysMetSer 260
QY 781 ACATACCTGTAGCCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACCTTCATCA 840
DB 261 ThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThrSerSer 280
QY 841 GGGGTCAAGGTGTCATCTATGATCCCGCAGACAAACGGAAATCAACACATTAATGCTTTG 900
DB 281 GlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyrAlaLeu 300
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DB 321 SerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsnTrpGly 340
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DB 361 LysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeu 380
QY 1141 GTCACAATGGAATGGGAAATGATATTTGGCTTAAAGAGGGTTTCCAAATACATGGAA 1200
DB 381 ValThrMetGlnTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyrMetGlu 400
QY 1201 CTTATCGCTGTTAATGCTACATATCCAGAGCTCAATTTTGATGACTATTTTGAATGTG 1260
DB 401 LeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeuAsnVal 420
QY 1261 TGTTTTGAAGTAATTAACAAAGATTCATTGAATTCATCCCGCCTATCTCCAAACACGCG 1320
DB 421 CysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLysProAla 440
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DB 461 IleLeuAsnMetLeuLysaspPheLeuGlyGluGluLysPheGlnLysGlyIleLeuGln 480
QY 1441 TACTTAAAGAAAGTTACGCTATAGAAATGCTAAGAATGCTAAGATGATGCTGGAGCAGTCTGCA 1500
DB 481 TyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspAspLeuTrpSerSerLeuSer 500
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QY 1561 ACAAGTAAACATGCTCCGCTTTCTGGGGGAAAAATGCAGAGCTCAAAGAGATGATGACTACA 1620
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QY 1681 CTGCAACAGGAGCGCTTCCTCCAGGGGGTTTCCAGGNAGACCTCGAATGGAGGGCCCTG 1740
DB 561 LeuGlnGlnGluArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArgAlaLeu 580
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DB 601 HisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThrSerTrp 620
QY 1861 GTGAAATTAATGTGACTCAATGGTTACTACATGTTCACTATCAGGGTCTGATGGTGG 1920
DB 621 ValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHisGlyTrp 640
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DB 641 AspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAspArgVal 660
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Db AspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAlaCysAsp 760
QY 2281 CTGAACCATGCTCCTTGGATCAGAAAGCTGCTGAACCTCTTCCAGTGGATGAATCC 2340
Db LeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMetGluSer 780
QY 2341 AGTGGAAATTAATATATACCAACAGATGCTTTTAAAGATTGTATTTCTGTGGTGCTCAG 2400
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QY 2401 ACAACAGCAGGATGGAATTTACTCTTTTAGCAATATGAACCTGTCNAATGTCAGTGTCAA 2460
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QY 2461 CAACACAAATTCGTATGCTTGTGACAGCAGCAGCATCGAAAGATTTACTGAAGTTA 2520
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QY 2581 GCGATTGCCAGCTGCCAAAGGGGAGCAACTAGCATGGATTTTGTGAAGAGAAATGG 2640
Db AlaIleAlaArgArgProLysGlyGlnGlnLeuAlaTrpAspPheValArgGluAsnTrp 880
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QY 2701 ACAACAGCTCACTTTTCTTCCAAGGATAAGTTGCAAGAGTGCAAACTATTTTGAATCT 2760
Db ThrThrAlaHisPheSerSerLysAspLysLeuGlnGluValLysLeuPhePheGluSer 920
QY 2761 CTTGAGGCTCAAGGATCATCTCGATATTTTCAAACTGTTCTGGAAACGATAACCAA 2820
Db LeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIleThrLys 940
QY 2821 AATATAAATGGCTGGAGAGNACTTCCGACTCTGAGGACTCTGCTAATGGTTAATACT 2880
Db AsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeuMetValAsnThr 960

RESULT 2

US-10-168-425-6
; Sequence 6, Application US/10168425
; Publication No. US20030124706A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YANG, Junming
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: BURFORD, Neil
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LU, Dyoung Aina M.
; APPLICANT: REDDY, Roopa
; APPLICANT: YUE, Henry
; APPLICANT: NGUYEN, Dannie B.
; APPLICANT: TANG, Y. Tom
; APPLICANT: YAO, Monique G.

; APPLICANT: LAL, Presti
; TITLE OF INVENTION: PROTEASES
; FILE REFERENCE: PI-0003 PCT
; CURRENT APPLICATION NUMBER: US/10/168,425
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/172,055; 60/177,334; 60/178,884; 60/179,903
; PRIOR FILING DATE: 1999-12-23; 2000-01-21; 2000-01-28; 2000-02-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PERL Program
; SEQ ID NO 6
; LENGTH: 960
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030124706A1 60116897CD1
US-10-168-425-6

Alignment Scores:
Pred. No.: 0 Length: 960
Score: 5052.00 Matches: 960
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.80% Indels: 0
DB: 14 Gaps: 0

US-10-039-073-3 (1-2883) x US-10-168-425-6 (1-960)

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Db 1 MetPheHisSerSerAlaMetValAsnSerHisArgLysProMetPheAsnIleHisArg 20
QY 61 GGATTTTACTGCTTAAACAGCCATCTTCCCAAATATGCAATTTGTTCTCAGTTCTCAGTG 120
Db 21 GlyPheTyrCysLeuThrAlaIleLeuProGlnIleCysIleCysSerGlnPheSerVal 40
QY 121 CCATCTAGTTATCATCTTCACTGAGGATCCTGGGCTTCCCAAGTAGCCACTAATGGGAA 180
Db 41 ProSerSerTyrHisPheThrGluAspProGlyAlaPheProValAlaThrAsnGlyGlu 60
QY 181 CGATTTCTTGGCAGGAGCTAAGGCTCCCACTGTGGTTCATTTCTCTCCATTATGACCTC 240
Db 61 ArgPheProTrpGlnGluLeuArgLeuProSerValValIleProLeuHisTyrAspLeu 80
QY 241 TTTGTCACCCCAATCTCACCTCTCTGACCTTTGTCATCTGAGAGATCGAAGTCTTG 300
Db 81 PheValHisProAsnLeuThrSerLeuAspPheValAlaSerGluLysIleGluValLeu 100
QY 301 GTCAGCAATGCTACCCAGTTTATCATCTTGCACAGCAAGATCTTGAATCAGCAATGCC 360
Db 101 ValSerAsnAlaThrGlnPheIleIleLeuHisSerLysAspLeuGluIleThrAsnAla 120
QY 361 ACCCTTCAGTCAGAGGAAGATTCAAGATACATGAAACCAGGAAAGAACTGAAAGTTTG 420
Db 121 ThrLeuGlnSerGluLysAspSerArgTyrMetLysProGlyLysGluLeuLysValLeu 140
QY 421 AGTTACCTGCTCATGAACAAATTTGCACTGCTGTTCCAGAGAACTTACCGCTCACCTG 480
Db 141 SerTyrProAlaHisGluGlnIleAlaLeuLeuValProGluLysLeuThrProHisLeu 160
QY 481 AATATCTATGTGGCTATGGACTTCCAGCCCAAGTTAGTGTATGGCTTTGAAGGTTTAT 540
Db 161 LysTyrTyrValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTyr 180
QY 541 AAAAGACATACAGAACTCTTGGTGGTGAACAAGAAATTTCTGCAAGTAAACAGATTTTGAG 600
Db 181 LysSerThrTyrArgThrLeuGlyGlyGluThrArgIleLeuAlaValThrAspPheGlu 200
QY 601 CCAACCCAGGACGATGGCTTTCCCTTGTGTTGATGAACCGTGTGTTCAAGGCCAACCTTT 660
Db 201 ProThrGlnAlaArgMetAlaPheProCysPheAspGluProLeuPheLysAlaAsnPhe 220
QY 661 TCATCATGATACGAAGAGAGAGCAGGCATATTCACACTATTCACACATGCCAAAGGTTAAG 720

Db 221 SerIleLysIleArgArgGluSerArgHisIleAlaLeuSerAsnMetProLysValLys 240
QY 721 ACAATTGAACCTGAGAGGCTCTTTGGAAGATCACCTTTGAAACTACTGTAAAAATGAGT 780
Db 241 ThrIleGluLeuGluGlyIleLeuLeuGluAspHisPheGluThrThrValLysMetSer 260
QY 781 ACATACCTTGTAGGCTACATAGTTTGTGATTTCACACTCTCTGAGTGGCTTCACATTCA 840
Db 261 ThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThrSerSer 280
QY 841 GGGGTCAAGGTGTCATCTATGCAATCCCGACAGAACCGAATCAAAACACATATTGCTTTG 900
Db 281 GlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyrAlaLeu 300
QY 901 CAGGCATCACTGAAGCTACTTGATTTTATGAAAGTACTTTGATATCTACTATCCACTC 960
Db 301 GlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyrProLeu 320
QY 961 TCCAAACTGGATTAAATTGCTATTCTGACTTTGCACTCGAGCCATGGAAAATTGGGGC 1020
Db 321 SerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsnTrpGly 340
QY 1021 CTCAATTACATATAGGAGAGCTCACTGCTTTTGAACCCCAAGACCTCTTCTGCTCCGAT 1080
Db 341 LeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAlaSerAsp 360
QY 1081 AACTGTGGGTCAACAGACTAGCCATGCACTGGCGCACCGATGGTTTGGCAACCTG 1140
Db 361 LysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeu 380
QY 1141 GTCAAACTGGAATGCTGGAAATGATTGTGGCTTAAGGAGGGTTTGGCAAAATACATGGAA 1200
Db 381 ValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyrMetGlu 400
QY 1201 CTATACGCTGTTAATGCTACATATCCAGAGCTGCAATTTGATGACTATATTTTGAATGTG 1260
Db 401 LeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeuAsnVal 420
QY 1261 TGTTTGAAGTAAATACAAAGATTCATTAAGTAAATTCATCCCGCCTATCTCCAAACGAGC 1320
Db 421 CysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLysProAla 440
QY 1321 GAAACCCGCACTCAAAATACAGGAAATGTTTGATGAAGTTTCTTATAACAAGGAGCTTGT 1380
Db 441 GluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGlyAlaCys 460
QY 1381 ATTTTGAATATGCTCAAGGATTTTCTGGTGAGGAGAAATTCAGAAAGGAATAATTCAG 1440
Db 461 IleLeuAsnMetLeuLysAspPheLeuGlyGluGluLysPheGlnLysGlyIleIleGln 480
QY 1441 TACTTAAAGAGTTCAGCTATAGAAATGCTAAGATGATGACTGTGGAGCAGTCTGTCA 1500
Db 481 TyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspAspLeuTrpSerSerLeuSer 500
QY 1501 AATAGTTGTTTAGAAAGTGAATTTTACATCTGGTGGAGTTTGTCAATCCGATCCCAAGATG 1560
Db 501 AsnSerCysLeuGluSerAspPheThrSerGlyValCysHisSerAspProLysMet 520
QY 1561 ACAAGTAACTGCTCGCTTTCTGGGGGAAATATGCAGAGGTCAAAAGAGATGATGACTACA 1620
Db 521 ThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGluValLysGluMetMetThrThr 540
QY 1621 TGGACTCTCCAGAAAGAAATCCCTGCTGGTGTAAACAAGACGGGTCTTCACTCCGA 1680
Db 541 TrpThrLeuGlnLysGlyIleProLeuLeuValValLysGlnAspGlyCysSerLeuArg 560
QY 1681 CTGCAACAGGAGCGCTTCTCCAGGGGTTTTCAGGAAGACCCCTGAATGGAGGGCCCTG 1740
Db 561 LeuGlnGlnGluArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArgAlaLeu 580
QY 1741 CAGGAGAGTACCTGTGGCATATCCCATTTGACCTTACCTCCACGAGTCTTCTAATGTGATC 1800

Db 581 GlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerThrSerSerSerAsnValIle 600
QY 1801 CACAGACACATTTCTAAATCAAAAGACAGATACCTCTGATCTACTCTGAAAGACAGTTGG 1860
Db 601 HisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThrSerTrp 620
QY 1861 GTCAAAATTTAATGTGACTCAAAATGTTTACTACATCGTTCTACCTATGAGGGTCTAGTGG 1920
Db 621 ValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHisGlyTrp 640
QY 1921 GACCAACTCATTTACACAGCTGAATCAGAACCAACACACTTCTCAGACTTAAGACAGAGTA 1980
Db 641 AspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAspArgVal 660
QY 1981 GGTCTCATTCATGATGCTGTTTACGTAGTTGGTCAGGGAGACTGACCTTAGACAAAGCT 2040
Db 661 GlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAspLysAla 680
QY 2041 CTTGACATGACTTACTACCTCCAACATGAAACAAAGCAGCCCGCACTTCTCGAAGTCTG 2100
Db 681 LeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProAlaLeuLeuGluGlyLeu 700
QY 2101 AGTTACTTGGAAATCGTTTACACATGATGGACAGAGGAATATTTTCAGATATCTCGAA 2160
Db 701 SerTyrLeuGluSerPheTyrHisMetMetAspArgArgAsnIleSerAspIleSerGlu 720
QY 2161 AACCTCAAGCGTTTACCTCTTCAAGTATTTTAAGCCAGTATTGACAGGCAAGCTGAGT 2220
Db 721 AsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSerTrpSer 740
QY 2221 GACAAGGCTCAGTCTGGGACAGGATGCTCCGCTCGGCTCTCTTGAAGCTGGCTGTGAC 2280
Db 741 AspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysAlaCysAsp 760
QY 2281 CTGAACCATGCTCTTGGCATCCAGAAAGCTGCTGAACTCTTCTCCAGCTGGATGGAATCC 2340
Db 761 LeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMetGluSer 780
QY 2341 AGTGGAAATTTAAATATACCAACAGATGTTTAAAGATTGTGTATTCTGTGGGTGCTCAG 2400
Db 781 SerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrSerValGlyAlaGln 800
QY 2401 ACAACAGCAGGATGGAATTACCTTTTAGAGCAATATGAACTGTCATGTCAAGTCTCGTAA 2460
Db 801 ThrThrAlaGlyTrpAsnTyrLeuLeuGluGlnTyrGluLeuSerMetSerSerAlaGlu 820
QY 2461 CAAAACAAAATCTGTATGCTTTGTCAACGAGCAACATCAGGAAAGATTACTGAAGTTA 2520
Db 821 GlnAsnLysIleLeuTyrAlaLeuSerThrSerLysHisGlnGluLysLeuLeuLysLeu 840
QY 2521 ATTGAACTAGGAATGGAAGGAAAGTTTATCAACACACAGAACTTGGCAGCTCTCTTCAT 2580
Db 841 IleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaLeuLeuHis 860
QY 2581 GCGATTGCCAGACGTCCTCAAGGGCAGCAACTAGCATGGGATTTTGTAAAGAGAAAATTGG 2640
Db 861 AlaIleAlaArgArgProLysGlyGlnGlnLeuAlaTrpAspPheValArgGluAsnTrp 880
QY 2641 ACCCATCTTCTGAAAAAATTTGACTTGGGCTCATATGACATAGGATGATCATCTCTGGC 2700
Db 881 ThrHisLeuLeuLysLysPheAspLeuGlySerTyrAspIleArgMetIleIleSerGly 900
QY 2701 ACAACAGCTCACCTTTTCTTCCAAGGATAAGTTTCAAGAGGTGAAACTATTTTTTGAATCT 2760
Db 901 ThrThrAlaHisPheSerSerLysAspLysLeuGlnGluValLysLeuPhePheGluSer 920
QY 2761 CTTGAGGCTCAAGGATCACATCTGGGATATTTTCAAACCTGTTCTGAAACAGGATAACAAA 2820
Db 921 LeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIleThrLys 940
QY 2821 AATATAAATGGCTGAGAGAAATCTCCGACTCTGAGGACTTGGCTAATGGTTAATCT 2880
Db 941 AsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeuMetValAsnThr 960

RESULT 3

US-10-363-616-459
 ; Sequence 459, Application US/10363616
 ; Publication No. US20040044181A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
 ; FILE REFERENCE: 21272-113 (793)
 ; CURRENT APPLICATION NUMBER: US/10/363,616
 ; CURRENT FILING DATE: 2003-03-03
 ; PRIOR APPLICATION NUMBER: 09/654,935
 ; PRIOR FILING DATE: 2000-09-01
 ; NUMBER OF SEQ ID NOS: 490
 ; SEQ ID NO 459
 ; LENGTH: 785
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-363-616-459

Alignment Scores:

Pred. No.:	0	Length:	785
Score:	4141.00	Matches:	782
Percent Similarity:	99.74%	Conservatives:	0
Best Local Similarity:	99.74%	Mismatches:	2
Query Match:	81.81%	Indels:	0
DB:	15	Gaps:	0

US-10-039-073-3 (1-2883) x US-10-363-616-459 (1-785)

QY	1	ATGTTCCATCTCTGCAATGTTTAATTCACACAGAAACCAATGTTTAACATTCACAGA	60
DB	1	MetPheHisSerSerAlaMetValAsnSerHisArgLysProMetPheAsnIleHisArg	20
QY	61	GGATTTTACTGCTTAACAGCCATCTGCCCAATATGCATTTGCTTCAGTTCACGTG	120
DB	21	GlyPheTyrCysLeuThrAlaIleLeuProGlnIleCysIleCysSerGlnPheSerVal	40
QY	121	CCATCTAGTTATCACTTCACTCAGGATCCTGGGGCTTTCCAGTAGCCCAATATGGGAA	180
DB	41	ProSerSerTyrHisPheThrGluAspProGlyAlaPheProValAlaThrAsnGlyGlu	60
QY	181	CGATTTCTTGGCAGAGCTAAGGCTCCCGAGTGGTCATTCCTCTCCATATGACCTC	240
DB	61	ArgPheProTrpGlnGluLeuArgLeuProSerValValIleProLeuHisTyrAspLeu	80
QY	241	TTTGTCCACCCCAATCTCACCTCTGCACTTTGTCATCTGAGAAGATCGAAGCTCTG	300
DB	81	PheValHisProAsnLeuThrSerLeuAspPheValAlaSerGluLysIleGluValLeu	100
QY	301	GTCAGCAATGCTACCCAGTTTATCATCTTGACACAGAAAGATCTTGAATCACGAATGCC	360
DB	101	ValSerAsnAlaThrGlnPheIleIleLeuHisSerLysAspLeuGluIleThrAsnAla	120
QY	361	ACCCTTCAGTCAGAGAAGATCAAGATACATGAAACACAGGAAAGAACTGAAAGTTTG	420
DB	121	ThrLeuGlnSerGluGluAspSerArgTyrMetLysProGlyLysGluLeuLysValLeu	140
QY	421	AGTTACCTGCTCATGACAAATTCGACCTGGTTCAGAGAACTTACGCCTCACCTG	480
DB	141	SerTyrProAlaHisGluGlnIleAlaLeuLeuValProGluLysLeuThrProHisLeu	160
QY	481	AAATACTATGTGGCTATGACTTCCAAGCCAAGTTAGGTGATGGCTTTGAAGGGTTTAT	540
DB	161	LysTyrTyrValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTyr	180
QY	541	AAAAGCACATACAGAACTCTTGGTGTGAAACAAGAAATTCCTTCAGTAAACAGATTTGAG	600
DB	181	LysSerThrTyrArgThrLeuGlyGlyGluThrArgIleLeuAlaValThrAspPheGlu	200
QY	601	CCAACCCAGCAGCATGCTTCCCTTGTGATGACCGTCTTCAAGCCCACTTT	660
DB	201	ProThrGlnAlaArgMetAlaPheProCysPheAspGluProLeuPheLysAlaAsnPhe	220

QY	661	TCAATCAAGATACGAAGAGAGAGAGAGGAGATATTCACATATTCACATGCCAAAGGTTAAG	720
DB	221	SerIleLysIleArgArgGluSerArgHisIleAlaLeuSerAsnMetProLysValLys	240
QY	721	ACAATTCGAACCTTGAAGGAGGCTTTTGGAGAGTCACTTTGAAACTACTGTAAAATAGT	780
DB	241	ThrIleGluLeuGluGlyGlyLeuLeuGluAspHisPheGluThrValLysMetSer	260
QY	781	ACATACCTTGTAGCCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACCTATCA	840
DB	261	ThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThrSerSer	280
QY	841	GGGTCAAGGTGCTCATCTATGCATCCCGACAGAAACGGAATCAACACATATGCTTTG	900
DB	281	GlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyrAlaLeu	300
QY	901	CAGGCATCAGTGAAGTACTTGTATTTATGAAAGTACTTTGATATCTACTATCTCACTC	960
DB	301	GlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyrProLeu	320
QY	961	TCCAAACTGGAATTTAATTTGCTATTCTCCTGACTTTTCACCTGGAGCCATCGAAAATGGGC	1020
DB	321	SerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsnTrpGly	340
QY	1021	CTCATTAATATAGGAGAGCGTCACTGCTTTTTCACCCCAAGACCTCTTCTGCTTCCGAT	1080
DB	341	LeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAlaSerAsp	360
QY	1081	AACTGTGGTGCACAGAGTCATAGCCCATGAACTGGCGCACCATGCTGTTGGCAACCTG	1140
DB	361	LysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeu	380
QY	1141	GTCAAAATGGAATCGTGAATGATATTTGGCTTAAGGAGGCTTTTGCAAAATACATGAA	1200
DB	381	ValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyrMetGlu	400
QY	1201	CTTATCGCTGTTAATGTACATATCCAGAGCTGCAATTTGATGACTATTTTGAATGTG	1260
DB	401	LeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeuAsnVal	420
QY	1261	TGTTTTCGAAGTAATACAAAGATTCATGAAATTCATCCCGCCCTATCTCCAAACCCAGCG	1320
DB	421	CysPheGluValIleThrLysAspSerLeuAsnSerArgProIleSerLysProAla	440
QY	1321	GAACCCCGACTCAAAATACAGGAAATGTTTGAATGAAGTTTCTATAAACAAGGAGCTTGT	1380
DB	441	GluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGlyAlaCys	460
QY	1381	ATTTTGAATATGCTCAAGGATTTTCTGGGTGAGAGAAATTCAGAAAGGAATATATTGAG	1440
DB	461	IleLeuAsnMetLeuLysAspPheLeuGlyGluGluLysPheGlnLysGlyIleIleGln	480
QY	1441	TACTTAAAGAGTTTCAGCTATAGAAATCTAAGATGATGATGACTTCTGGAGCAGCTGTCA	1500
DB	481	TyrLeuLysLysPheSerTyrArgAsnAlaAsnAsnAspAspLeuTrpSerSerLeuSer	500
QY	1501	AATAGTTTGTAGAAAGTATTTTACATCTCGTGGAGTTTGTTCATTCGGATCCCAGATG	1560
DB	501	AsnSerCysLeuGluSerAspPheThrSerGlyValCysHisSerAspProLysMet	520
QY	1561	ACAAAGTAACTGCTCGCTTTCTCGGGGAAATGCAGAGGTCAAAGAGATGATGACTACA	1620
DB	521	ThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGluValLysGluMetMetThrThr	540
QY	1621	TGGACTCTCCAGAAAGAAATCCCTGCTGTGGTTAAACAAGCGGTGTTCTACTCGA	1680
DB	541	TrpThrLeuGlnLysGlyIleProLeuLeuValLysGlnAspGlyCysSerLeuArg	560
QY	1681	CTGCAACAGGAGCCCTCTCCAGGGGTTCCTCAGGAAGACCCCTGAATGAGGGCCCTG	1740
DB	561	LeuGlnGlnGluArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArgAlaLeu	580

QY 1741 CAGGAGAGTACCTGTGGCATATCCCATTTGACCTACCTCCAGAGTCTCTTCTTAATGTGATC 1800
Db |||||||GlnGluArgTyrLeuThrPheHisLeuProLeuThrTyrSerThrSerSerAsnValIle 600
QY 1801 CACAGACACATTCATAAATCAAGACAGATACCTCTGGATCTACCTGAAAGACCAAGTTGG 1860
Db |||||||HisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThrSerTrp 620
QY 1861 GTGAAATTTAATGTGGACTCAAATGGTTACTACATCGTTCACTATGAGGGTCTAGGATGG 1920
Db |||||||ValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHisGlyTrp 640
QY 1921 GACCACTCATTAACAGCTGAATCAGAACACACACTTCTCAGACCTTAAGACAGAGTA 1980
Db |||||||AspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAspArgVal 660
QY 1981 GGTCTGATTCTATGATGTGTTTCAGCTAGTTGGTCAGGAGACTGACCTAGACAAAGCT 2040
Db |||||||GlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAspLysAla 680
QY 2041 CTTGACATGACTTACTACCTCCAACTCAACATGAACAAGCAGCCCCGCACTTCTCGAAGGTCTG 2100
Db |||||||LeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProAlaLeuLeuGluGlyLeu 700
QY 2101 AGTTACTTGGAAATCGTTTTACCACATGATGACAGAGAAGGAATATTTTCAGATATCTCGAA 2160
Db |||||||SerTyrLeuGluSerPheTyrHisMetMetAspArgAsnIleSerAspIleSerGlu 720
QY 2161 AACCTCAAGCGTTACCTTCTCAGTATTTAAGCCAGTGTGACAGGCAAGCTGGAGT 2220
Db |||||||AsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSerTrpSer 740
QY 2221 GACAAGGCTCAGTCTGGGACAGGATGCTCGCTCGGCTCTCTTGAAGCTGGCTGTGAC 2280
Db |||||||AspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAlaCysAsp 760
QY 2281 CTGAACCATGCTCTTGATCCAGAAAGCTGCTGAATCTTCTCCAGTGGATGCCATCC 2340
Db |||||||LeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPhePheGlnTrpMetGluSer 780
QY 2341 AGTGGAAATTA 2352
Db |||||||SerGlyLysLeu 784

RESULT 4
US-09-764-853-646
; Sequence 646: Application US/09764853
; Patent No. US2002090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P0206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 646
; LENGTH: 728
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-853-646

Alignment Scores:
Pred. No.: 0 Length: 728
Score: 3799.00 Matches: 722
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 75.05% Indels: 0
DB: 9 Gaps: 0

US-10-039-073-3 (1-2883) x US-09-764-853-646 (1-728)

QY 715 GTTAAAGCAATTTGAAGAGGCTCTTTTGGAAAGATCACATTTGAAACACTACTGTAAAA 774
Db |||||||ValLysThrIleGluLeuGluGlyGlyLeuLeuGluAspHisPheGluThrThrValLys 26
QY 775 ATGAGTACATACCTTTAGCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACT 834
Db |||||||MetSerThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThr 46
QY 835 TCATCAGGGGTCAAGGTGTCCATCTATGCATCCCCAGACAAACCGAATCAACACACATTAT 894
Db |||||||SerSerGlyValLysValSerIleTyrAlaSerProAspLysArgGlnThrHisTyr 66
QY 895 GCTTTCCAGGCATCCTCAGAGCTACTTGATTTTTATGAAAAGTACTTTGATATCTACTAT 954
Db |||||||AlaLeuGlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyr 86
QY 955 CCNCTCTCCAACTGATTTAATTGCTATTTCTGACTTTTGCACCTGGAGCCATGGAAAT 1014
Db |||||||ProLeuSerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsn 106
QY 1015 TGGGGCTCATTTACATATAGGGAGAGCTCAGTCTCTTTTGGACCCCAAGACCTCTCTGCT 1074
Db |||||||TrpGlyLeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAla 126
QY 1075 TCCGATAAACTGTGGTCCACAGAGTCATAGCCCATGAATGGCGCCACAGTGGTTGGC 1134
Db |||||||SerAspLysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGly 146
QY 1135 AACCTGGTCACATGAAGTGGATGATATTTGGCTTTAAGGAGGTTTTCAGAAATAC 1194
Db |||||||AsnLeuValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyr 166
QY 1195 ATGGAATTTATCGCTGTTAATGCTACATATCCAGAGCTGCAATTTTGATGACTATTTTGTG 1254
Db |||||||MetGluLeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspLysTyrPheLeu 186
QY 1255 AATGTGTGTTTGAAGTAATTCAAAAAGATTCATTAATTCATCCCGCCCTATCTCCAAA 1314
Db |||||||AsnValCysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLys 206
QY 1315 CCAGCGGAACCCGACTCAATACAGGAAATGTTTGTAGTGAAGTTTCTCATACAGGGA 1374
Db |||||||ProAlaGluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGly 226
QY 1375 GCTTGTATTTTGAATATGCTCAAGGATTTTCTGGGTGAGGAGAAATTCAGAAAGGAATA 1434
Db |||||||AlaCysIleLeuAsnMetLeuLysAspPheLeuGlyGluGluLysPheGlnLysGlyIle 246
QY 1435 ATTCACTACTTAAAGAAAGTTTCAGCTATAGAAATGCTAAGATGATGACTTTGTGGAGAGT 1494
Db |||||||IleGlnTyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspLeuTrpSerSer 266
QY 1495 CTGTCAATAGTTGTTAGAAAGTATTTTACATCTGTGGAGTTTGTTCATTCGGATCCC 1554
Db |||||||LeuSerAsnSerCysLeuGluSerPheThrSerGlyValCysHisSerAspPro 286
QY 1555 AAGATGACAAGTAAACATGCTCGCTTCTCGGGGAAAAATTCAGAGTCAAAAGAGATGATG 1614
Db |||||||LysMetThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGluValLysGluMetMet 306
QY 1615 ACTACATGACTCTCCAGAAAGAAATCCCCCTGCTGGTGGTTAAACAAGACGGGTGTTC 1674
Db |||||||ThrThrTrpThrLeuGlnLysGlyIleProLeuLeuValLysGlnAspGlyCysSer 326
QY 1675 CTCGAGTCCAAAGAGGAGGCTTCTCCAGGGGGTTTTCCAGGAAGACCTGATCGAGG 1734
Db |||||||LeuArgLeuGlnGlnGluArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArg 346
QY 1735 GCCTCCAGGAGAGGTACCTGTGGCATATCCCATTCACCTACTCCACGAGTCTTCTTAAT 1794
Db |||||||AlaLeuGlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerThrSerSerAsn 366
QY 1795 GTGATCCACAGACACATTTCAAATCAAAAGACAGATACCTCTGGATCTCTGAAAAGACC 1854

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Db 367 ValIleHisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThr 386
QY 1855 AGTTGGGTGAATTTAAATGTGGACTCAAAATGGTTACTACATCGTTCACTATGAGGGTCAT 1914
Db 387 SerTrpValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHis 406
QY 1915 GGATGGGACCAACTATTACACAGCTGAATCAGAACCCACACACTCTCAGACCTAAGAC 1974
Db 407 GlyTrpAspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAsp 426
QY 1975 ACAGTAGGTCTGATTCATGATCTGTTTCAGCTAGTTGGTGCAGGAGACTGACCCCTAGAC 2034
Db 427 ArgValGlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAsp 446
QY 2035 AAAGCTCTTGACATGACTTACTCTCCAACTGAACAAAGCAGCCCGCACTTCTCGAA 2094
Db 447 LysAlaLeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProAlaLeuLeuGlu 466
QY 2095 GGTCTGAGTTACTTGGATCGTTTTACCATGATGGACAGAAAGAAATATTCAGATATC 2154
Db 467 GlyLeuSerTyrLeuGluSerPheTyrHisMetMetAspArgAsnIleSerAspIle 486
QY 2155 TCTGAAACCTCAAGCGTTACCTCTTCCAGTATTTTAAGCCAGTATTCAGACGCAAGC 2214
Db 487 SerGluAsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSer 506
QY 2215 TGGAGTCAACAGGGCTCAGTCTGGACAGGATGCTCCGCTCGCTCTCTTGAAGCTGGCC 2274
Db 507 TrpSerAspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAla 526
QY 2275 TGAGCTGAACCATGCTCTTTCATCCAGAAAGCTGCTGAACCTCTTCCAGTGGATG 2334
Db 527 CysAspLeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMet 546
QY 2335 GAATCCAGTGGAAATTAATATATACCAACAGATGTTTAAAGATTTGTGTATCTGTGGT 2394
Db 547 GluSerSerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrSerValGly 566
QY 2395 GCTCAGACAAACAGCAGGATGGAATTTACCTTTTAGAGCAATATGAACCTGTCAATGTCAAGT 2454
Db 567 AlaGlnThrThrAlaGlyTrpAsnTyrLeuLeuGluGlnTyrGluLeuSerMetSerSer 586
QY 2455 GCTGAACAAACAAATCTGTATGCTTTGTCAACGAGCAAGCATCAGGAAAAGTTACTG 2514
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QY 2515 AAGTTAATGACTAGGATGAAGAAAGTTATCAAGACACACAACTTGGCAGCTCTC 2574
Db 607 LysLeuIleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaAlaLeu 626
QY 2575 CTTTCATGCGATTGCCAGACGTCCTCAAGGGGAGCAACTAGCATGGGATTTTGTAAAGAA 2634
Db 627 LeuHisAlaIleAlaArgArgProLysGlyGlnGlnLeuAlaIleTrpAspPheValArgGlu 646
QY 2635 AATGGACCCCATCTTCTGAAAATAATTTGACTTGGGCTCATATGACATGAAGGATGATCATC 2694
Db 647 AsnTrpThrHisLeuLeuLysLysPheAspLeuGlySerTyrAspIleArgMetIleIle 666
QY 2695 TCTGCCACACAGCTCATCTTTCTTCCAAAGGATAAGTTGCAAGAGGTGAACACTATTTTTT 2754
Db 667 SerGlyThrThrAlaHisPheSerSerLysAspLysLeuGlnGlnValLysLeuPhePhe 686
QY 2755 GAATCTCTTGAGGCTCAAGGATCACATCTGGATATTTTCAACCTGTTCTCGAAGCAGATA 2814
Db 687 GluSerLeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGlnThrIle 706
QY 2815 ACCAAAAATATAAATGGCTGGAGAAAGATCTTCCGACTCTCAGGACTTGGCTTAATGGTT 2874
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QY 2875 AATACT 2880
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Db 727 AsnThr 728
RESULT 5
US-09-764-853-819
; Sequence 819, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 819
; LENGTH: 722
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: SITE
; LOCATION: (237)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (296)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (719)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (720)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (721)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-853-819
Alignment Scores:
Pred. No.: 0 Length: 722
Score: 3770.00 Matches: 717
Percent Similarity: 99.31% Conservative: 0
Best Local Similarity: 99.31% Mismatches: 5
Query Match: 74.48% Indels: 0
DB: 9 Gaps: 0
US-10-039-073-3 (1-2883) x US-09-764-853-819 (1-722)
QY 715 GTTAAGCAATTTGAACCTTGAAGGAGTCTTTTGAAGATCACTTTGAACTACTCTAAA 774
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QY 775 ATGAGTACATACCTTGTAGCCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACT 834
Db 21 MetSerThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThr 40
QY 835 TCATCAGGGGTCAAGGTGTCCATCTATGCATCCCGACAAACCGAAATCAACACATTAT 894
Db 41 SerSerGlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyr 60
QY 895 GCTTTGACGGCATCACATGAAGCTACTGATTTTATGAAAAGTACTTTGATATCTACTAT 954
Db 61 AlaLeuGlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyr 80
QY 955 CCATCTCCAAACCTGGATTTAATTGCTATTCTCAGCTTTTGACCTGGAGCCATGGAAAT 1014
Db 81 ProLeuSerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsn 100
QY 1015 TGGGGCTCATTTACATATAGGAGACGTCATCTGCTTTTTTGACCCCAAGACCTTCTGCT 1074
Db 101 TrpGlyLeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAla 120
QY 1075 TCCGATAACTGTGGGTCCACAGAGTCATGCCCATGAACTGGCGCACCAGTGGTTGGC 1134
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Db 121 SerAspLysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGly 140
Qy 1135 AACCTGGTCACAAATGGAATGGTGAATATGATATTTGGCTTAAGGAGGGTTTTGCAAAATAC 1194
Db 141 AsnLeuValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyr 160
Qy 1195 ATGGAACATTATCGCTGTTAATGCTACATATCCAGAGCTGCAATTTGATGACTATTTTGTG 1254
Db 161 MetGluLeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeu 180
Qy 1255 AATGTGTGTTTGAAGTAATACAAAAGATTCATTGAATCATCCCGCCCTATCTCCAAA 1314
Db 181 AsnValCysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLys 200
Qy 1315 CCAGCGAAACCCCGACTCAAAATACAGAAATGTTTGCATGAAGTTTCTCTATAACAAGGGA 1374
Db 201 ProAlaGluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGly 220
Qy 1375 GCTTGTATTTTGAATATGCTCAAGGATTTTCTGGTGAGGAGAAATTCAGAAAGGAATA 1434
Db 221 AlaCysIleLeuAsnMetLeuLysAspPheLeuGlyGluLysPhe**LysGlyIle 240
Qy 1435 ATTCACTACTTAAAGAAGTTCAGCTATAGAAATCTAAGAAATGATGACTTGTGGACAGT 1494
Db 241 IleGlnTyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspLeuTrpSerSer 260
Qy 1495 CTGTCAAATAGTGTAGAAAGTGAATTTACATCTGCTGGAGTTCGTCAATCGGATCCC 1554
Db 261 LeuSerAsnSerCysLeuGluSerAspPheThrSerGlyValCysHisSerAspPro 280
Qy 1555 AAGATGACAAATACATGCTCGCTTCTCTGGGGGAAATGCAGAGGTCAAAGAGATGATG 1614
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Db 301 ThrThrTrpThrLeuGlnLysGlyIleProLeuLeuValValLysGlnAspGlyCysSer 320
Qy 1675 CTCCGACTGCAACAGGAGCGCTTCTCTCAGGGGGTTTTCCAGGAAGACCCCTGAATGGAGG 1734
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Qy 1735 GCCTTCGAGGAGAGGTACCTGTGGCATATCCATTGACCTACCTCCAGAGTTCCTTAAT 1794
Db 341 AlaLeuGlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerThrSerSerSerAsn 360
Qy 1795 GTGATCCACAGACACATCTAAATCAAGACATACTCTGGATCTACCTGAAAGACC 1854
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Qy 1855 AGTTGGGTGAAATTTAATGTGCACTCAAATGGTTACTACATCGTTCACTATGAGGGTCA 1914
Db 381 SerTrpValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHis 400
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Db 401 GlyTrpAspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAsp 420
Qy 1975 AGAGTAGGCTGATTCATGATGTGTTTCAGCTAGTTCGTGTCAGGAGACTGACCCCTAGAC 2034
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Qy 2035 AAAGCTCTTGACATGACTTACTACTCTCAACATCAACAGACAGCCCCCGCACTTCTCGAA 2094
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Qy 2095 GGTCTGATTTACTTGGAAATCGTTTTTACCATGATGACAGAAAGAAATATTTCAATATC 2154
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Qy 2155 TCTGAACACCTCAGCGGTACTCTTCTCAGTATTTTAAAGCCAGTGATGACAGCGCAAGC 2214
Db 481 SerGluAsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSer 500

Qy 2215 TCGAGTGACAAGGGCTCAGTCTGGGACAGGATGCTCGGCTCGGCTCTCTTTGAAAGCTGGCC 2274
Db 501 TrpSerAspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAla 520
Qy 2275 TGTGACTGAACCATGCTCTTGCATCCAGAAAGCTGCTGAACTCTTCTCCAGTGGATG 2334
Db 521 CysAspLeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMet 540
Qy 2335 GAATCAGTGGAAAAATTAAATATACCAACAGATGTTTAAAGATTGTGTATTTCTGTGGGT 2394
Db 541 GluSerSerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrSerValGly 560
Qy 2395 GCTCAGACAACAGCAGGATGGAATTACCTTTTAGAGCAATATGAACTGTCAATGTCAAGT 2454
Db 561 AlaGlnThrThrAlaGlyTrpAsnTyrLeuLeuGluGlnTyrGluLeuSerMetSerSer 580
Qy 2455 GCTGAACAAAACAAAATTCGTATGCTTGTGTCAACGAGCAGCATCAGGAAAGTACTG 2514
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Qy 2515 AGTTTAATTGAACCTAGGAATGGAAGGAAAGGTTTATCAAGACACAGAACTTGGCAGCTCTC 2574
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Qy 2575 CTTCATCGCATTCGCCAGATGCCAAAGGGCAGCAACTAGCATGGGATTTTGTAAAGAGAA 2634
Db 621 LeuHisAlaIleAlaArgArgProLysGlyGlnGlnLeuAlaTrpAspPheValArgGlu 640
Qy 2635 AATTGACCCATCTTCTGAAAAATTTGACTTGGGCTCATATGACATAGGATGATCATC 2694
Db 641 AsnTrpThrHisLeuLeuLysLysPheAspLeuGlySerTyrAspIleArgMetIleIle 660
Qy 2695 TCTGGCACAAACAGCTCACCTTTCTTCCAAAGGATAAGTTGCAAGAGGTGAAACTATTTT 2754
Db 661 SerGlyThrThrAlaHisPheSerSerLysAspLysLeuGlnGluValLysLeuPhePhe 680
Qy 2755 GAATCTCTTGAGGCTCAAGGATCACATCTCGATATTTTCAAACTGTTCGAAACGATA 2814
Db 681 GluSerLeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIle 700
Qy 2815 ACCAAAAATATAAATGGCTGGAGAGAATCTCCGACTGAGGACTTGGCTAATGGTT 2874
Db 701 ThrLysAsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeu***** 720
Qy 2875 AATACT 2880
Db 721 ***Thr 722
RESULT 6
US-10-220-443-2
; Sequence 2, Application US/10220443
; Publication No. US20030215820A1
; GENERAL INFORMATION:
; APPLICANT: Levine, Stewart
; TITLE OF INVENTION: REGULATORS OF TYPE-1 TUMOR NECROSIS FACTOR RECEPTOR AND OTHER CYT
; TITLE OF INVENTION: RECEPTOR SHEDDING
; FILE REFERENCES: 218732
; CURRENT APPLICATION NUMBER: US/10/220, 443
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06464
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/185,586
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 941
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-220-443-2
Alignment Scores:

Pred. No.:	5.2e-228	Length:	.941
Score:	2516.50	Matches:	478
Percent Similarity:	69.34%	Conservative:	171
Best Local Similarity:	51.07%	Mismatches:	268
Query Match:	49.71%	Indels:	19
DB:	15	Gaps:	7

US-10-039-073-3 (1-2883) x US-10-220-443-2 (1-941)			
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Qy	127	AGTTATCACTTCACGTAGGATCCCTGGGGCTTTCCAGTAGCCACTAATAGGGAACGATTT	186
Db	31	TrpCysGlnSerThrGlu-----AlaSerProLysArgSerAspGlyThrProPhe	47
Qy	187	CCTTGGCAGGAGCTAAGGCTCCCGAGTCGTGTCATTCCTCCATTATGACCTCTTTGTC	246
Db	48	ProTrpAsnLysIleArgLeuProGluTyrValIleProValHisIleThrAspLeuLeuIle	67
Qy	247	CACCCCAATCTCACCTCTCGACTTTGTCATCTGAGAAGATCGAAGTCTTGTCAGC	306
Db	68	HisAlaLeuLeuThrThrLeuThrPheTrpGlyThrThrLysValGluIleThrAlaSer	87
Qy	307	AATGCTACCCAGTTTATCATCTTCACAGCAAGAATCTTGAATCAGCAATGCCACCCCTT	366
Db	88	GlnProThrSerThrIleLeuHisSerHisIleLeuGlnIleSerArgAlaThrLeu	107
Qy	367	CAGTCAGGAGGAAATTCAGATACATGAAACAGAGAAAGAACTGAAAGTTTGTAGTTAC	426
Db	108	ArgLysGlyAlaGlyGluArgLeuSerGlu-----GluProLeuGlnValLeuGluHis	125
Qy	427	CCTGCTCATGAACAAATGCACTGCTGTTCCAGAGAACTTACGCTCACCTGAAATAC	486
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Qy	547	ACATACAGAACTCTTGGTGGTGAACAAAGAAATCTTGCAGTAAACAGATTTTGAGCCAAC	606
Db	166	ThrTyrArgThrLysGluGlyGluLeuArgIleLeuAlaSerThrGlnPheGluProThr	185
Qy	607	CAGCAGCATGGCTTTCCCTTGTGATCAACCGTTGTTCAAGCCAACTTTTCAATC	666
Db	186	AlaAlaArgMetAlaPheProCysPheAspGluProAlaPheLysAlaSerPheSerIle	205
Qy	667	AAGATACGAAGAGAGCAGGCATATTGCACATATCCAAATGCGCCAAAGGTTTAAGACAA	726
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Qy	727	GAACTTGAAGGAGTCTTTTGGAGATCACTTTGAACACTCTGATAAAATAGTACATAC	786
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Qy	787	CTTGTAGCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCATTCATCAGGGGTC	846
Db	246	LeuValAlaPheIleIleSerAspPheGluSerValSerTyrIleThrLysSerGlyVal	265
Qy	847	AAGGTGTCCATCTATGATCCCCAGACAAACGGAAATCAACACATTTATGCTTTCAGGCA	906
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Qy	907	TCACTGAAGCTACTTGATTTTATGAAAGTACTTTGTATCTACTACTATCCACTCTCCAA	966
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Qy	967	CTGATTTAATTCCTATTCCTGACTTTGACACTGGAGCCATGGAAAATTTGGGGCTCAT	1028
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Qy 2221 GACAAGGGCTCAGTCTCGGACAGATGCTCCGCTCGGCTCTCTTGAAGCTGGCTGTGAC 2280
Db 718 AspGluGlySerValSerGluArgMetLeuArgSerGlnLeuLeuLeuLeuAlaCysVal 737
Qy 2281 CTGAACCATGCTCTTCAGATCCAGAAAGCTGCTGAACTCTTCCAGTGGATGGAATCC 2340
Db 738 HisAsnTyrGlnProCysValGlnArgAlaGluGlyTyrPheArgLysTrpLysGluSer 757
Qy 2341 AGTGGAAAAATATAATATACCAACAGATGTTTAAAGATTGTGTATCTGTGGGTGCTCAG 2400
Db 758 AsnGlyAsnLeuSerLeuProValAspValThrLeuAlaValPheAlaValGlyAlaGln 777
Qy 2401 ACAACAGCAGATGGAATTAACCTTTTAGAGCAATATGAACCTGTCATGTCAAGTGTGAA 2460
Db 778 SerThrGluGlyTrpAspPheLeuTyrSerLysTyrGlnPheSerLeuSerSerThrGlu 797
Qy 2461 CAAAACAAATCTGTATGCTTGTCAACGAGCAAGCATCAGGAAAGTGTACTGAATTA 2520
Db 798 LysSerGlnIleGluPheAlaLeuCysArgThrGlnAsnLysGluLysLeuGlnTrpLeu 817
Qy 2521 ATTCAACTAGGAATGGAAGAAAGGTTATCAAGACACAGAACTTGGCAGCTCTCCTTCAT 2580
Db 818 LeuAspGluSerPheLysGlyAspLysIleLysThrGlnGluPheProGlnIleLeuThr 837
Qy 2581 GCGAATTCGACAGCTCCAAAGGGGCAGCAACTAGCATGGATTTTGTAAAGAAATGG 2640
Db 838 LeuIleGlyArgAsnProValGlyTyrProLeuAlaTrpGlnPheLeuArgLysAsnTrp 857
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Qy 2701 ACAACAGCTCACTTTCTTCCAAGGATAAGTTGCAAGCGTGAACACTATTTTGAATCT 2760
Db 878 ThrThrAsnGlnPheSerThrArgThrArgLeuGluGluValLysGlyPhePheSerSer 897
Qy 2761 CTGAGGCTCAAGGATCACATCTGGATATTTTCAAACTGTCTCGAAACGATAACAAA 2820
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Qy 2821 AATATAAATGGCTGGAGAGAATCTTCGCACTCTGAGGACTGGGCTA 2868
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RESULT 7

US-10-264-237-2723
; Sequence 2723, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P131P1
; CURRENT APPLICATION NUMBER: US/10/264, 237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2723
; LENGTH: 941
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-264-237-2723

Alignment Scores:
Pred. No.: 6,46e-228 Length: 941
Score: 2515.50 Matches: 477
Percent Similarity: 69.34% Conservative: 172
Best Local Similarity: 50.96% Mismatches: 268
Query Match: 49.69% Indels: 19
DB: 15 Gaps: 7
US-10-039-073-3 (1-2883) x US-10-264-237-2723 (1-941)
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Db 15 PheLeuLeuSerSerLeuLeuAlaLeuLeuThrVal-----SerThrProSer 30
Qy 127 AGTTATCACTTCACTCAGGATCCTGGGGCTTCCAGTAGTCCACTAATGGGAACGATTT 186
Db 31 TrpCysGlnSerThrGlu-----AlaSerProLysArgSerAspGlyThrProPhe 47
Qy 187 CTTGCGCAGGAGCTAAGGCTCCCGAGTGGTGCATTCCTCTCCATATGACCTTTGTGTC 246
Db 48 ProTrpAsnLysIleArgLeuProGluTyrValIleProValHisTyrAspLeuLeu 67
Qy 247 CACCCCAATCTCACTCTCTGGACTTTGTTGCATCTGAGAGATCGAAGTCTTGGTCAGC 306
Db 68 HisAlaAsnLeuThrThrLeuThrPheTrpGlyThrLysValGluIleThrAlaSer 87
Qy 307 AATGCTACCCAGTTTATCATCTTGCACAGCAAGAGATCTTGAATCAGCAATGCCACCTT 366
Db 88 GlnProThrSerThrIleLeuHisSerHisLeuGlnIleSerArgAlaThrLeu 107
Qy 367 CAGTCAGAGGAAGATTCAAGATACATGAAACCAAGGAAAGAAAGTTTTGGATTAC 426
Db 108 ArgLysGlyAlaGlyGluArgLeuSerGlu-----GluProLeuGlnValLeuGluHis 125
Qy 427 CTGCTCATGAAACAAATTCGACTGCTGTTTCAGAGAAAATTCAGCTCACCTGAAATAC 486
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Qy 487 TATGTGGCTATGGACTTCCAAGCAAGTAGTGGTGTGAGGGTTTGAAGGTTTATAAAGC 546
Db 146 ThrValValIleHisTyrAlaGlyAsnLeuSerGluThrPheHisGlyPheTyrLysSer 165
Qy 547 ACATACAGAACTCTTGGTGTGAAACAAAGATTTCTTGCAGTAAACAGATTTTGGACCAAC 606
Db 166 ThrTyrArgThrLysGluGlyGluLeuArgIleLeuAlaSerThrGlnPheGluProThr 185
Qy 607 CAGGCACGATCGCTTTCCTTCTGATGACCGTGTTCCTCAAGCCCACTTTTCAATC 666
Db 186 AlaAlaArgMetAlaPheProCysPheAspGluProAlaPheLysAlaSerPheSerIle 205
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Qy 847 AAGGTGTCATCTATGCATCCCGCAGACAAACCGAATCAAAACATTTATGTTTGCAGGCA 906
Db 266 LysValSerValTyrAlaValProAspLysMetAsnGlnAlaAspTyrAlaLeuAspAla 285
Qy 907 TCACTGAAGCTACTTGATTTTATGAAAGTACTTTTGATATCTTATCTATCCACTCTCAAA 966
Db 286 AlaValThrLeuLeuGluPheTyrGluAspTyrPheSerIleProFyrProLeuProLys 305
Qy 967 CTGGATTTAATGCTATTCTGACTTTGCACCTGGAGCCATCGAAATTTGGGGCCTCAT 1026
Db 306 GlnAspLeuAlaAlaIleProAspPheGlnSerGlyAlaMetGluAsnTrpGlyLeuThr 325

; ORGANISM: Homo sapiens			
US-10-472-533-329			
Alignment Scores:			
Pred. No.:	6,46e-228	Length:	941
Score:	2515.50	Matches:	477
Percent Similarity:	69.34%	Conservative:	172
Best Local Similarity:	50.96%	Mismatches:	268
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Qy	67	TACTGCTTAACAGGCATCTGCCCAATATGCAATGTTGTTCTCAGTTCCTCAGTCCCATCT	126
Db	15	PhelLeuLeuSerSerLeuLeuAlaLeuLeuThrVal-----SerThrProSer	30
Qy	127	AGTTATCATCTTCATGAGGATCTGGGGCTTCCAGTAGCCACCAATATGGGAACGATTT	186
Db	31	TrpCysGlnSerThrGlu-----AlaSerProLysArgSerAspGlyThrProPhe	47
Qy	187	CTTTGGCAGGAGCTAAGCTCCCGAGTGTGGTCAATCTCTCCATTTATGACCTCTTTGTC	246
Db	48	ProTrpAsnLysIleArgLeuProGluTyrValIleProValHisTyrAspLeuLeuIle	67
Qy	247	CACCCCAATCTCAGTCTGAGCTTTGTTGCATCTGAGAGATCGAAGTCTTGGTCAGC	306
Db	68	HisAlaLeuLeuThrLeuThrPheTrpGlyThrThrLysValGluIleThrAlaSer	87
Qy	307	AATGCTACCCAGTTTATCATCTTCACAGCAAGATCTTGAATACGAATGCGACCCCTT	366
Db	88	GlnProThrSerThrIleLeuHisSerHisLeuGlnIleSerArgAlaThrLeu	107
Qy	367	CAGTCAGGAGGATTCAGATACATGAAACACGAGAAAGAGTGAAGTTTTCAGTTAC	426
Db	108	ArgLysGlyAlaGlyGluArgLeuSerGlu-----GluProLeuGlnValLeuGluHis	125
Qy	427	CTGCTCATGAACAAATGCACTGCTGGTCCAGAGAAATCTTACGCTCACCTGAAATAC	486
Db	126	ProProGlnGluGlnIleAlaLeuLeuAlaProGluProLeuLeuValGlyLeuProTyr	145
Qy	487	TATGTGCTATGAGCTTCCAGCCCAAGTTAGTGTATGCTTTGAAGGTTTATAAAGC	546
Db	146	ThrValValIleHisTyrAlaGlyAsnLeuSerGluThrPheHisGlyPheTyrLysSer	165
Qy	547	ACATACAGACTCTGGTGGTGAACAGAGATTTCTGCAGTAAACAGATTTTGACCCAAC	606
Db	166	ThrTyrArgThrLysGluGlyGluLeuArgIleLeuAlaSerThrGlnPheGluProThr	185
Qy	607	CAGCAGCATGGCTTTCCTTGTGTTGATCAACCGTTGTTCAAGCCCACTTTTCAATC	666
Db	186	AlaAlaArgMetAlaPheProCysPheAspGluProAlaPheLysAlaSerPheSerIle	205
Qy	667	AAGATACGAAGAGAGAGCAGCATATTGCATCTTCCAAATGCCAAAGGTTAAGACAATT	726
Db	206	LysIleArgGluProArgHisLeuAlaIleSerAsnMetProLeuValLysSerVal	225
Qy	727	GAACCTGAGAGGCTTTTGGAGATCAGCTTTGAACTACTGTAAAAATGAGTACATAC	786
Db	226	ThrValAlaGluGlyLeuIleGluAspHisPheAspValThrValLysMetSerThrTyr	245
Qy	787	CTGTGAGCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACTTCATCAGGGGTC	846
Db	246	LeuValAlaPheIleIleSerAspPheGluSerValSerLysIleThrLysSerGlyVal	265
Qy	847	AAGGTGTCATCTATGCAATCCCGACAGCAACCGGAATCAACACATTAATGCTTTCCAGCA	906
Db	266	LysValSerValTyrAlaValProAspLysMetAsnGlnAlaAspTyrAlaLeuAspAla	285
Qy	907	TCAGTGAAGCTACTGATTTTATGAAAGTACTTTGATATCTACTATCCACTCTCCAAA	966
Db	286	AlaValThrLeuLeuGluPheTyrGluAspTyrPheSerIleProTyrProLeuProLys	305
Qy	967	CTGGATTTAATGCTATTCTGCTGCTTTGCACCTGGAGCCATGGAATAATGGGCGCTCAT	1026
Db	306	GlnAspLeuAlaAlaIleProAspPheGlnSerGlyAlaMetGluAsnTrpGlyLeuThr	325
Qy	1027	ACATATAGGAGAGAGCTCAGTCTTTTGGACCCCAAGACCTCTTCTGCTCCGATAAAGTG	1086
Db	326	ThrTyrArgGluSerAlaLeuLeuPheAspAlaGluLysSerSerAlaSerLysLeu	345
Qy	1087	TGGGTCCACAGAGCTATAGCCCATGAATGCGCCACAGTGGTTTGGCAACCTGGTCACA	1146
Db	346	GlyIleThrMetThrValAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeuValThr	365
Qy	1147	ATGGAATGTGGGAATGATATTTGGCTTAAGAGGGTTTTGCAAAATACATGGAACCTATC	1206
Db	366	MetGluTrpTrpAsnAspLeuTrpLeuAsnGluGlyPheAlaLysPheMetGluPheVal	385
Qy	1207	GCTGTTAATGCTACATATCCAGAGCTGCAATTTGATGACTATTTTTTGAATGTGTGTTT	1266
Db	386	SerValSerValThrHisProGluLeuLysValGlyAspTyrPheGlyLysCysPhe	405
Qy	1267	GAAGTAATTACAAAAGATTCATTGAATTCATCCCGCTCTATCTCCAAACAGCGGAACC	1326
Db	406	AspAlaMetGluValAspAlaLeuAsnSerSerHisProValSerThrProValGluAsn	425
Qy	1327	CCGACTCAAAATACAGGAATGTTTGTGAAGTTTCTATAACAAGGAGCTTGTATTTTG	1386
Db	426	ProAlaGlnIleArgGluMetPheAspAspValSerTyrAspLysGlyAlaCysIleLeu	445
Qy	1387	AATATGCTCAAGATTTTCTGGGTGAGGAGAAATTCAGNAAGGAATATTTAGTACTTA	1446
Db	446	AsnMetLeuArgGluTyrLeuSerAlaAspAlaPheLysSerGlyIleValGlnTyrLeu	465
Qy	1447	AAGAAGTTCAGCTATAGAAATCTAAGATGATGACTTGTGGAGCAGTCTGTCAAAATAGT	1506
Db	466	GlnLysHisSerTyrLysAsnThrLysAsnGluAspLeuTrpAspSerMetAlaSerIle	485
Qy	1507	TGTTTGAAGATGATTTTACATCTGGT-----GGAGTTTGTCTCGGATCCCAAGATG	1560
Db	486	Cys---ProThrAspGlyValLysGlyMetAspGlyPheCys---SerArgSerGlnHis	503
Qy	1561	ACAAGTAACATGCTCGCTTCTGGGGGAAATGCAGAGGTCAAGAGATGATGACTACA	1620
Db	504	SerSerSerSerSerHisTrpHisGlnGluGlyValAspValLysThrMetMetAsnThr	523
Qy	1621	TGACTCTCCAGAAAGGAATCCCTGCTGGTGTAAACAAGACGGGTCTTCACTCCGA	1680
Db	524	TrpThrLeuGlnArgGlyPheProLeuIleThrIleThrValArgGlyArgAsnValHis	543
Qy	1681	CTGCAACAGGAGCGCTTCTCCAGGGGGTTTTCCAGGAAGACCTGAAATGGAGGGCCCTG	1740
Db	544	MetLysGlnGluHisTyrMetLysGly-----SerAspGlyAlaPro	557
Qy	1741	CAGAGAGGTACCTGTGGCATATCCCATTCAGTACTCCACGAGTCTTCTAATGTGATC	1800
Db	558	AspThrGlyTyrLeuTrpHisValProLeuThrPheIleThrSerLysSerAspMetVal	577
Qy	1801	CACAGACACATCTTAAATCAAAAGACAGATCTCTGATCTACTCTGAAAAACAGTTGG	1860
Db	578	HisArgPheLeuLeuLysThrLysThrAspValLeuLeuProGluGluValGluTrp	597
Qy	1861	GTGAAATTTAATGTGAGCTCAAAATGGTTACTACATCGTTCATGAGGGTCAATGATGG	1920
Db	598	IleLysPheAsnValGlyMetAsnGlyTyrTyrIleValHisTyrGluAspAspGlyTrp	617
Qy	1921	GACCACTCATACAGCTGAATCAGAACCAACACACTTCTCAGACCTTAAGGACAGATA	1980
Db	618	AspSerLeuThrGlyLeuLeuLysGlyThrHisThrAlaValSerSerAsnAspArgAla	637
Qy	1981	GGTCTGATTCATGCTGTTTACGTAGTTTGGTGGAGGAGACTGACCTTAGACAAAGCT	2040
Db	638	SerLeuIleAsnAsnAlaPheGlnLeuValSerIleGlyLysLeuSerIleGluLysAla	657
Qy	2041	CTTGACATGACTTACTACCTCCCAACATGAAACAAGCAGCCCCCGACTTCTTCGAAGGCTG	2100

Db 658 LeuAspLeuSerLeuTyrLeuLysHisGluThrGluLeuMetProValPheGlnGlyLeu 677
Qy 2101 AGTTACTTGGAAATCGTTTACACATGATGGACAGAGGAATATTTTCAGATATCTCTGAA 2160
Db 678 AsnGluLeuLeuProMetTyrLysLeuMetGluLysArgAspMetAsnGluValGluThr 697
Qy 2161 AACCTCAAGCGTTACTCTTTCAGTATTTTAAAGCAGAGTATTCAGAGCAAGCTGGAGT 2220
Db 698 GlnPheLysAlaPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 717
Qy 2221 GACAAAGGCTCAGTCTGGACAGGATGCTCCGCTCGGCTCTCTCAAGCTGSCCTGTGAC 2280
Db 718 AspGluGlySerValSerGluArgMetLeuArgSerGluLeuLeuLeuLeuLeuAlaCysVal 737
Qy 2281 CTGAACCATGCTCTTGGCATCCAGAAAGCTGCTGAACCTCTTCTCCAGTGGATGAATCC 2340
Db 738 HisAsnTyrGlnProCysValGlnArgAlaGluGlyTyrPheArgLysTrpLysGluSer 757
Qy 2341 AGTGAATAATTAATATACCAACAGATGTTTAAAGATTGTATTCGTGGTCTGCTCAG 2400
Db 758 AsnGlyAsnLeuSerLeuProValAspValThrLeuAlaValPheAlaValGlyAlaGln 777
Qy 2401 ACAACAGCAGGATGAATTACCTTTAGAGCAATATGAACCTCAATGTCAGTCTGAA 2460
Db 778 SerThrGluGlyTrpAspPheLeuTyrSerLysTyrGlnPheSerLeuSerSerThrGlu 797
Qy 2461 CAAACAAATAATCTGTATGCTTTGCAACGACCAAGCATCAGAAAGTACTGAAGTTA 2520
Db 798 LysSerGlnIleGluPheAlaLeuCysArgThrGlnAsnLysGluLysLeuGlnTrpLeu 817
Qy 2521 ATTGAATAGGAATCGAAGAAAGTTATCAAGACACAGAACTTGGCAGCTCTCTTCAT 2580
Db 818 LeuAspGluSerPheLysGlyAspLysIleLysThrGlnGluPheProGlnIleLeuThr 837
Qy 2581 GCGATTGCGCAGCGTCCAAAGGGCAGCAACTAGCATGGATTTTGTAAAGAGAAATGG 2640
Db 838 LeuIleGlyArgAsnProValGlyTyrProLeuAlaTrpGlnPheLeuArgLysAsnTrp 857
Qy 2641 ACCCATCTTCTGAAATAATTTGACTTGGCTCATATGACATAAGGATGATCTCTGCG 2700
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Qy 2761 CTTGAGGCTCAAGATCATCTGGATATTTTCAAACTGTCTCGAAACGATACCAAA 2820
Db 898 LeuLysGluAsnGlySerGlnLeuArgCysValGlnGlnThrIleGluThrIleGluGlu 917
Qy 2821 AATATAAATGGCTGGAGAAGATCTCCGACTCTGAGGACTTGGCTA 2868
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RESULT 9

US-10-106-698-6381
; Sequence 6381, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA05P1
; CURRENT APPLICATION NUMBER: US/10106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: Patentin Ver. 3.0

; SEQ ID NO 6381
; LENGTH: 944
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-106-698-6381
Alignment Scores:
Pred. No.: 6,47e-228 Length: 944
Score: 2515.50 Matches: 477
Percent Similarity: 69.34% Conservative: 172
Best Local Similarity: 50.96% Mismatches: 268
Query Match: 49.69% Indels: 19
DB: 14 Gaps: 7
US-10-039-073-3 (1-2883) x US-10-106-698-6381 (1-944)
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Qy 127 AGTTATCATCTTCATCAGGATCTCTGGGGCTTCCAGTAGCCACTTAATGGGAACGATT 186
Db 34 TrpCysGlnSerThrGlu-----AlaSerProLysArgSerAspGlyThrProPhe 50
Qy 187 CTTGGCAGGAGCTAAAGCTCCCGAGTGTGCTCATCTCTCCATTATGACCTCTTTGTC 246
Db 51 ProTrpAsnLysIleArgLeuProGluTyrValIleProValHisTyrAspLeuLeu 70
Qy 247 CACCCCAATCTCCTCTGAGCTTTGTTGCATCTGAGAAGATCGAAGTCTTGGTCAGC 306
Db 71 HisAlaAsnLeuThrThrLeuThrPheTrpGlyThrThrLysValGluIleThrAlaSer 90
Qy 307 AATGCTACCCAGTTTATCATCTTCACAGCAAGATCTTGAATCAGCAATGCCACCTT 366
Db 91 GlnProThrSerThrIleLeuLeuHisSerHisLeuGlnIleSerArgAlaThrLeu 110
Qy 367 CAGTCAGAGGAGGATCAAGATACATGAAACCAGGAAGAACTGAAAGTCTTGGATTAC 426
Db 111 ArgLysGlyAlaGlyGluArgLeuSerGlu-----GluProLeuGlnValLeuGluHis 128
Qy 427 CTTGCTCATGAACAAATTTGCACTGCTGTTCCAGAGAACTTACGCTCCTCAGTGAATAC 486
Db 129 ProGlnGluGlnIleAlaLeuLeuAlaProGluProLeuLeuValGlyLeuProTyr 148
Qy 487 TATGCTGCTAGTACTTCCAGCCCAAGTTAGGTAGTGGCTTTGAAGGGTTTATAAAGC 546
Db 149 ThrValValIleHisTyrAlaGlyAsnLeuSerGluThrPheHisGlyPheTyrLysSer 168
Qy 547 ACATACAGAACTCTTGGTGAACAGAAATCTTCCAGTAAACAGATTTTGAGCCCAACC 606
Db 169 ThrTyrArgThrLysGluGlyGluLeuArgIleLeuAlaSerThrGlnPheGluProThr 188
Qy 607 CAGCAGCAGTGGCTTTCCCTTGTGTTGATGAACCGTTGTTCAAGCCCACTTTTCAATC 666
Db 189 AlaAlaArgMetAlaPheProCysPheAspGluProAlaPheLysAlaSerPheSerIle 208
Qy 667 AAGATACGAAGAGAGAGCAGCATATTCGACTATCCAACTCCCAAGAGGTTTAAGCAAT 726
Db 209 LysIleArgArgGluProArgHisLeuAlaIleSerAsnMetProLeuValLysSerVal 228
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Db 229 ThrValAlaGluGlyLeuIleGluAspHisPheAspValThrValLysMetSerThrTyr 248
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Qy 907 TCACTGAAGTACTTGTGATTTTATGAAAGTACTTTTGTATATCTACTACTCTCCAAA 966

APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC63
CURRENT APPLICATION NUMBER: US/09/989,722
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535

QY	DB	Seq1	Seq2	Seq3	Seq4	Seq5	Seq6	Seq7	Seq8	Seq9	Seq10	Seq11	Seq12	Seq13	Seq14	Seq15	Seq16	Seq17	Seq18	Seq19	Seq20	Seq21	Seq22	Seq23	Seq24	Seq25	Seq26	Seq27	Seq28	Seq29	Seq30	Seq31	Seq32	Seq33	Seq34	Seq35	Seq36	Seq37	Seq38	Seq39	Seq40	Seq41	Seq42	Seq43	Seq44	Seq45	Seq46	Seq47	Seq48	Seq49	Seq50	Seq51	Seq52	Seq53	Seq54	Seq55	Seq56	Seq57	Seq58	Seq59	Seq60	Seq61	Seq62	Seq63	Seq64	Seq65	Seq66	Seq67	Seq68	Seq69	Seq70	Seq71	Seq72	Seq73	Seq74	Seq75	Seq76	Seq77	Seq78	Seq79	Seq80	Seq81	Seq82	Seq83	Seq84	Seq85	Seq86	Seq87	Seq88	Seq89	Seq90	Seq91	Seq92	Seq93	Seq94	Seq95	Seq96	Seq97	Seq98	Seq99	Seq100	Seq101	Seq102	Seq103	Seq104	Seq105	Seq106	Seq107	Seq108	Seq109	Seq110	Seq111	Seq112	Seq113	Seq114	Seq115	Seq116	Seq117	Seq118	Seq119	Seq120	Seq121	Seq122	Seq123	Seq124	Seq125	Seq126	Seq127	Seq128	Seq129	Seq130	Seq131	Seq132	Seq133	Seq134	Seq135	Seq136	Seq137	Seq138	Seq139	Seq140	Seq141	Seq142	Seq143	Seq144	Seq145	Seq146	Seq147	Seq148	Seq149	Seq150	Seq151	Seq152	Seq153	Seq154	Seq155	Seq156	Seq157	Seq158	Seq159	Seq160	Seq161	Seq162	Seq163	Seq164	Seq165	Seq166	Seq167	Seq168	Seq169	Seq170	Seq171	Seq172	Seq173	Seq174	Seq175	Seq176	Seq177	Seq178	Seq179	Seq180	Seq181	Seq182	Seq183	Seq184	Seq185	Seq186	Seq187	Seq188	Seq189	Seq190	Seq191	Seq192	Seq193	Seq194	Seq195	Seq196	Seq197	Seq198	Seq199	Seq200	Seq201	Seq202	Seq203	Seq204	Seq205	Seq206	Seq207	Seq208	Seq209	Seq210	Seq211	Seq212	Seq213	Seq214	Seq215	Seq216	Seq217	Seq218	Seq219	Seq220	Seq221	Seq222	Seq223	Seq224	Seq225	Seq226	Seq227	Seq228	Seq229	Seq230	Seq231	Seq232	Seq233	Seq234	Seq235	Seq236	Seq237	Seq238	Seq239	Seq240	Seq241	Seq242	Seq243	Seq244	Seq245	Seq246	Seq247	Seq248	Seq249	Seq250	Seq251	Seq252	Seq253	Seq254	Seq255	Seq256	Seq257	Seq258	Seq259	Seq260	Seq261	Seq262	Seq263	Seq264	Seq265	Seq266	Seq267	Seq268	Seq269	Seq270	Seq271	Seq272	Seq273	Seq274	Seq275	Seq276	Seq277	Seq278	Seq279	Seq280	Seq281	Seq282	Seq283	Seq284	Seq285	Seq286	Seq287	Seq288	Seq289	Seq290	Seq291	Seq292	Seq293	Seq294	Seq295	Seq296	Seq297	Seq298	Seq299	Seq300	Seq301	Seq302	Seq303	Seq304	Seq305	Seq306	Seq307	Seq308	Seq309	Seq310	Seq311	Seq312	Seq313	Seq314	Seq315	Seq316	Seq317	Seq318	Seq319	Seq320	Seq321	Seq322	Seq323	Seq324	Seq325	Seq326	Seq327	Seq328	Seq329	Seq330	Seq331	Seq332	Seq333	Seq334	Seq335	Seq336	Seq337	Seq338	Seq339	Seq340	Seq341	Seq342	Seq343	Seq344	Seq345	Seq346	Seq347	Seq348	Seq349	Seq350	Seq351	Seq352	Seq353	Seq354	Seq355	Seq356	Seq357	Seq358	Seq359	Seq360	Seq361	Seq362	Seq363	Seq364	Seq365	Seq366	Seq367	Seq368	Seq369	Seq370	Seq371	Seq372	Seq373	Seq374	Seq375	Seq376	Seq377	Seq378	Seq379	Seq380	Seq381	Seq382	Seq383	Seq384	Seq385	Seq386	Seq387	Seq388	Seq389	Seq390	Seq391	Seq392	Seq393	Seq394	Seq395	Seq396	Seq397	Seq398	Seq399	Seq400	Seq401	Seq402	Seq403	Seq404	Seq405	Seq406	Seq407	Seq408	Seq409	Seq410	Seq411	Seq412	Seq413	Seq414	Seq415	Seq416	Seq417	Seq418</
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; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.:	1,248-227	Length:	941
Score:	2512.50	Matches:	477
Percent Similarity:	69.34%	Conservative:	172
Best Local Similarity:	50.96%	Mismatches:	268
Query Match:	49.63%	Indels:	19
DB:	9	Gaps:	7

US-10-039-073-3 (1-2883) x US-09-989-723-353 (1-941)

Qy	67	TACTGCTTTAAGCAGCCATCTTGGCCCCAAATATATGATTTGTTCTCAGTTCTCAGTGCCATCT	126
Db	15	PhelLeuSerSerLeuLeuAlaLeuLeuThrVal-----SerThrProSer	30
Qy	127	AGTTATCATCTTACATGAGGATCCTGGGCTTTCCAGTAGCCACTAAATGGGGAACGATTT	186
Db	31	TrpCysGlnSerThrGlu-----AlaSerProLysArgSerAspGlyThrProPhe	47
Qy	187	CCTTGGCAGGAGACTAAGGCTCCCCAGTGGTGCATTCTCTCATTTAGACCTCTTTGTC	246
Db	48	ProTrpAsnLysIleArgLeuProGluTrpValIleProValHisTyrAspLeuLeuIle	67
Qy	247	CACCCCAATCTCACCTCTCTGACCTTTGTTGCATCTGAGAAGATCGAAGTCTTGTGTACG	306
Db	68	HisAlaAsnLeuThrLeuThrLeuThrPheTrpGlyThrThrLysValGluIleThrAlaSer	87
Qy	307	AATGCTACCCAGTTTATCATCTTGCACAGCAAGATCTTGAATCAGCAATGCCACCCTT	366
Db	88	GlnProThrSerThrIleLeuHisSerHisLeuGlnIleSerArgAlaThrLeu	107
Qy	367	CAGTCAGGAGGAGATTCAAGATACATGAATCAAGCAAGAAAGAACTTGAAGTTTGGAGTTAC	426
Db	108	ArgLysGlyAlaGlyArgLeuSerGlu-----GluProLeuGlnValLeuGluHis	125
Qy	427	CCTGCTCATGAACAAATTTGCACTGTGCTTTCAGAGAACTTACGCTCACCCTGAATAC	486
Db	126	ProProGlnGluGlnIleAlaLeuLeuAlaProGluProLeuLeuValGlyLeuProTyr	145
Qy	487	TATGTGGCTATGGACTTCCAGGCCAAGTTAGTGTGATGGCTTTGAAGGGTTTTATAAAGC	546
Db	146	ThrValValIleHisTyrAlaGlyAsnLeuSerGluThrPheHisGlyPheTyrLysSer	165
Qy	547	ACATACAGAACTCTTGTGGTGGTGAACAAGAATTTCTTGCAGTAACAGATTTTTCAGGCCAAC	606
Db	166	ThrTyrArgThrLysGluGlyGluLeuArgIleLeuAlaSerThrGlnPheGluProThr	185
Qy	607	CAGCAGCATGGCTTTCCCTTGTGATGACCGTTGTTTCAAGCCAACTTTTCAATC	666
Db	186	AlaAlaArgMetAlaPheProCysPheAspGluProAlaPheLysAlaSerPheSerIle	205
Qy	667	AAGATACGAGAGAGAGCAGCATATTCACATATCCACATGCCAAGGTTAAAGCAATT	726
Db	206	LysIleArgArgGluProArgHisLeuAlaIleSerAsnMetProLeuValLysSerVal	225
Qy	727	GAACTTGAAGGAGGCTTTTGGGAAGATCATTCTTGAATCTACTGTAAAAATCAGTACATAC	786
Db	226	ThrValAlaGluGlyLeuIleGluAspHisPheAspValThrValLysMetSerThrTyr	245
Qy	787	CTTGTAGCTACATAGTTTGTGATTTTCCACTCTCTGAGTGGCTTCACCTTCATCAGGGGTC	846
Db	246	LeuValAlaPheIleIleSerAspPheGluSerValSerLysIleThrLysSerGlyVal	265
Qy	847	AAGGTGTCATCTATGTCATCCCCAGACAAACCGAATCAAAACACATATTATGCTTTGCAGCA	906
Db	266	LysValSerValTyrAlaValProAspLysIleAsnGlnAlaAspTyrAlaLeuAspAla	285
Qy	907	TCACTGAAGCTACTTGATTTTTTATGAAAAAGTACTTTGATATCTACTATCTCCACTCTCCAAA	966

286	AlaValThrLeuLeuGluPheTyrGluAspTyrPheSerIleProTyrProLeuProLys	305
967	CTGATTAAATGCTATTCCTGACTTTGACCTGGAGCCATGAAAAATGGGCGCTCAT	1026
306	GlnAspLeuAlaIleProAspPheGlnSerGlyAlaMetGluAsnTrpGlyLeuThr	325
1027	ACATATAGGAGAGCTCATGCTGCTTTTGGACCCCAAGACCTCTTCTGCTTCCGATAAATCG	1086
326	ThrTyrArgGluSerAlaLeuLeuPheAspAlaGluLysSerSerAlaSerSerLysLeu	345
1087	TGGGTCACAGAGCTCATAGCCCATGAACCTGGCCGACCACTGGTTTGGCAACCTGGTCA	1146
346	GlyIleThrValThrValAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeuValThr	365
1147	ATGGAATGGTGGGAATGATATTTGGCTTTAAGGAGGGTTTGCAAAATACATCGAACTTATC	1206
366	MetGluTrpTrpAsnAspLeuTrpLeuAsnGluGlyPheAlaLysPheMetGluPheVal	385
1207	GCTGTTAAATGCTATCATATCCAGAGCTGCAATTTGATGACTATTTTGAATGTGCTTTT	1266
386	SerValSerValThrHisProGluLeuLysValGlyAspTyrPhePheGlyLysCysPhe	405
1267	GAAGTAATACAAAAGNTTCATTGAATTCATCCCGCCCTATCTCCAAAACGACGGGAACC	1326
406	AspAlaMetGluValAspAlaLeuAsnSerHisProValSerThrProValGluAsn	425
1327	CCGACTCAAAATACAGAAATGTTTGATGAAGTTTCTATAACAAGGAGAGCTGTATTTTG	1386
426	ProAlaGlnIleArgGluMetPheAspAspValSerTyrAspLysGlyAlaCysIleLeu	445
1387	AATATGCTCAAGGATTTTCTGGGTGAGAGAAATTCAGAAAAGGAATAATTCAGTACTTA	1446
446	AsnMetLeuArgGluTyrLeuSerAlaAspAlaPheLysSerGlyIleValGlnTyrLeu	465
1447	AAGAAGTTCAGCTATAGAATAAGCTAGAAATGATGACTTGTGGAGCAGTCTGTCAATAGT	1506
466	GlnLysHisSerTyrLysAsnThrLysAsnGluAspLeuTrpAspSerMetAlaSerIle	485
1507	TGTTTAGAAGTCATTTTACATCTGCT-----GGAGTTTGTTCATTCGGATCCCAAGATG	1560
486	Cys---ProThrAspGlyValLysGlyMetAspGlyPheCys---SerArgSerGlnHis	503
1561	ACAAGTAACATGCTCCCTTCTGGGGGAAAATGTCAGAGGTCAAAGAGATGACTACATA	1620
504	SerSerSerSerHisTrpHisGlnGluGlyValAspValLysThrMetMetAsnThr	523
1621	TGCACTCTCCAGAAAGGAATCCCTCTGCTGGTGGTTAAACAAGACGGGTGTTCACTCCGA	1680
524	TrpThrLeuGlnArgGlyPheProLeuIleThrIleThrValArgGlyArgAsnValHis	543
1681	CTCAACAGAGAGCGCTTCTCCAGAGGGGTTTTCCAGGAAGACCCCTGAATGGAGGGCCCTG	1740
544	MetCysGlnGlnHisTyrMetLysGly-----SerAspGlyAlaPro	557
1741	CAGGAGAGGTACCTGTGGCATATCCCATCTACTCCACAGATGTTCTTCTAATGTGATC	1800
558	AspThrGlyTyrLeuTrpHisValProLeuThrPheIleThrSerLysSerAsnMetVal	577
1801	CACAGACATTTCTAAATCAAAGACAGATATCTCTGGATCTCTACCTGAAAAGACCACTGG	1860
578	HisArgPheLeuLysThrLysThrAspValLeuIleLeuProGluGluValGluTrp	597
1861	GTCAAAATTAATGTGGACTCAATAGTTACTACATCTGTTCACTATGAGGGTCACTGATCG	1920
598	IleLysPheAsnValGlyMetAsnGlyTyrTyrIleValHisTyrGluAspAspGlyTyr	617
1921	GACCAACTATTACACAGCTGAATCAGAACACCACACTTCTCAGACCTTAAGGACAGATGA	1980
618	AspSerLeuThrGlyLeuLeuLysGlyThrHisThrAlaValSerSerAsnAspArgAla	637
1981	GGTCTGATTCATGATGTGTTTCAGCTAGTTGGTGTGAGGAGACTGACCCCTAGACAAAGCT	2040
638	SerLeuIleAsnAsnAlaPheGlnLeuValSerIleGlyLysLeuSerIleGlyLysAla	657

Db 108 ArgLysGlyAlaGlyGluArgLeuSerGlu-----GluProLeuGlnValLeuGluHis 125
Qy 427 CCTGCTCATGAACAAATTCGACTGCTGGTCCAGAGAAACTTACGCCTCACCTGAAATAC 486
Db 126 ProProGlnGluGlnIleAlaLeuLeuAlaProGluProLeuLeuValGlyLeuProTyr 145
Qy 487 TATGTGGCTATGGACTTCCCAAGCCAAAGTATGGTATGGCTTTGAAGGGTTTATAAAGC 546
Db 146 ThrValValIleHisTyrAlaGlyAsnLeuSerGluThrPheHisGlyPheTyrLysSer 165
Qy 547 ACATACAGAAGCTCTGGTGGTGAACAAGATTCCTGCAGTACACAGATTTTGACCAACC 606
Db 166 ThrTyrargThrLysGluGlyGluArgIleLeuAlaSerThrGlnPheGluProThr 185
Qy 607 CAGCAGCATGGCTTCCCTTGTCTTGTATGAACCGTTGTTCAAGCCAACTTTTCAATC 666
Db 186 AlaAlaargMetAlaPheProCysPheAspGluProAlaPheLysAlaSerPheSerIle 205
Qy 667 AAGATACGAAGAGAGAGAGCATATTGCGACTATCCCAACATGCCAAAGGTTAAGACAATT 726
Db 206 LysIleArgArgGluProArgHisLeuAlaIleSerAsnMetProLeuValLysSerVal 225
Qy 727 GAACCTGAGAGAGCTTTTGGAGATCACCTTTCGAAACTACTGTAAAAAGTACATAC 786
Db 226 ThrValAlaGluGlyLeuIleGluAspHisPheAspValThrValLysMetSerThrTyr 245
Qy 787 CTTGTAGCCTACATAGTTGTGATTTCCACTCTCTGAGTGGCTTCACTTCATCAGGGGTC 846
Db 246 LeuValAlaPheIleIleSerAspPheGluSerValSerLysIleThrLysSerGlyVal 285
Qy 847 AAGGTGTCATATGATGCCAGACCCAGACAAACGGGAATCAACACATATTGCTTTGCAAGCA 906
Db 266 LysValSerValTyrAlaValProAspLysIleAsnGlnAlaAspTyrAlaLeuAspAla 285
Qy 907 TCACTGAAGTACTGATTTTATGAAGTACTTTGATCTACTATCTCACTCCACTCCAAA 966
Db 286 AlaValThrLeuLeuGluPheTyrGluAspTyrPheSerIleProTyrProLeuProLys 305
Qy 967 CTGGATTAAATTGCTATTCCTGACTTTGACCTGGAGCCATGGAATAATGGGGCTCATTT 1026
Db 306 GlnAspLeuAlaIleProAspPheGlnSerGlyAlaMetGluAsnTrpGlyLeuThr 325
Qy 1027 ACATATAGGAGAGCGTCACCTGCTTTTGGACCCCAAGACCTCTCTGCTTCGTAATAACTG 1086
Db 326 ThrTyrargGluSerAlaLeuLeuPheAspAlaGluLysSerSerAlaSerLysLeu 345
Qy 1087 TGGGTCCACGAGTCATAGCCCATGAACTGGCGCACAGTGGTGTGGCAACCTGGTCACA 1146
Db 346 GlyIleThrValThrValAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeuValThr 365
Qy 1147 ATGGAATGGTGGAAATGATATTGCTTAAAGAGGGTTTTCGAAATAACATGGAACTTATC 1206
Db 366 MetGluTrpTrpAsnAspLeuTrpLeuAsnGluGlyPheAlaLysPheMetGluPheVal 385
Qy 1207 GCTGTTAATGCTACATATCCAGAGCTGCAATTTGATGATCATTTTGTGAATGTGTGTTT 1266
Db 386 SerValSerValThrHisProGluLeuLysValGlyAspTyrPhePheGlyLysCysPhe 405
Qy 1267 GAAGTAATCAAAAGATTTCATTAATTCATCCCGCCTATCTCCAAACCCAGCGGAACC 1326
Db 406 AspAlaMetGluValAspAlaLeuAsnSerHisProValSerThrProValGluAsn 425
Qy 1327 CCGACTCAAAATACAGGAAATGTTTGATGAAGTTTTCCTATAAACAGGGAGCTGTGATTTTG 1386
Db 426 ProAlaGlnIleArgGluMetPheAspAspValSerTyrAspLysGlyAlaCysIleLeu 445
Qy 1387 AATATGCTCAAGGATTTTCTGGTGAGGAGAAATTCAGAAAGGAATAATTCAGTACTTA 1446
Db 446 AsnMetLeuArgGluTyrLeuSerAlaAspAlaPheLysSerGlyIleValGlnTyrLeu 465
Qy 1447 AAGNAGTTCAGTATAGAAATGCTAAGAATGATGACTTGTGGACGACTGTGCAATAGT 1506
Db 466 GlnLysHisSerTyrLysAsnThrLysAsnGluAspLeuTrpAspSerMetAlaSerIle 485

Qy 1507 TGTTTAGAAAGTGATTTTACATCTGGT-----GGAGTTTGTTCATTCGGATCCCAAGATG 1560
Db 486 Cys--ProThrAspGlyValLysGlyMetAspGlyPheCys---SerArgSerGlnHis 503
Qy 1561 ACAAGTAACATGCTCCGCTTTCTGGGGGAAAATGCAGAGGTCAAGAGATGATGACTACA 1620
Db 504 SerSerSerSerHisTrpHisGlnGluGlyValAspValLysThrMetMetAsnThr 523
Qy 1621 TGGACTCTCCAGAAAGGAATCCCCCTGCTGGTGTGTTAAACAAGACGGGTCTTCACCTCGA 1680
Db 524 TrpThrLeuGlnArgGlyPheProLeuIleThrIleThrValargGlyArgAsnValHis 543
Qy 1681 CTGCAACAGAGGCGTTCCTCCAGGGGTTTTCAGGAAGACCCCTCAATCGAGGCGCTG 1740
Db 544 MetLysGlnGluHisTyrMetLysGly-----SerAspGlyAlaPro 557
Qy 1741 CAGGAGAGTACTGTGGCATATCCCATTTGACCTACTCCACGAGTTCCTCTAATGTGATC 1800
Db 558 AspThrGlyTyrLeuTrpHisValProLeuThrPheIleThrSerLysSerAsnMetVal 577
Qy 1801 CACAGACACATCTTAAATCAAAGACAGACATCTCTGATCTACCTCGAAAGACCACTGG 1860
Db 578 HisArgPheLeuLeuLysThrLysThrAspValLeuLeuProGluGluValGluTrp 597
Qy 1861 GTGAAATTTAATGTGACTCAAATGGTTACTTACATCGTTCACTATCAGGGTTCATGGATGG 1920
Db 598 IleLysPheAsnValGlyMetAsnGlyTyrTyrIleValHisTyrGluAspAspGlyTrp 617
Qy 1921 GACCAACTCATATACACAGCTGAATCAGAACCAACACACTCTCTCAGACTTAAGGACAGAT 1980
Db 618 AspSerLeuThrGlyLeuLeuLysGlyThrHisThrAlaValSerSerAsnAspArgAla 637
Qy 1981 GGTCTCATTCATGATGTGTTTCAGCTAGTGGTGAGGGAGACTGACCTAGACAAAGCT 2040
Db 638 SerLeuIleAsnAsnAlaPheGlnLeuValSerIleGlyLysLeuSerIleGlyLysAla 657
Qy 2041 CTTGACATCACTTACTCTCCAAACATGAAACAGCAGCGCCGACACTCTCTGAAAGTCTG 2100
Db 658 LeuAspLeuSerLeuTyrLeuLysHisGluThrGluIleMetProValPheGlnGlyLeu 677
Qy 2101 AGTTACTTGGATCGTTTACCATGATGGAGAGAAATATTTTCAGATATCTCTGAA 2160
Db 678 AsnGluLeuIleProMetTyrLysLeuMetGluLysArgAspMetAsnGluValThr 697
Qy 2161 AACCTCAAGCGTTACCTCTTCAGTATTTTAAGCCAGTATTGACAGGCAAGCTCGAGT 2220
Db 698 GlnPheLysAlaPheLeuIleArgLeuLeuArgAspLeuIleAspLysGlnTrpThr 717
Qy 2221 GACAAGGCTCAGTCTGGGACAGGATGCTCCGCTCGGCTCTCTTGAAGCTGGCTGTGAC 2280
Db 718 AspGluGlySerValSerGluGlnMetLeuArgSerGluLeuLeuLeuAlaCysVal 737
Qy 2281 CTGAACCATGCTCTTGCATCCAGAAAGCTGCTGAATCTTCTCCAGTGGATGGAATCC 2340
Db 738 HisAsnTyrGlnProCysValGlnArgAlaGluGlyTyrPheArgLysTrpLysGluSer 757
Qy 2341 AGTGGAAAATTAATATACCAACAGATGTTTAAAGATTGTGTATCTCTGGGTGCTCAG 2400
Db 758 AsnGlyAsnLeuSerLeuProValAspValThrLeuAlaValPheAlaValGlyAlaGln 777
Qy 2401 ACAACAGCAGGATGGAATTACCTTTTAGAGCAATATGAATGTCTCAATGTCAAGTGTGAA 2460
Db 778 SerThrGluGlyTrpAspPheLeuTyrSerLysTyrGlnPheSerLeuSerSerThrGlu 797
Qy 2461 CAAAACAAAATTCGTATGCTTTGTCAACAGCAGCAGCATCAGGAAAGTTACTGAAATTA 2520
Db 798 LysSerGlnIleGluPheAlaLeuCysArgThrGlnAsnLysGluLysLeuGlnTrpLeu 817
Qy 2521 ATTGAACAGGAATGGAAGGAAAGTTATCAAGACACAGAACTTGGCAGCTCTCTTCAT 2580
Db 818 LeuAspGluSerPheLysGlyAspLysIleThrGlnGluPheProGlnIleLeuThr 837

QY 967 CTGGATTAAATTCCTGCTATTCGACCTTGCACCTCGAGCGCATGGAAAAATTTGGGCGCTCATTT 1026
Db 306 GlnAepLeuAlaAilaileProAepPheGlnSerGlyAlaMetGluAenTrpGlyLeuThr 325
QY 1027 ACATATAGGAGACGCTCACTGCTTTTTCACCCCAAGACCTCTTCCTGCTTCGATATAAATCG 1086
Db 326 ThrTyArgGluSerAlaLeuLeuPheAepAlaGluLysSerSerAlaSerSerLysLeu 345
QY 1087 TGGGTACACAGAGTCATACCCCATGAATTCAGTGGCGCACCAAGTGGTTGGCAACCTCGTCA 1146
Db 346 GlyIleThrValThrValAlaHisGluLeuAlaHisGlnTrpPheGlyAenLeuValThr 365
QY 1147 ATGGAATGGTGAATGATATTTGGCTTAAGAGGGTTTTGCAAAATACATACGAATTCATC 1206
Db 366 MetGluTrpTrpAenAepLeuTrpLeuAenGluGlyPheAlaLysPheMetGluPheVal 385
QY 1207 GCTGTTAATGCTACATATCCAGAGCTGCAATTTGTATGACTATTTTTCGAAATGCTGTTT 1266
Db 386 SerValSerValThrHisProGluLeuLysValGlyAepTyPhePheGlyLysCysPhe 405
QY 1267 GAAGTAATTTACAAAAGATTCATGAATTCATCCCGCCCTATCTCCAAACCCAGCGGAAC 1326
Db 406 AspAlaMetGluValAspAlaLeuAenSerSerHisProValSerThrProValGluAen 425
QY 1327 CCGACTCAATACAGAAATGTTTCATGAATTCATCCCGCCCTATCTCCAAACCCAGCGGAAC 1386
Db 426 ProAlaGlnIleArgGluMetPheAepAepValSerTyAepLysGlyAlaCysIleLeu 445
QY 1387 AATATGCTCAAGGATTTCTGGTGGAGGAGAAATTCAGAAAGGAATTAATTCAGTACTTA 1446
Db 446 AenMetLeuAaggluTyLysSerAlaAepAlaPheLysSerGlyIleValGlnTyLeu 465
QY 1447 AAGAAATTCAGCTATAGAAATCTAAGAAATGATGACTTGTGAGCAGTCTGTCAAATAGT 1506
Db 466 GlnLysHisSerTyLysAenThrLysAenGluAepLeuTrpAepSerMetAlaSerIle 485
QY 1507 TGTTTAGAAAGTATTTACATCTCGT-----GGAGTTTGTCTCGGATCCCAAGATG 1560
Db 486 Cys----ProThrAepGlyValLysGlyMetAepGlyPheCys--SerArgSerGlnHis 503
QY 1561 ACAAGTACATGCTCGCTCTTCGGGGGAAATGCAGAGGTCAAGAGATGATGACTACA 1620
Db 504 SerSerSerSerHisIleThrHisGlnGluGlyValAepValLysThrMetMetAenThr 523
QY 1621 TGGACTCTCCAGAAAGGAATCCCTGCTGTGGTTAAACAAGACGGGTTCCTACCTCGA 1680
Db 524 TrpThrLeuGlnArgGlyPheProLeuIleThrIleThrValArgGlyArgAenValHis 543
QY 1681 CTGCAACAGGAGCGCTTCTCCAGGGGGTTTTCCAGGAAGACCCCTGAATGGAGGGCCCTG 1740
Db 544 MetLysGlnGluHisTyMetLysGly-----SerAepGlyAlaPro 557
QY 1741 CAGGAGAGGTACCTGTGGCATATCCATTTGACCTACTCCAGAGTTCCTTAATGTGATC 1800
Db 558 AspThrGlyTyLeuTrpHisValProLeuThrPheIleThrSerLysSerAenMetVal 577
QY 1801 CACAGACATCTCTAAAATCAAGACAGATACCTCTGGATCTACCTCGAAAGACCAAGTGG 1860
Db 578 HisArgPheLeuLeuLysThrLysThrAepValLeuIleLeuProGluGluValGluTrp 597
QY 1861 GTGAAATTAATGTGGACTCAAAATGGTTACTACATCGTTTCACTATGAGGGTTCATGGATGG 1920
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QY 1921 GACCAACTCATTTACACAGCTGAATCAGAACACACACTTCTCAGACCTTAAGCACAGATA 1980
Db 618 AepSerLeuThrGlyLeuLysGlyThrHisThrAlaValSerSerAenAargAla 637
QY 1981 GGTCTGATTTCATGATGTTTTCAGCTAGTTGGTCAGGGAGACTGACCTAGACAAAGCT 2040
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QY 2041 CTTGACATGACTTACTCTCAACATGAACAGCAGCCCGCACCTTCTCGAAGGCTGTG 2100
Db 658 LeuAepLeuSerLeuTyLeuLysHisGlnThrGluLeuMetProValPheGlnGlyLeu 677
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QY 2581 GCGATTGCCAGACCTCCAAAGGGCAGCAACTACAGTGGGATTTTGTAAAGAGAAATGG 2640
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RESULT 14
US-09-989-731-353
; Sequence 353, Application US/09989731
; Patent No. US20020103125A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaud, J. Christopher

; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PLC70
; CURRENT APPLICATION NUMBER: US/09/989,731
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.: 1.24e-227 Length: 941
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Percent Similarity: 69.34% Conservative: 172
Best Local Similarity: 50.96% Mismatches: 268
Query Match: 49.63% Indels: 19
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US-10-039-073-3 (1-2883) x US-09-989-732-353 (1-941)

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Db 88 GlnProThrSerThrIleLeuHisSerHisHisLeuGlnIleSerArgAlaThrLeu 107

Qy 367 CAGTCAGGAGGATTCAGATACATGAACACGAGAAAGAACTGAAAGTTTCAGTTAC 426
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Db 108 ArgLysGlyAlaGlyGluArgLeuSerGlu-----GluProLeuGlnValLeuGluHis 125

Qy 427 CCTGCTCATGAACAAATGCACTGCTGCTCCAGAAACATTTACGCTCCTCACTGAAATAC 486
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Db 306 GlnAspLeuAlaAlaIleProAspPheGlnSerGlyAlaMetGluAseTnpGlyLeuThr 325

Qy 1027 ACATATAGGAGAGAGCTACCTGCTTTTGGACCCCAAGACCTCTTCTGCTTCCGATAAATCG 1086
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Qy 1267 GAAGTAATTAACAAAGATTCAATTCATCCCGCCTTATCTCCAAACCCAGCGGAAACC 1326
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Db 406 AspAlaMetGluValAspAlaLeuAsnSerSerHisProValSerThrProValGluAsn 425

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Db 426 ProAlaGlnIleArgGluMetPheAspAspValSerTyrAspLysGlyAlaCysIleLeu 445

Qy 1387 AATATCTCAAGGATTTTCTGGGTGAGGAGAAATTCAGAAAGGATTAATTCAGTACTTA 1446
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Db 446 AsnMetLeuArgGluTyrLeuSerAlaAspAlaPheLysSerGlyIleValGlnTyrLeu 465

Qy 1447 AAGAACTTCAGCTATAGAATGCTAAGATGATGACTTGTGGAGCAGTCTGTCAAAATAGT 1506
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Db 466 GlnLysHisSerTyrLysAsnThrLysAsnGluAspLeuTrpAspSerMetAlaSerIle 485

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Db 486 Cys---ProThrAspGlyValLysGlyMetAspGlyPheCys---SerArgSerGlnHis 503

Qy 1561 ACAGTAAACATGCTCCCTTTCTGGGGGAAATGACAGAGTCAAGAGATGATGACTACA 1620
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Qy 1621 TGGACTCTCCAGAAAGAAATCCCTGCTGGTGTGTTTAAACAGACGGGTGTTTCACTCCGA 1680
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Db 524 TrpThrLeuGlnArgGlyPheProLeuIleThrIleThrValArgGlyArgAsnValHis 543

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Qy 1861 GTGAAATTAATGTGAGCTCAATGTTACTACATCGTTCACTATGAGGGTTCATGATGG 1920
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Qy 1921 GACCAACTCATTACAGCTGAATCAGAACCCACACTTCTCAGACCTTAAGGACAGGTA 1980
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Db 618 AspSerLeuThrGlyLeuLeuLysGlyThrHisThrAlaValSerSerAsnAspAla 637

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Qy	2161	AACCTCAAGCGTTACCTCTTCTTCACTATTTTAAAGCCAGTGAATTGACAGGCAAGCTGGAGT	2220
Db	698	GlnPheLysAlaPheLeuIleArgLeuLeuArgAspLeuIleAspLysGlnThrTrpThr	717
Qy	2221	GACAAGGGCTCAGTCTGGGACAGATGCTCGCTCGGCTCTCTTGAAGCTGGCTGTGAC	2280
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Qy	2521	ATTCAACTAGGAATGGAAAGAAAGTTATCAAGACACAGAACTTGGCAGCTCTCCTTCAT	2580
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Qy	2701	ACACAGCTCACTTTCTTCCACGATAAGTTGCAAGAGGTGAACTATTTTGGATCT	2760
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Qy	2761	CTTCAGGCTCAAGGATCACATCTCGATATTTTCCAACTGTCTTCGGAACCGATAACCA	2820
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Job time : 463.314 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 26, 2005, 06:11:31 ; Search time 70.8178 Seconds
(without alignments)
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Searched: 513545 seqs, 74649064 residues

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	5052	99.8	960	3	US-09-345-650-1
2	2507.5	49.5	948	4	US-09-620-312D-1105
3	2027	40.0	1025	2	US-08-530-792D-23
4	2016.5	39.8	1026	2	US-08-530-792D-22
5	1444	28.5	957	4	US-09-949-016-6154
6	1440	28.4	964	4	US-09-949-016-7431
7	1264.5	25.0	967	3	US-09-139-802-201
8	1264.5	25.0	967	4	US-09-659-786-201
9	1225	24.2	919	4	US-09-919-039-222
10	1165	23.0	977	3	US-08-335-844A-22
11	1165	23.0	977	4	US-09-129-366-22
12	1117	22.1	972	3	US-08-335-844A-24

13	1117	22.1	972	4	US-09-129-366-24	Sequence 24, Appl
14	1100	21.7	972	3	US-08-335-844A-23	Sequence 23, Appl
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16	1083	21.4	699	4	US-09-270-767-45507	Sequence 45507, A
17	986	19.5	593	4	US-08-637-670-38	Sequence 38, Appl
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19	884	17.5	850	4	US-09-902-540-10199	Sequence 10199, A
20	868	17.1	990	4	US-09-657-931A-11	Sequence 11, Appl
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22	863	17.0	995	4	US-09-657-931A-1	Sequence 1, Appl
23	844	16.7	815	4	US-09-107-433-5059	Sequence 5059, Ap
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37	477.5	9.4	346	4	US-08-637-670-24	Sequence 24, Appl
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39	460.5	9.1	359	4	US-08-637-670-37	Sequence 37, Appl
40	459	9.1	350	4	US-08-637-670-39	Sequence 39, Appl
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42	440	8.7	680	4	US-09-902-540-11278	Sequence 11278, A
43	392.5	7.8	867	4	US-09-602-777A-104	Sequence 104, App
44	379.5	7.5	242	4	US-09-248-796A-18160	Sequence 18160, A
45	364.5	7.2	380	4	US-09-270-767-44186	Sequence 44186, A

ALIGNMENTS

RESULT 1
US-09-345-650-1
; Sequence 1, Application US/09345650
; Patent No. 6362324
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: 17867, A No. 6362324e1 Human Amino acid
; FILE REFERENCE: 5800-36
; CURRENT APPLICATION NUMBER: US/09/345,650
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 960
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-345-650-1

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Best Local Similarity: 100.00%
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US-10-039-073-3 (1-2883) x US-09-345-650-1 (1-960)

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QY 1447 AAGAAGTTCAGCTATAGAATCTGAAGATCATGACTTGTGGAGCACTGTGCAATAGT 1506
Db 466 GlnLysHisSerTyrLysAsnThrLysAsnGluAspLeuTrpAspSerMetAlaSerIle 485
QY 1507 TGTTTAGAAAGTATTTACATCTGGT-----GGAGTTTGTCTATCCGATCCCAAGATG 1560
Db 486 Cys---ProThrAspGlyValLysGlyMetAspGlyPheCys---SerArgSerGlnHis 503
QY 1561 ACAAGTAACATGCTCGCTCTTGGGGGAAATTCAGAGGTCAAAGAGATGATGACTACA 1620
Db 504 SerSerSerSerHisTrpHisGlnGluGlyValAspValLysThrMetMetAsnThr 523
QY 1621 TGGACTCTCAGAAAGAAATCCCTCTGCTGTGTTAAACAAGCGGTGTTCACTCCGA 1680
Db 524 TrpThrLeuGlnArgGlyPheProLeuIleThrIleThrValArgGlyArgAsnValHis 543
QY 1681 CTGCAACAGGAGCGCTTCCTCCAGGGGTTTTCAGGAAGACCTGATGGAGGCCCTG 1740
Db 544 MetLysGlnGluHisTyrMetLysGly-----SerAspGlyAlaPro 557
QY 1741 CAGGAGAGGTACCTGTGGCATATCCCATATGACCTATCCACGAGTTCTTCTAATGTGATC 1800
Db 558 AspThrGlyTyrLeuTrpHisValProLeuThrPheIleThrSerLysSerAspMetVal 577
QY 1801 CACGACACATTTCAAAATCAAGACAGATCTCTGGATCTACTGAAAGACAGGTGG 1860
Db 578 HisArgPheLeuLysThrLysThrAspValLeuIleLeuProGluGluValGluTrp 597
QY 1861 GTGAAATTTAATGGACTCAATGGTTACTACATCGTTCACTATGAGGTCATGATGG 1920
Db 598 IleLysPheAsnValGlyMetAsnGlyTyrTyrIleValHisTyrGluAspAspGlyTrp 617
QY 1921 GACCAACTATTACACAGCTGAATCAGAACCCACACTTCTCAGACCTTAAGGACAGGTA 1980
Db 618 AspSerLeuThrGlyLeuLeuLysGlyThrHisThrAlaValSerSerAsnAspArgAla 637
QY 1981 GGCTCTGATTCATGATGTTTACGCTAGTGGTCAGGAGAGCTGACCTTAGACAAAGCT 2040
Db 638 SerLeuIleAsnAsnAlaPheGlnLeuValSerIleGlyLysLeuSerIleGluLysAla 657

QY 2041 CTTGACATGACTTACTACCTCCAAACATGAAACAAGCAGCCCGCCTTCTCGAAGGTCTG 2100
Db 658 LeuAspLeuSerLeuTyrLeuLysHisGluThrGluIleMetProValPheGlnGlyLeu 677
QY 2101 AGTTACTTGGAAATCGTTTTTACCACATGATGACAGAGGAATATTTTCAGATATCTCTGAA 2160
Db 678 AsnGluLeuIleProMetTyrLysLeuMetGluLysArgAspMetAsnGluValGluThr 697
QY 2161 AACCTCAAGGTTACCTTCTTCAGTATTTTAAGCCAGTATGTCACAGGCAAGCTGAGT 2220
Db 698 GlnPheLysAlaPheLeuIleArgLeuLeuArgAspLeuIleAspLysGlnThrTrpThr 717
QY 2221 GACCAAGGCTCAGCTCGGACAGAGTCCCGCTCGGCTCTCTTGAAGCTGGCTGTGAC 2280
Db 718 AspGluGlySerValSerGluGlnMetLeuArgSerGluLeuLeuLeuLeuAlaCysVal 737
QY 2281 CTGAACCATGCTCTCTTGCATCCAGAAAGCTGTCTGAACTCTCTCCAGCTGGATGGAATCC 2340
Db 738 HisAsnTyrGlnProCysValGlnArgAlaGluGlyTyrPheArgLysTrpLysGluSer 757
QY 2341 AGTGGAAATTAATATACACAGATGTTTAAAGATTGTGTATCTGTGGTGTCTCAG 2400
Db 758 AsnGlyAsnLeuSerLeuProValAspValThrLeuAlaValPheAlaValGlyAlaGln 777
QY 2401 ACAACAGCAGGATGGAATTAACCTTTTAGAGCAATATGAACTGTCAATGTCAAGTCTGAA 2460
Db 778 SerThrGluGlyTrpAspPheLeuTyrSerLysTyrGlnPheSerLeuSerSerThrGlu 797
QY 2461 CAAACAAAAATTTCTGTATGCTTTGTCAACGAGCAAGCATCAGGAAAGTTTACTGAAAGTTA 2520
Db 798 LysSerGlnIleGluPheAlaLeuCysArgThrGlnAsnLysGluLysLeuGlnTrpLeu 817
QY 2521 ATTGAACATAGGAATGGAAGAAAGTTATCAAGACACAGAACTTGGCAGCTCTCTTCAT 2580
Db 818 LeuAspGluSerPheLysGlyAspLysIleLysThrGlnGluPheProGlnIleLeuThr 837
QY 2581 GCATTGTCAGAGCTCCAAAGGGGAGCAACTAGCATGGATTTTCTAGAGAAAATTTGG 2640
Db 838 LeuIleGlyArgAsnProValGlyTyrProLeuAlaTrpGlnPheLeuArgLysAsnTrp 857
QY 2641 ACCATCTTCTGAAAAAATTTGACTTTGGCTCATATGACATAGGATGATCATCTCTGCG 2700
Db 858 AsnLysLeuValGlnLysPheGluLeuGlySerSerSerIleAlaHisMetValMetGly 877
QY 2701 ACAACAGCTCACTTTTCTCCAGGATAAGTTGCAAGAGGTGAACTATTTTGAATCT 2760
Db 878 ThrThrAsnGlnPheSerThrArgThrArgLeuGluValLysGlyPhePheSerSer 897
QY 2761 CTTGAGGCTCAAGGATCACATCTGGATATTTTCAAACCTGTTCTGGAACGATAACCAA 2820
Db 898 LeuLysGluAsnGlySerGlnLeuArgCysValGlnThrIleGlnThrIleGluGlu 917
QY 2821 AATATAAATGGCTGGAGAAGAATTTCCGACTCTGAGGACTTGGCTA 2868
Db 918 AsnIleGlyTrpMetAspLysAsnPheAspLysIleArgValTrpLeu 933

RESULT 3

US-08-530-792D-23
; Sequence 23, Application US/08530792D
; Patent No. 5972680
; GENERAL INFORMATION:
; APPLICANT: Knowles, W. J.; Guraleski, D.; Haigh, W.; Letsinger, J. T.;
; APPLICANT: Clairmont, K.; and Hart, J.
; TITLE OF INVENTION: Glucose Transporter Vesicle Amino-peptidase
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bayer Corporation
; STREET: 400 Morgan Lane
; CITY: West Haven
; STATE: Connecticut
; COUNTRY: U.S.A.
; ZIP: 06516

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" diskette, 1.44 Mb Storage

COMPUTER: Dell Windows 95 PC

OPERATING SYSTEM: Windows 95

SOFTWARE: WordPerfect for Windows 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US-08/530,792D

FILING DATE: 09/19/95

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/309,232

FILING DATE: 09/20/94

ATTORNEY/AGENT INFORMATION:

NAME: Brewer, Alice A.

REGISTRATION NUMBER: 32888

REFERENCE/DOCKET NUMBER: MWH 323P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (203) 812-2705

TELEFAX: (203) 812-5492

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 1025 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein;

ORIGINAL SOURCE:

ORGANISM: Rattus norvegicus

STRAIN: Sprague-Dawley

DEVELOPMENTAL STAGE: adult

TISSUE TYPE: skeletal muscle

IMMEDIATE SOURCE:

LIBRARY: Clontech rat skeletal muscle cDNA library in lambda

LIBRARY: gtl1 and mRNA isolated from rat skeletal muscle

CLONE: 12.1 (from lambda gtl1 library), PCR product clones 5,

CLONE: 334, and KC44.

FEATURES:

NAME/KEY: complete amino acid sequence for GTvap, long version

IDENTIFICATION METHOD: translation from cDNA

US-530-792D-23

Alignment Scores:

No.:	Length:	Matches:
2,576-194	1025	402
2027,00		Conservative: 158
Local Similarity:		Mismatches: 310
Indels:		Gaps: 5
Match:		

US-039-073-3 (1-2883) x US-08-530-792D-23 (1-1025)

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150 CCAGTAGGACCAATATGGGAACGATTCTTGTGGAGGAGCTAAGGCTCCCGAGTGTC 219
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
153 ProfileAlaThrAsnGlyValPheProTrpAlaGlnIleArgLeuProThraIaile 172
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
220 ATTCTCTCCATTATGACTCTTTGTGCACCCCAATCTCACCTCTCTGGACTTTGTGCA 279
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
173 IleProGlnArgTyrgluSerLeuHisProAsnLeuThrSerMetThrPheArggly 192
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
280 TCTGAGAAGATCGAAGTCTGTGTGACGAATGCTACCAGTTTATCATCTTTCGACAGCAA 339
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
193 SerValThrIleSerLeuGlnAlaLeuGlnAsePThrArgAspIleIleLeuHisSerThr 212
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
340 GATCTTGAATCACAAGATGCCACCTTTCAGTCAGAGGAGATTCAAGATACATGAACCA 399
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
213 GlyHisAsnIleSerValThrPheMetSerAlaValSerGln----- 228
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
400 GGAAAGAACTGAAAGTTTGTAGTTTACCTGCTCATGAACAAATGCACTGCTGTGTCCA 459
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
229 GluLysGlnValGluIleLeuGluTyrrProTyrrHisGluGlnIleAlaValAlaPro 248
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
460 GAGAAACCTTACGCCTCACCTGAAATTAATATGTGGCTATGTGGCTTCCAAAGCCCAAGTTAGT 519
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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QY	1120	CACAGTGGTTGGCAACCTGGTCACAATGAATGTTGGNAATCATATTGGCTTAAGGAG	117
Db	468	HISGLNTRPPhEGlyAsnLeuValThrMetGLNtrPrAsnAaspLeuTrpIeuAenGIU	487
QY	1180	GGTITTGCAAAATAATCAGGAACATTATCGCTGTTTAATGCTACATATCCAGAGCTGC	123
Db	488	GlyPheAlaThrPheMetGLUTyrPheSerValGLULysILEphElysGLIUleuAenSer	507
QY	1240	GATGACTATTTTTGAATGTGTGTTTTGAAGTAATTTACAAGAATTCATTGAATTCATCC	129
Db	508	TyrGLAaspPheLeuAapAlaArgPheLYeThrMetArgLysAaspSerLeuAenSerSer	527
QY	1300	CGCCCTATCTCCAACACAGCGGAAACCCCAGACTCAAATACAGAAAATGTTTGAATGAAGTT	135
Db	528	HISProIIeSerSerSerValGLINserSerGluGLINleuGLUMetPheAepSerLeu	547
QY	1360	TCCTATAACAGGAGGCTTGTTATTTGAATATGCTCAAGGATTTTCTGGTGAGGAGAA	141
Db	548	SerTyrPheLysGLyAlaSerLeuLeuLeuMetLeuLysSerTyrZeuSerGluAapVal	567
QY	1420	TTCCAGAAAGGAATAATTCAGTACTTAAAGAAGTTCCAGCTPATAGAANAATGCTAAGAATGAT	147
Db	568	PheGLNHISAlaIElleLeuTyRLeuHISasnHISerTyRAlaAlaILEGLINserAap	587
QY	1480	GACTTGTGGAGCAGCTGCTCAAATAGTTGTTTAGAAGTGATTTTACATCTGCTGGAGTT	153
Db	588	AapLeuIrrPaspSerPheAenGLU-----	595
QY	1540	TGTCATTCGGATCCCAAGATGACAAGTAACATGCTGCCCTTTTCTGGGGAAAAATGCAGAG	159
Db	596	-----ValThrGLyLysThrLeuAap	602

Alignment Scores:

Pred. No.: 2,928-193 Length: 1026
 Score: 2016.50 Matches: 402
 Percent Similarity: 61.74% Conservative: 158
 Best Local Similarity: 44.32% Mismatches: 310
 Query Match: 39.84% Indels: 37
 DB: 2 Gaps: 6

US-10-039-073-3 (1-2883) x US-08-530-7920-22 (1-1026)

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Qy 160 CCAGTAGCCACTAATGGGGAACGATTTCTTGGCAGAGCTAAGCTCCCGAGTGTGTC 219
Db 153 ProilealaThrAsnGlyValPheProTrpAlaGlnIleArgLeuProThraIaIle 172

Qy 220 ATTCTCTCCATTATGACTCTTTGTCCACCCCAATCTCAGCTCTCTGGACTTTGTGCA 279
Db 173 IleProGlnArgTyrrGluLeuSerLeuHisProAlaLeuThrSerMetThrPheArgGly 192

Qy 280 TCTGAGAGATCGAAGTCTTGGTCAGCAATGCTACCCAGTTTATCATCTTCACAGCAAA 339
Db 193 SerValThrIleSerLeuGlnAlaLeuGlnAspThrArgAspIleIleLeuHisSerThr 212

Qy 340 GATCTTGAATCACCAGATGCCACCTTCAGTCAGAGGAAGATTCAAGATACATGAAACCA 399
Db 213 GlyHisAsnIleSerSerValThrPheMetSerAlaValSerSerGln----- 228

Qy 400 GGAAGAAGTGAAGTTTGGATTACCTCTCATGAACAATTTGCACTCTCTGTTCCA 459
Db 229 GluLysGlnValGluIleLeuGluTyrrProTyrrHisGluGlnIleAlaValAlaPro 248

Qy 460 GAGAACTTACGCTCCTCAGTGAATATGCTGCTATGGCTATGGACTTCCAGCCCAAGTTAGGT 519
Db 249 GluSerLeuLeuThrGlyHisAsnTyrrThrLeuLysIleGluTyrrSerAlaAsnIleSer 268

Qy 520 GATGCTTTGAAGGGTTTATAAAAGCACATACAGAACTCTTGGTGGTGAACAAGAAATT 579
Db 269 AsnSerTyrrGlyPheTyrrGlyLeuThrTyrrAspLysSerAsnGluLysIleAsn 288

Qy 580 CTTCAGTAAACAGATTTTGAAGCAACCCAGCAGCATGGCTTTCCCTTGTCTGTGATGAA 639
Db 289 PheAlaAlaThrGlnPheGluProLeuAlaAlaArgSerAlaPheProCysPheAspGlu 308

Qy 640 CCGTGTTCAGGCACTTTTCAATCAAGATACGAGAGAGAGAGAGAGCATATTGCACTA 699
Db 309 ProAlaPheLysAlaThrPheIleLysIleThrArgAspGluHisThrAlaLeu 328

Qy 700 TCCAACTGTCAGAGTTTAAAGCAATTCGAACCTTGAAGGAGTCTTTTGGAGAGTCACTTT 759
Db 329 SerAsnMetProLysLysSerSerValProThrGluGluGlyLeuIleGlnAspGluPhe 348

Qy 760 GAAACTACTGTAAATAGTACATACCTTTGAGCTACATAGTTTGTGATTTCCACTCT 819
Db 349 SerGluSerValLysMetSerThrTyrrLeuValAlaPheIleValGlyGluMetArgAsn 368

Qy 820 CTGAGTGGCTTCACTTCAATCAGGGGTCAAGGTGTCATCTATGATCCCAAGCAAAAGG 879
Db 369 LeuSerGln---AspValAsnGlyThrLeuValSerValTyrrAlaValProGluLysIle 387

Qy 880 AATCAACACATATGCTTTCAGGCATCATCTGAAGCTACTTGTATTTTATGAAAGTAC 939
Db 388 AspGlnValTyrrHisAlaLeuAspThrTyrrValLysLeuLeuGluPheTyrrGlnAsnTyrr 407

Qy 940 TTTGATATCTACTATCCACTCTCCAACTGGATTTAATGTCTATTTCTCTGACTTTGACCT 999
Db 408 PheGluIleGlnTyrrProLeuLysLysLeuAspLeuValAlaIleProAspPheGluAla 427

Qy 1000 GGAGCCATGGAAATTTGGGGCTCTATTACATATAGGGAGAGCTCAGCTGCTTTTGACCCC 1059
Db 428 GlyAlaMetGluAsnTrpGlyLeuLeuThrPheArgGluGluThrLeuLeuTyrrAspAsn 447

Qy 1060 AAGACCTCTTCTGCTTCCGATAACTGGGTGCTCAGAGTTCATAGCCCATGACTGGCG 1119
Db 448 AlaThrSerSerValAlaAspArgLysLeuValThrLysIleIleAlaHisGluLeuAla 467
  
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Qy 1120 CACCACTGGTTTGGCAACCTGGTGCACAAATGGAATGGTGAATGATATTTGGCTTAAGGAG 1179
Db 468 HisGlnTrpPheGlyAsnLeuValThrMetGlnTrpTrpAsnAspLeuLeuTrpLeuAsnGlu 487

Qy 1180 GGTTCCTCAAAATACATGGAACCTTATCGCTGTTAATGCTACATATCCAGAGCTGCAATTT 1239
Db 488 GlyPheAlaThrPheMetGluTyrrPheSerValGluLysIlePheLysGluLeuAsnSer 507

Qy 1240 GATGACTATTTTGAATGTGTGTTTGAAGTAAATACAAAAGATTTCATTTGAATTCATCC 1299
Db 508 TyrGluAspPheLeuAspAlaArgPheLysThrMetArgLysAspSerLeuAsnSerSer 527

Qy 1300 CGCCTATCTCCAAACAGCGGAAACCCGACTCAATATACAGAAATTTGTTGATGAAGTT 1359
Db 528 HisProIleSerSerSerValGlnSerSerGluGlnIleGluGluMetPheAspSerLeu 547

Qy 1360 TCCTATAACAAG--GGAGCTTGTATTTTGAATATGCTCAAGGATTTTCTGGGTGAGGAG 1416
Db 548 SerTyrrPheLysGlnGlyAlaSerLeuLeuLeuMetLeuLysSerTyrrLeuSerGluAsp 567

Qy 1417 AAATTCAGAAAGGAATAATTCACTTAAAGAAAGTTTCAGCTATAGAAATGCTAAGAAAT 1476
Db 568 ValPheGlnHisAlaIleIleLeuTyrrLeuHisAsnHisSerTyrrAlaAlaIleGlnSer 587

Qy 1477 GATGACTTGTGGAGCAGCTCTGTCAAATGATGTTGTTTGAAGATGATTTTACATCTGGTGA 1536
Db 588 AspAspLeuTrpAspSerPheAsnGlu----- 596

Qy 1537 GTTGTGCTTCGGATCCCAAGATCAACAAGTAAACATGCTCGCTTCTGGGGGAAAAATGCA 1596
Db 597 -----ValThrGlyLysThrLeu 602

Qy 1597 GAGTCAAGAGATGATGACTACATGAGCTCTCCAGAAAGAAATCCCGCTGCTGCTGTT 1656
Db 603 AspValLysLysMetMetLysThrTrpThrLeuGlnLysGlyPheProLeuValThrVal 622

Qy 1657 AAACAAGACGGGTGTTTCACTCCGACTGCAACAGAGAGCGCTTCTCCAGGGGGTTTTCCAG 1716
Db 623 GlnArgLysGlyThrGluLeuLeuGlnGlnGlnArgPhePheProSerMet----- 640

Qy 1717 GAAGACCTCAATCGAGGGCCCTCCAGAGAGGTACCTGGGCATATCCCATTCACCTAC 1776
Db 641 ---GlnProGluIleGlnAspSerAspThrSerHisLeuTrpHisIleProIleSerTyrr 659

Qy 1777 TCCACAGAGTTCTTCTAATGTGATCCACAGACAC-----ATTCTAAATCAAGACAC 1827
Db 660 ValThrAspGlyArgAsnTyrrSerGluTyrrArgSerValSerLeuLeuAspLysLysSer 679

Qy 1828 GATACCTCGATCTACCTGAAAGACCAAGTGGGTGAAATTTAATGTGGACTCAATGTT 1887
Db 680 AspValIleAsnLeuThrGluGlnValGlnTrpValLysValAsnThrAsnMetThrGly 699

Qy 1888 TACTACATCTTCACTATGAGGTGTCATGGAGCCCACTCATTTACAGCTCAATGATCAG 1947
Db 700 TyrrTyrrIleValHisTyrrAlaHisAspGlyTrpAlaAlaLeuIleAsnGlnLeuLysArg 719

Qy 1948 AACACACACACTTCTCAGACCTAAGGACAGAGTAGGTCTGATGATGATGTTTTCAGCTA 2007
Db 720 AsnProTyrrValLeuSerAspLysAspArgAlaAsnLeuLeuAsnAsnIlePheGluLeu 739

Qy 2008 GTTGGTGCAGGAGAGTCCCTTAGACAAAGCTCTTGCATAGCTTTACTACTCTCAACAT 2067
Db 740 AlaGlyLeuGlyLysValProLeuGlnMetAlaPheAspLeuIleAspTyrrLeuArgAsn 759

Qy 2068 GAAACAGACAGCCCGCACTTCTCGAGGTCGTGATGTTTGGATCGTTTGGATCCCATG 2127
Db 760 GluThrHisThrAlaProIleThrGluAlaLeuPheGlnThrAspLeuIleTyrrAsnLeu 779

Qy 2128 ATGACAGAGGAAGTAATTTTCAGATATCTCTGAAACCTCAAGCGTTACCTTCTTCTCAGTAT 2187
Db 780 LeuGluLysLeuGlyHisMetAspLeuSerSerArgLeuValThrArgValHisLysLeu 799
  
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Qy 2188 TTTAAGCCAGTGATTGACAGCAAGCTGAGTGACAAAGGGCTCAGTCTGGGACAGGATG 2247
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
800 LeuGlnAsnGlnIleGlnGlnThrTrpThrAspGluGlyThrProSerMetArgGlu 819
Qy 2248 CTCGGCTCGGCTCTCTTGAAGCTGGCTGTGACCTGAACCATGCTCTTCATCCAGAAA 2307
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
820 LeuArgSerAlaLeuLeuGluPheAlaCysAlaHisSerLeuGluAsnCysThrThrMet 839
Qy 2308 GCTGCTCAACTCTCTCCAGTGAGTGAATCCAGTGGAAAAATTAAATATACCAACAGAT 2367
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
840 AlaThrLysLeuPheAspGlyTrpMetAlaSerAsnGlyThrGlnSerLeuProThrAsp 859
Qy 2368 GTTTTAAAGATTGTGTAATCTGTGGGTCTCAGACACAGCAGGATGAATTAACCTTTTA 2427
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
860 ValMetThrThrValPheLysValGlyAlaArgThrGluLysGlyTrpLeuPheLysPhe 879
Qy 2428 GAGCAATATGAACTGTCAATGTCAAGTCTGAAGTCTGAACAAACAAAATTCGTATGCTGTCA 2487
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
880 SerMetTyrSerSerMetGlySerGluAlaGluLysAspLysIleLeuGluAlaLeuAla 899
Qy 2488 ACGAGCAAGCATCAGGAAAAAGTTACTGAAGTTAATTCGAATAGGAAGGAAAGGTT 2547
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
900 SerSerAlaAspAlaHisLysLeuTyrTrpLeuMetLysSerSerLeuAspGlyAspIle 919
Qy 2548 ATCAAGACACAGAACTTGGCAGCTCTCTTCATCGGATTCGCCAGACGTCCAAAAGGGCAG 2607
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
920 IleArgThrGlnLysLeuSerLeuIleileArgThrValGlyArgGlnPheProGlyHis 939
Qy 2608 CAACTACATGGGATTTTGAAGAAAAATTTGGACCCATCTTCGAAAAAATTTGACTTG 2667
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
940 LeuLeuAlaTrpAspPheValLysGluAsnTrpAsnLysLeuValHisLysPheHisLeu 959
Qy 2668 GGCTCATATGACATAAGGATGATCATCTCTGGCACAAACACTCACTTTTCTTCCAGGAT 2727
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
960 GlySerTyrThrIleGlnSerIleValIleGlySerThrHisLeuPheSerThrLysThr 979
Qy 2728 AAGTTGCAAGAGGTGAACATAATTTTTGAATCTCTTGGAGCTCAAGGATCACATCTGGAT 2787
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
980 HisLeuSerGluValGlnGluPhePheGluAsnGlnSerGluAlaThrLeuGlnLeuArg 999
Qy 2788 ATTTTCAAACCTGTTGGAACAGATAACCAAAAATATAAAATGCGTGGAGAGAATCTT 2847
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
1000 CysValGlnGluAlaPheGluValIleGluLeuAsnIleGlnTrpMetAlaArgAsnLeu 1019
Qy 2848 CCGACTCTGAGGACTTCGCTA 2868
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
1020 LysThrLeuThrLeuTrpLeu 1026
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RESULT 5

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US-09-949-016-6154
; Sequence 6154, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6154
; LENGTH: 957
; TYPE: PR1
; ORGANISM: Human
US-09-949-016-6154
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Alignment Scores: 9.45e-136 Length: 957
Pred. No.: 1444.00 Matches: 323
Score: 53.07% Conservative: 178
Percent Similarity: 34.22% Mismatches: 361
Best Local Similarity: 28.53% Indels: 82
Query Match: 4 Gaps: 19
DB: 19

US-10-039-073-3 (1-2883) x US-09-949-016-6154 (1-957)

Qy 118 GTGCCATCTAGTATATCACTCTCAGTGGGCTTTCCAGTA----- 155
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
60 LeuProSerSer-----ThrAlaSerProSerGlyProProAlaGlnAspGlnAsp 76
Qy 166 -----GCCACTAATCGGGAACGATTCTTGGCAGGAGCTAAGGCTCCCGAGTGTG 216
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
77 IleCysProAlaSerGluAspGluSerGlyGlnTrpLysAsnPheArgLeuProAspPhe 96
Qy 217 GTCATTCTCTCCATTTATGACCTCTTTGTCCACCCTCCTCACCTCTCTGGACTTTGTT 276
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
97 ValAsnProValHisTyrAspLeuHisValLysProLeuLeuGluAspThrTyrThr 116
Qy 277 GCATCTGAGAAGATCGAAGTCTTGGTCAGCAATGCTACCAGTTTATCATCTTGCACAGC 336
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
117 GlyThrValSerIleSerIleAsnLeuSerAlaProThrArgTyrLeuTrpLeuHisLeu 136
Qy 337 AAAGATCTTGAATATCAAGAAATGCCACCTTCAGTCAGAGGAAGATTCAAGATACATGAA 396
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
137 ArgGluThrArgIleThrArgLeu-----ProGluLeuLysArg 149
Qy 397 CCA-----GGAAGAAAGAACTGAAAGTT-----TTGAGTTTACCTCTCATGAACAAAT 444
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
150 ProSerGlyAspGlnValGlnValArgCysPheGluTyrLysLysGlnGluTyrVal 169
Qy 445 GCATCTCTGGTCCAGAGAACTTACGCTCCTACCTG-----AAATCATATGTGGCT 495
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
170 ValValGluAlaGluGluLeuThrProSerSerGlyAspGlyLeuTyrLeuLeuThr 189
Qy 496 ATGGACTCTCCAAAGCCAAAGTTAGTGATGCTTTGAAGGGTTTTATAAAGACACATACAGA 555
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
190 MetGluPheAlaGlyTrpLeuAsnGlySerLeuValGlyPheTyrArgThrTyr--- 208
Qy 556 ACTCTTGGTGGTGAACAACAAGAAATTTCTGCAGTAACAGATTTTGGAGCAACCCAGGACGC 615
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
209 ThrGluAsnGlyArgValLysSerIleAlaAlaThrAspHisGluProThrAspAlaArg 228
Qy 616 ATGGCTTTCCCTGCTTTCATGAACCGTTGTTCAAGCCCAACTTTTCAATCAAGATACGA 675
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
229 LysSerPheProCysPheAspGluProAsnLysLysAlaThrTyrThrIleSerIleThr 248
Qy 676 AGAGAGAGCAGGCATATTGCACATATCCAAATGCCAAAGGTTAAGACAATTGAACCTTGA 735
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
249 HisProLysGluTyrGlyAlaLeuSerAsnMetProValAlaLysGluSerValAsp 268
Qy 736 GGAGGTCTTTTGAAGATCACTTTGAAACTACTGTAATAAATGAGTACATACCTTTGTAGCC 795
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
269 AspLysTrpThrArgThrThrPheGluLysSerValProMetSerThrTyrLeuValCys 288
Qy 796 TACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCATCATCAGGGGTCAAGGTGTC 855
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
289 PheAlaValHisGlnPheAspSerValLysArgIleSerAsnSerGlyLysProLeuThr 308
Qy 856 ATCTATGCATCCCGACACAAACGGATCAACACATATTATGCTTTGCGAGCATCCTGTAAG 915
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
309 IleTyrValGlnProGluGlnLysHisThrAlaGluTyrAlaAlaAsnIleThrLysSer 328
Qy 916 CTACTTGTATTTTATGAAAGTACTTTTGATCTACTACTCTCCAACTCTCCAACTGATTTA 975
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
329 ValPheAspTyrPheGluGluTyrPheAlaMetAsnTyrSerLeuProLysLeuAspLys 348
Qy 976 ATTGCTATTCTCGACTTTCACCTGAGCCATCGGAAATTTGGGGCTCTATTACATATAGG 1035
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
349 IleAlaIleProAspPheGlyThrGlyAlaMetGluAsnTrpGlyLeuIleThrTyrArg 368
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; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7431
; LENGTH: 964
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7431

Alignment Scores:
Pred. No.:      2.39e-135      Length:      964
Score:          1440.00      Matches:      322
Percent Similarity: 52.97%      Conservative: 178
Best Local Similarity: 34.11%      Mismatches: 362
Query Match:      28.45%      Indels:      82
DB:              4          Gaps:      19

US-10-039-073-3 (1-2883) x US-09-949-016-7431 (1-964)

QY 118 GTGCCATCTAGTTATCATCTTCACTGAGGATCCTCGGGCTTCCAGTA----- 165
DB 118 GTGCCATCTAGTTATCATCTTCACTGAGGATCCTCGGGCTTCCAGTA----- 165
QY 166 -----GCCACTAATGGGAACGATTCCTTGGCAGGAGCTAAGCTCCCGAGTGTG 216
DB 166 -----GCCACTAATGGGAACGATTCCTTGGCAGGAGCTAAGCTCCCGAGTGTG 216
QY 84 IleCysProAlaSerGluAspGluSerGlyGlnTrpLysAsnPheArgLeuProAspPhe 103
DB 84 IleCysProAlaSerGluAspGluSerGlyGlnTrpLysAsnPheArgLeuProAspPhe 103
QY 217 GTCATCTCTCCATTATGACCTCTTGTCCACCCCAATCTCACCTCTCTGGACTTTGTT 276
DB 217 GTCATCTCTCCATTATGACCTCTTGTCCACCCCAATCTCACCTCTCTGGACTTTGTT 276
QY 104 ValAsnProValHisTrpAspLeuHisValLysProLeuLeuGluAspThrTyrThr 123
DB 104 ValAsnProValHisTrpAspLeuHisValLysProLeuLeuGluAspThrTyrThr 123
QY 277 GCATCTGAGAAGATCGAAGTCTTGGTCAGCAATGCTACCCAGTTTATCATCTTCACAGC 336
DB 277 GCATCTGAGAAGATCGAAGTCTTGGTCAGCAATGCTACCCAGTTTATCATCTTCACAGC 336
QY 124 GlyThrValSerIleSerIleAsnLeuSerAlaProThrArgTyrLeuTrpLeuHisLeu 143
DB 124 GlyThrValSerIleSerIleAsnLeuSerAlaProThrArgTyrLeuTrpLeuHisLeu 143
QY 337 AAGATCTTGAATCAGCAATGCCACCTTCAGTCAGAGGAAGATTCAGATCATGAAGA 396
DB 337 AAGATCTTGAATCAGCAATGCCACCTTCAGTCAGAGGAAGATTCAGATCATGAAGA 396
QY 144 ArgGluThrArgIleThrArgLeu-----ProGluLeuLysArg 156
DB 144 ArgGluThrArgIleThrArgLeu-----ProGluLeuLysArg 156
QY 397 CCA---CGAAGAAGCTGAAGTT-----TTGAGTTACCTGCTCATGACAATTT 444
DB 397 CCA---CGAAGAAGCTGAAGTT-----TTGAGTTACCTGCTCATGACAATTT 444
QY 157 ProSerGlyAspGlnValGlnValArgArgCysPheGluTyrLysLysGlnGluTyrVal 176
DB 157 ProSerGlyAspGlnValGlnValArgArgCysPheGluTyrLysLysGlnGluTyrVal 176
QY 445 GCATCTGGTTCAGAGAACTTACCGCTCACCTG-----AAATACTATGTGGCT 495
DB 445 GCATCTGGTTCAGAGAACTTACCGCTCACCTG-----AAATACTATGTGGCT 495
QY 177 ValValGluAlaGluGluLeuThrProSerSerGlyAspGlyLeuTyrLeuLeuThr 196
DB 177 ValValGluAlaGluGluLeuThrProSerSerGlyAspGlyLeuTyrLeuLeuThr 196
QY 496 ATGCACTCCAGCAAGTTAGTGATGGCTTTGAAGGGTTTATAAAGCACATACAGA 555
DB 496 ATGCACTCCAGCAAGTTAGTGATGGCTTTGAAGGGTTTATAAAGCACATACAGA 555
QY 197 MetGluPheAlaGlyTrpLeuAsnGlySerLeuValGlyPheTyrArgThrThrTyr--- 215
DB 197 MetGluPheAlaGlyTrpLeuAsnGlySerLeuValGlyPheTyrArgThrThrTyr--- 215
QY 556 ACTCTTGGTGTGAACACAGAAATCTTGCAGTAACAGATTTTGAGCCAAACCCAGGCACGC 615
DB 556 ACTCTTGGTGTGAACACAGAAATCTTGCAGTAACAGATTTTGAGCCAAACCCAGGCACGC 615
QY 216 ThrGluAsnGlyArgValLysSerIleValAlaThrAspHisGluProThrAspAlaArg 235
DB 216 ThrGluAsnGlyArgValLysSerIleValAlaThrAspHisGluProThrAspAlaArg 235
QY 616 ATGGCTTTCCCTTCTGTTGATGAACCGTTGTTCAAGCCCAACTTTTCAATCAAGATACGA 675
DB 616 ATGGCTTTCCCTTCTGTTGATGAACCGTTGTTCAAGCCCAACTTTTCAATCAAGATACGA 675
QY 236 LysSerPheProCysPheAspGluProAsnLysLysAlaThrTyrThrIleSerIleThr 255
DB 236 LysSerPheProCysPheAspGluProAsnLysLysAlaThrTyrThrIleSerIleThr 255
QY 676 AGAGAGAGCGGCATATTGCATATCAACATGCCAAAGGTTTAAGACAATTTGAACCTGAA 735
DB 676 AGAGAGAGCGGCATATTGCATATCAACATGCCAAAGGTTTAAGACAATTTGAACCTGAA 735
QY 256 HisProLysGluTyrGlyAlaLeuSerAsnMetProValAlaLysGluGluSerValAsp 275
DB 256 HisProLysGluTyrGlyAlaLeuSerAsnMetProValAlaLysGluGluSerValAsp 275
QY 736 GGAGGTCTTTGGAGATCACTTTGAACACTGTAAATATGATACATACCTTTGTAGCC 795
DB 736 GGAGGTCTTTGGAGATCACTTTGAACACTGTAAATATGATACATACCTTTGTAGCC 795
QY 276 AspLysTrpThrArgThrThrPheGluLysSerValProMetSerThrTyrLeuValCys 295
DB 276 AspLysTrpThrArgThrThrPheGluLysSerValProMetSerThrTyrLeuValCys 295
QY 796 TACATAGTTTGTGATTTCCACTCTCTCGAGTGGCTTCACTTCATCAGGGGTCAAGGGTGC 855
DB 796 TACATAGTTTGTGATTTCCACTCTCTCGAGTGGCTTCACTTCATCAGGGGTCAAGGGTGC 855
QY 296 PheAlaValHisGlnPheAspSerValLysArgIleSerAsnSerGlyLysProLeuThr 315
DB 296 PheAlaValHisGlnPheAspSerValLysArgIleSerAsnSerGlyLysProLeuThr 315
QY 856 ATCTATGCATCCCGACACAACGGAATCAACACATTTATGCTTTGCGGCGATCCTGAAG 915
DB 856 ATCTATGCATCCCGACACAACGGAATCAACACATTTATGCTTTGCGGCGATCCTGAAG 915
QY 316 IleTyrValGlnProGluGlnLysHisThrAlaGluTyrAlaAlaAsnIleThrLysSer 335
DB 316 IleTyrValGlnProGluGlnLysHisThrAlaGluTyrAlaAlaAsnIleThrLysSer 335
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QY 916 CTACTTGTATTTTATGAAAGTACTTTTGATATCTACTATCTCACTCTCCAAACTGGATTTA 975
DB 916 CTACTTGTATTTTATGAAAGTACTTTTGATATCTACTATCTCACTCTCCAAACTGGATTTA 975
QY 336 ValPheAspTyrPheGluGlyPheAlaMetAsnTyrSerLeuProLysLeuAspLys 355
DB 336 ValPheAspTyrPheGluGlyPheAlaMetAsnTyrSerLeuProLysLeuAspLys 355
QY 976 ATTGCTATTCTCGACTTTGCACCTGGAGCCATCGAAATTTGGGGCCTCATATCATAGG 1035
DB 976 ATTGCTATTCTCGACTTTGCACCTGGAGCCATCGAAATTTGGGGCCTCATATCATAGG 1035
QY 356 IleAlaIleProAspPheGlyThrGlyAlaMetGluAsnTrpGlyLeuIleThrTyrArg 375
DB 356 IleAlaIleProAspPheGlyThrGlyAlaMetGluAsnTrpGlyLeuIleThrTyrArg 375
QY 1036 GAGACGTCACTGCTTTTTCACCCCAAGACCTCTTCTGCTTCCGATAAACTGGGTCACC 1095
DB 1036 GAGACGTCACTGCTTTTTCACCCCAAGACCTCTTCTGCTTCCGATAAACTGGGTCACC 1095
QY 376 GluThrAsnLeuLeuTyrAspProLysGluSerAlaSerAsnGlnGlnArgValAla 395
DB 376 GluThrAsnLeuLeuTyrAspProLysGluSerAlaSerAsnGlnGlnArgValAla 395
QY 1096 AGAGTCATAGCCCATGAACTGGCGCACCTGCTTTGGCAACTCTGTCTACAATGGAATGG 1155
DB 1096 AGAGTCATAGCCCATGAACTGGCGCACCTGCTTTGGCAACTCTGTCTACAATGGAATGG 1155
QY 396 ThrValValAlaHisGluLeuValHisGlnTrpPheGlyAsnIleValThrMetAspTrp 415
DB 396 ThrValValAlaHisGluLeuValHisGlnTrpPheGlyAsnIleValThrMetAspTrp 415
QY 1156 TGGAAATGATATTGCTTAAGGAGGCTTTTGCAAAATATCATGGAACCTTATCGCTGTTAAT 1215
DB 1156 TGGAAATGATATTGCTTAAGGAGGCTTTTGCAAAATATCATGGAACCTTATCGCTGTTAAT 1215
QY 416 TrpGluAspLeuTrpLeuAsnGluGlyPheAlaSerPhePheGluPheLeuGlyValAsn 435
DB 416 TrpGluAspLeuTrpLeuAsnGluGlyPheAlaSerPhePheGluPheLeuGlyValAsn 435
QY 1216 GCTACATATCCAGAGCTGCAATTT---GATGACTATTTTTCGATGTGTTTTGAAGTA 1272
DB 1216 GCTACATATCCAGAGCTGCAATTT---GATGACTATTTTTCGATGTGTTTTGAAGTA 1272
QY 436 HisAlaGluThrAspTrpGlnMetArgAspGlnMetLeuLeuGluAspValLeuProVal 455
DB 436 HisAlaGluThrAspTrpGlnMetArgAspGlnMetLeuLeuGluAspValLeuProVal 455
QY 1273 ATTACAAAAGATTCATTGAATTCATCCCGCTCTATCTCCAAACCGCGAAACCCCGACT 1332
DB 1273 ATTACAAAAGATTCATTGAATTCATCCCGCTCTATCTCCAAACCGCGAAACCCCGACT 1332
QY 456 GlnGluAspAspSerLeuMetSerSerHisPheIleValThrValThrThrProAsp 475
DB 456 GlnGluAspAspSerLeuMetSerSerHisPheIleValThrValThrThrProAsp 475
QY 1333 CAAATACAGGAATGTTTGTATGAAGTTTCTCTATAACAAGGAGCTTGTATTTTGAATATG 1392
DB 1333 CAAATACAGGAATGTTTGTATGAAGTTTCTCTATAACAAGGAGCTTGTATTTTGAATATG 1392
QY 476 GluIleThrSerValPheAspGlyIleSerTyrSerLysGlySerSerIleLeuArgMet 495
DB 476 GluIleThrSerValPheAspGlyIleSerTyrSerLysGlySerSerIleLeuArgMet 495
QY 1393 CTCAGGATTTTCTGGGTGAGGAGAAATTCAGAAAGGAATTAATTCAGTACTTTAAAGAG 1452
DB 1393 CTCAGGATTTTCTGGGTGAGGAGAAATTCAGAAAGGAATTAATTCAGTACTTTAAAGAG 1452
QY 496 LeuGluAspTrpIleLysProGluAsnPheGlnLysGlyCysGlnMetTyrLeuGluLys 515
DB 496 LeuGluAspTrpIleLysProGluAsnPheGlnLysGlyCysGlnMetTyrLeuGluLys 515
QY 1453 TTCAGCTATAGAAATGCTAAGAATGATGCTTGTGTGAGCAGCTGTGCAAAATAGTTGTTA 1512
DB 1453 TTCAGCTATAGAAATGCTAAGAATGATGCTTGTGTGAGCAGCTGTGCAAAATAGTTGTTA 1512
QY 516 TyrGlnPheLysAsnAlaLysThrSerAspPheTrpAlaAlaLeuGluAla----- 533
DB 516 TyrGlnPheLysAsnAlaLysThrSerAspPheTrpAlaAlaLeuGluAla----- 533
QY 1513 GAAAGTGATTTTACATCTCGTGGAGTTTGTTCATTCGGATCCCAAGATGACAAGTAAATG 1572
DB 1513 GAAAGTGATTTTACATCTCGTGGAGTTTGTTCATTCGGATCCCAAGATGACAAGTAAATG 1572
QY 533 ----- 533
DB 533 ----- 533
QY 1573 CTCGCCCTTCTGGGGGAAAATGCAGAGTCAAGAGATGATGACTACATGAGCTCTCCAG 1632
DB 1573 CTCGCCCTTCTGGGGGAAAATGCAGAGTCAAGAGATGATGACTACATGAGCTCTCCAG 1632
QY 534 -----SerArgLeuProValLysGluValMetAspThrTrpThrArgGln 548
DB 534 -----SerArgLeuProValLysGluValMetAspThrTrpThrArgGln 548
QY 1633 AAAGGAATCCCTCTGCTGGTGTAAACAAGACGGGTGTTCACTCCGACTGCAACAGGAG 1692
DB 1633 AAAGGAATCCCTCTGCTGGTGTAAACAAGACGGGTGTTCACTCCGACTGCAACAGGAG 1692
QY 549 MetGlyTyrProValLeuAsnVal-----AsnGlyValLys---AsnIleThrGlnLys 565
DB 549 MetGlyTyrProValLeuAsnVal-----AsnGlyValLys---AsnIleThrGlnLys 565
QY 1693 CGCTTCTCCAGGGGGTTTTCCAGGAAGACCTGTAATGAGGGCCCTGCAGGAG----- 1746
DB 1693 CGCTTCTCCAGGGGGTTTTCCAGGAAGACCTGTAATGAGGGCCCTGCAGGAG----- 1746
QY 566 ArgPheLeuLeu-----AspProArgAlaAsnProSerGlnProProSer 580
DB 566 ArgPheLeuLeu-----AspProArgAlaAsnProSerGlnProProSer 580
QY 1747 -----AGTACTGTGGCATATCCCATTTGACCTAC-----TCCAGAGTTCTTCT 1791
DB 1747 -----AGTACTGTGGCATATCCCATTTGACCTAC-----TCCAGAGTTCTTCT 1791
QY 581 AspLeuGlyTyrThrTrpAsnIleProValLysTrpThrGluAspAsnIleThrSerSer 600
DB 581 AspLeuGlyTyrThrTrpAsnIleProValLysTrpThrGluAspAsnIleThrSerSer 600
QY 1792 AATGTCTCCACACACACATCTTAAATCAAGACAGATACCTGTGATCTCTCTGAGAAAG 1851
DB 1792 AATGTCTCCACACACACATCTTAAATCAAGACAGATACCTGTGATCTCTCTGAGAAAG 1851
QY 601 ValLeuPheAsnArgSerGluLysGluGlyIleThrLeuAsnSerSerAsnProSerGly 620
DB 601 ValLeuPheAsnArgSerGluLysGluGlyIleThrLeuAsnSerSerAsnProSerGly 620
QY 1852 ACCAGTTGGGTGAAATTTAATGTGGACTCAAAATGGTTACTACATCTTCACTATGAGGT 1911
DB 1852 ACCAGTTGGGTGAAATTTAATGTGGACTCAAAATGGTTACTACATCTTCACTATGAGGT 1911
QY 621 AsnAlaPheLeuLysIleAsnProAspHisIleGlyPheTyrArgValAsnTyrGluVal 640
DB 621 AsnAlaPheLeuLysIleAsnProAspHisIleGlyPheTyrArgValAsnTyrGluVal 640
QY 1912 CATGGATGGGACCACTATTACACAGCTGAATCAGAACCCACACACTTCTCAGACCTAAG 1971
DB 1912 CATGGATGGGACCACTATTACACAGCTGAATCAGAACCCACACACTTCTCAGACCTAAG 1971
QY 641 AlaThrTrpAspSerIleAlaThrAlaLeuSerLeuAsnHisLysThrPheSerSerAla 660
DB 641 AlaThrTrpAspSerIleAlaThrAlaLeuSerLeuAsnHisLysThrPheSerSerAla 660
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Qy	1330	ACTCAAAATACAGGAATGTTTGATGAAGTTTCTCTATAACAAGGAGGAGCTTGATTTTGAAT	1389
Db	466	AlaGlnIleSerGluLeuPheAspAlaIleSerTyrSerLysGlyAlaSerValLeuArg	485
Qy	1390	ATGCTCAAGGATTTTCTGGGTGAGGAGAAATCCAGAAAGCAATAATTCAGTACTCTAAAG	1449
Db	486	MetLeuSerSerPheLeuSerGluAspValPheLysGlnGlyLeuAlaSerTyrLeuHis	505
Qy	1450	AAGTTCAGCTATCAAAATGCTTAAGAATCATGACTTGTGGAGCAGCTCTG-----	1497
Db	506	ThrPheAlaTyrGlnAsnThrIleTyrLeuAsnLeuTrpAspHisLeuGlnGluAlaVal	525
Qy	1498	TCAAAATAGTTGTTTAGAAAGATGATTTTACATCTCGTGGAGTTTGCTCATTCGGATCCCAAG	1557
Db	526	AsnAsnArgSerIleGlnLeuProThrThr-----	535
Qy	1558	ATGACNAGTAACATGCTCGCTTCTCGGGGAAAAATGCAGAGGTCAAAGAGATCATGACT	1617
Db	536	-----ValArgAspIleMetAsn	541
Qy	1618	ACATGGACTCTCCAGAAAGGAATCCCCTGCTGGTGGTATAACAAGACGGGTGTTCTACTC	1677
Db	542	ArgTrpThrLeuGlnMetGlyPheProValIleThrVal-----AspThrSerThrGly	559
Qy	1678	CGACTCAACACAGGACGGCTTCTCCAGGGGGTTTTCCAGGAAGACCTGAA-----	1728
Db	560	ThrLeuSerGlnGluHisPheLeuLeu-----AspProAspSerAsnVal	574
Qy	1729	TGGAGGGCCCTGCAGGAGAGGTACTGTGGCATATCCCATTTGACC-----	1773
Db	575	ThrArgProSerGluPheAsnTyrValTrpIleValProIleThrSerIleArgAspGly	594
Qy	1774	-----TACTCCACG	1782
Db	595	ArgGlnGlnGlnAspTyrTrpLeuIleAspValArgAlaGlnAsnAspLeuPheSerThr	614
Qy	1783	AGTTCTTCTAATGTGATCCACAGACACATCTTAAAAATCAAAGACAGATATCTTGGATCTA	1842
Db	615	SerGlyAsn-----	617
Qy	1843	CCTGAAAGACCACTTGGTGGAAATTTAATGTGGACTCAAATGGTTACTACATCGTTCAAC	1902
Db	618	-----GluTrpValLeuLeuAsnLeuAsnValThrGlyTyrTyrArgValAsn	633
Qy	1903	TATGAGGTCATGATCGGACCAACTCATATACACAGCTGAATCAGAACCACACACTTCTC	1962
Db	634	TyrAspGluGluAsnTrpArgLysIleGlnThrGlnLeuGlnArgAspHisSerAlaIle	653
Qy	1963	AGACCTAAGGACAGAGTAGGTCTGATTCATGATGTTTTCAGCTAGTTGGTCGAGGAGAGA	2022
Db	654	ProValIleAsnArgAlaGlnIleAsnAspAlaPheAsnLeuAlaSerAlaHisLys	673
Qy	2023	CTGACCTTAGCAAAAGCTTTGACATGACTTACTACCTCCAAATGAAACAGACGAGCCCC	2082
Db	674	ValProValThrLeuAlaLeuAsnAsnThrLeuPheLeuIleGluGluArgGlnTyrMet	693
Qy	2083	GCACCTCTCGAAGCTCTGAGTTACTTCGAATCGTTTACCACATGATGGACAGAGGAAT	2142
Db	694	ProTrpGluAlaAlaLeuSerSerLeuSerTyrPheLysLeuMetPheAspArg-----	711
Qy	2143	ATTTTCAGATATCTCTGAAAACCTCAAGCGTTTACCTCTTTCAGTATTTTAAAGCCAGTGATT	2202
Db	712	--SerGluValTyrGlyProMetLysAsnTyrLeuLysLysGlnValThrProLeuPhe	730
Qy	2203	-----GACAGCAAAAGCTGGAGTGCAC-----AAGGCTCTGAGTCTGGGACAGG	2244
Db	731	IleHisPheArgAsnAsnThrAsnAsnTrpArgGluIleProGluAsnLeuMetAspGln	750
Qy	2245	ATGCTCCGCTCGGCTCTCTTGAAGCTGGCTGTGACCTGGAACCATGCTCTTCGATCCAG	2304
Db	751	TyrSerGluValAsnAlaIleSerThrAlaCysSerAsnGlyValProGluCysGluGlu	770
Qy	2305	AAAGCTGCTGAACCTCTTCTCCAGCTGGATGGAATCCAGTGGAAAATTAATATATACCAACA	2364

Db	771	MetValSerGlyLeuPheLysGlnTrpMetGluAsnProAsnAsnAsnProIleHisPro	790
Qy	2365	GATCTTTTAAAGATTGTGTAT-----TCTGTGGTGCTCAGACAACAGCAGGATGGAAT	2418
Db	791	AsnLeuArgSerThrValTyrCysAsnAlaIleAlaGlnGlyGlyGluGluTrpAsp	810
Qy	2419	TACCTTTTAGACAAATATGAACCTGTCAATGTCAAGTGTGAACAAACAAAAATCTGTAT	2478
Db	811	PheAlaTrpGluGlnPheArgAsnAlaThrLeuValAsnGluAlaAspLysLeuArgAla	830
Qy	2479	GCITTTGTCAAGCAGCAGCATCAGGAAGATTACTGAAGTTAATTGAATAGCTAGGAATGGAA	2538
Db	831	AlaLeuAlaCysSerLysGluLeuTrpIleLeuAsnArgTyrLeuSerTyrThrLeuAsn	850
Qy	2539	GGAAAGGTATCAAGACACAGAAGCTTGGCAGCTCTCTCTCATCGGATTGGCAGACGTCCA	2598
Db	851	ProAspLeuIleArgLysGlnAspAlaThrSerThrIleIleSerIleThrAsnAsnVal	870
Qy	2599	AAGGGGAGCAACTAGCATCGGATTTTGTGAAGAGAAATTTGGACCCATCTTCTGAAAAA	2658
Db	871	IleGlyGlnGlyLeuValTyrAspPheValGlnSerAsnTrpLysLysLeuPheAsnAsp	890
Qy	2659	TTTGACTTGGGTCATATGACATAAGGATGATCATCTCTGGCACACAGCTCCTTTCT	2718
Db	891	TyrGlyGlySerPheSerPheSerAsnLeuIleGlnAlaValThrArgArgPheSer	910
Qy	2719	TCCAAGGATAGTTGCAAGAGGTGMAACTATTTTTTGAATCTCTTGAGGCTCAA-----	2772
Db	911	ThrGlyTyrGluLeuGlnGlnLeuGlnPheLysAspAsnGluThrGlyPhe	930
Qy	2773	GGATCACATCTGGATATTTTTTCAAACCTGTCTCGAAACGATAACCAAAAATATAAATGG	2832
Db	931	GlySerGlyThrArgAlaLeuGluGlnAlaLeuGluLysThrLysAlaAsnIleLysTrp	950
Qy	2833	CTGGAGAAGAACTTCCGACTCTGAGACTTGGCTAATGGTTTAACT	2880
Db	951	VallysGluAsnLysGluValValLeuGlnTrpPheThrGluAsnSer	966
RESULT 9			
US-09-919-039-222			
; Sequence 222, Application US/09919039			
; Patent No. 6727066			
; GENERAL INFORMATION:			
; APPLICANT: Kaser, Matthew R.			
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES			
; FILE REFERENCE: PA-0035 US			
; CURRENT APPLICATION NUMBER: US/09/919,039			
; CURRENT FILING DATE: 2002-09-09			
; PRIOR APPLICATION NUMBER: 60/222,113			
; PRIOR FILING DATE: 2000-07-28			
; NUMBER OF SEQ ID NOS: 401			
; SOFTWARE: PERL Program			
; SEQ ID NO 222			
; LENGTH: 919			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: misc_feature			
; OTHER INFORMATION: Incyte ID No. 6727066 2278688CD1			
US-09-919-039-222			
Alignment Scores:			
Pred. No.:	9	36e-114	Length: 919
Score:	1225.00	Matches:	309
Percent Similarity:	49.74%	Conservative:	163
Best Local Similarity:	32.56%	Mismatches:	351
Query Match:	24.20%	Indels:	126
DB:	4	Gaps:	26
US-10-039-073-3 (1-2883) x US-09-919-039-222 (1-919)			
Qy	163	GTAGCCCAATATGGGGACGATTCTCTTGGCAGGAGCTAAGGCTCCACAGTGGTGCTATT	222


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QY 2260 CTCTTGAAGCTGGCCTGTGACCTGAACCATGCTCTTCATCCAGAAAGCTGCTGAATC 2319
Db :|||
709 ValLeuGlyLysLeuGlyLysAlaGlyHisLysAlaThrLeuGluGluAlaArgArg 728
QY 2320 TTCTCCAGTGGATGGAATCCAGTGGAAATTAATAATATACCAAGATGTTTAAAGATT 2379
Db :|||
729 PheLysAspHisValGlu-----GlyLysGlnLeuSerAlaAspLeuArgSerPro 746
QY 2380 GTGTATTCTGTG-----GGTGCTCAGACACAGCAGGATGGAATTACCTTTTA 2427
Db :|||
747 ValTyrLeuThrValLeuLysHisGlyAspGlyThrThrLeu-----AspIleMetLeu 764
QY 2428 GAGCAATATGAATGTCATCAAGTCTGAACAAACAAAATTCGTATGCTTTTGTCA 2487
Db :|||
765 LysLeuHisLysGlnAlaAspMetGlnGluGlyLysAsnArgIleGluArgValLeuGly 784
QY 2488 ACGAGCAAGCATCAGGAAAGTTACTGAAGTTAATGAATAGGAATGGAAGGAAGTT 2547
Db :|||
785 AlaThrLeuLeuProAspLeuIleGlnLysValLeuThrPheAlaLeuSerGluGluVal 804
QY 2548 ATCAAGACACAGACTTGGCAGCTCTCTTCATCGGATTGCCAGACGTCCTCAAG--GGG 2604
Db :|||
805 ---ArgProGlnAspThrValSerValIleGlyValAlaGlyGlySerLysHisGly 823
QY 2605 CAGCAACTAGCATGGGATTTGTAAAGAGAAATTTGGACCCCATCTTCTCAAAAATTTGAC 2664
Db :|||
824 ArgLysAlaAlaTrpLysPheIleLysAspAsnTrpGluGluLeuTyrAsnArgTyrGln 843
QY 2665 TTGGGCTCATATGACATAAGGATGATCATCTCTGGCACACAGCTCACTTTCTTCCAA 2724
Db :|||
844 ---GlyGlyPheLeuIleSerArgLeuIleLysLeuSerValGluGlyPheAlaValAsp 862
QY 2725 GATAAGTTGCAAGAGTGAACATAATTTTCAATCTCTTGAGGCTCAAGGATCATCTG 2784
Db :|||
863 LysMetAlaGlyGluValLysAlaPhePheGlnSerHisProAlaProSerAlaGluArg 882
QY 2785 GATATTTTCAAACTGTTCTGGAACGATAACCAACAAAATATATAATGCTGGAGAAAG 2844
Db :|||
883 ThrIle---GlnGlnCysCysGluAsnIleLeuLeuAsnAlaAlaTrpLeuLysArgAsp 901
QY 2845 CTTCGCACTCGAGGACTTGGCTAATG 2871
Db :|||
902 AlaGluSerIleHisGlnTyrLeuLeu 910

RESULT 10
US-08-335-844A-22
; Sequence 22, Application US/08335844A
; Patent No. 6066503
; GENERAL INFORMATION:
; APPLICANT: GRAHAM, MARGARET
; APPLICANT: SMITH, TREVOR STANLEY
; APPLICANT: MUNN, EDWARD ALBERT
; APPLICANT: KNOX, DAVID PATRICK
; APPLICANT: OLIVER, JOANNA JANE
; APPLICANT: NEWTON, SUSAN ELIZABETH
; TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING
; TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE PREPARATION OF
; TITLE OF INVENTION: VACCINES AGAINST HELMINTH INFECTIONS
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz
; STREET: Suite 701-E, 555 Thirteenth St., N.W
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/335,844A
; FILING DATE: 09-JAN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB PCT/GB93/00943
; FILING DATE: 06-MAY-1993
; APPLICATION DATA:
; APPLICATION NUMBER: GB 9209936
; FILING DATE: 08-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: WALKER, Barbara W.
; REGISTRATION NUMBER: 35,400
; REFERENCE/DOCKET NUMBER: 1181-223A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)783-6040
; TELEFAX: (202)783-6031
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 977 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-335-844A-22

Alignment Scores:
Pred. No.: 1,04e-107 Length: 977
Score: 1165.00 Matches: 280
Percent Similarity: 49.22% Conservative: 192
Best Local Similarity: 29.20% Mismatches: 411
Query Match: 23.01% Indels: 76
DB: 3 Gaps: 21

US-10-039-073-3 (1-2883) x US-08-335-844A-22 (1-977)

QY 115 TCAGTGCCTCTAGTATTATCATCTTCACT-----GAGGAT 147
Db :|||
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QY 148 CTGGGGCTTTCCAGCTAGCCACTAATGGGAACGATTTCTTGGCAGGAGCTAAGGCTC 207
Db :|||
61 LysGlyAspGlnProIleValAspAsnSerProSerAla---GluGluLeuArgLeu 79
QY 208 CCAGTGTGGTCANTCTCTCCATTATGACCTTTGTTCAC-----CCCAATCTC 258
Db :|||
80 ProThrThrIleLysProLeuThrTyrAspLeuValIleLysThrTyrLeuProAsnTyr 99
QY 259 ACCTCTCTG-----GACTTT-----GTTGCATCTGAG 285
Db :|||
100 ValAsnTyrProProGluLysAspPheAlaIleAspGlyThrValValIleAlaMetGlu 119
QY 286 AAGATCGAAGTCTTGGTCAGCAATGCTACCCAGTTTATCATCTTGCACAGCAAGATCTT 345
Db :|||
120 ValValGlu-----ProThrLysSerIleValLeuAsnSerLysAsnIle 134
QY 346 GAAATCACAAGATCCCACTTCCAGTCCAGGAGAGATCAAGATACATGAACACCGAGAAA 405
Db :|||
135 ProVal-----IleAlaAspGlnCysGluLeuPheSerAsnAsnGlnLysLeuAspIle 152
QY 406 GAAGTGAAGTTTGTAGTTACCTGCTCATGACAAATTCACATGCTGCTGGTTCAGAGAAA 465
Db :|||
153 Glu---LysValValAspGlnProArgLeuGluLysValGluPheValLeuLysLysLys 171
QY 466 CTTACGCTCACCTGAAATACTATGTGGTCTATGGATCTTCCAGCCCAAGTTAGTGTGGC 525
Db :|||
172 LeuGluLysAsnGlnLysIleThrLeuLysIleValTyrIleGlyLeuIleAsnAspMet 191
QY 526 TTTGAAGGGTTTATAAAGCACATACAGAACTCTTGGTGGTGAAACAGAAATCTTGCA 585
Db :|||
192 LeuGlyGlyLeuTyrArgThrThrTyrThrAspLysAspGlyThrThrLysIleAlaAla 211
QY 586 GTAAACAGATTTTGAGCCACCCAGGACCGATGGCTTCCCTTGTGATGAACCGCTTG 645
Db :|||
212 CysThrHisMetGluProThrAspAlaArgLeuMetValProCysPheAspGluProThr 231
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Db 931 LeuLysAsnLeuTyrLysAsn---AspLysArgAlaArgGluTyrGlyAlaPheGlyGly 949
Qy 2800 GTTCTGGAACGATAACCAAAATATAAATGGCTGGAGAGATCTTCCGACTCTG 2856
Db 950 AlaileGluArgSerGluHisArgValLysTrpIleGluLysHisPheArgLysLeu 968
RESULT 11
US-09-129-366-22
; Sequence 22, Application US/09129366
; Patent No. 6534638
; GENERAL INFORMATION:
; APPLICANT: GRAHAM, MARGARET
; APPLICANT: SMITH, TREVOR STANLEY
; APPLICANT: MUNN, EDWARD ALBERT
; APPLICANT: KNOX, DAVID PATRICK
; APPLICANT: OLIVER, JOANNA JANE
; APPLICANT: NEWTON, SUSAN ELIZABETH
; TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING
; TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE PREPARATION OF
; TITLE OF INVENTION: VACCINES AGAINST HELMINTH INFECTIONS
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz
; STREET: Suite 701-E, 555 Thirteenth St., N.W
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/129,366
; FILING DATE: 05-AUG-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/335,844
; FILING DATE: 09-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB PCT/GB93/00943
; FILING DATE: 06-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9209936
; FILING DATE: 08-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, Barbara G.
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1181-241A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)783-6040
; TELEFAX: (202)783-6031
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 977 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-129-366-22
Alignment Scores:
Pred. No.: 1,04e-107 Length: 977
Score: 1165.00 Matches: 280
Percent Similarity: 49.22% Conservative: 192
Best Local Similarity: 29.20% Mismatches: 411
Query Match: 23.01% Indels: 76
DB: 4 Gaps: 21
US-10-039-073-3 (1-2883) x US-09-129-366-22 (1-977)
Qy 115 TCAGTGCATCTAGTATTATCACTTCACT-----GAGGAT 147

Db 41 SerIleGlyLeuThrTyrTyrPheThrArgLysAlaPheAspThrThrGlyGlyAsnGly 60
Qy 148 CTTGGGGCTTTCCAGTAGCCACTAATGGGAACGATTTCTTGGGAGGAGCTTAAGGCTC 207
Db 61 LysGlyAspGlnProIleValAspAspAsnSerProSerAla---GluGluLeuArgLeu 79
Qy 208 CCCAGTGTGGTCATTCCTCTCCATTATGACCTCTCTTGTCCAC-----CCCAATCTC 258
Db 80 ProThrThrIleLysProLeuThrTyrAspLeuValIleLysThrTyrLeuProAsnTyr 99
Qy 259 ACCTCTCTG-----GACTTT-----GTTGCATCTGAG 285
Db 100 ValAsnTyrProProGluLysAspPheAlaIleAspGlyThrValValIleAlaMetGlu 119
Qy 286 AAGATCGAAGTCTTGGTCAGCAATGCTACCCAGTTTATCATCTTGCACAGCAAGATCTT 345
Db 120 valValGlu-----ProThrLysSerIleValLeuAsnSerLysAsnIle 134
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Qy 406 GAACTGAAAGTTTGTAGTTACCTGCTCATGAACAAATTCCACTGCTGTTCCAGAGAAA 465
Db 153 Glu---LysValValAspGlnProArgLeuGluLysValGluPheValLeuLysLys 171
Qy 466 CTTACGCTCACCTGAAATACTATGTGGCTATGCTGCTTCCAGCCCAAGTAGGTGGC 525
Db 172 LeuGluLysAsnGlnLysIleThrLeuLysIleValTyrIleGlyLeuIleAsnAspMet 191
Qy 526 TTTGAAAGGGTTTATAAAGCACATACAGAACTCTTGGTGGTGAACAAAGAATTTCTTGA 585
Db 192 LeuGlyGlyLeuTyrArgThrThrTyrThrAspLysAspGlyThrLysIleAlaAla 211
Qy 586 GTAACAGATTTTGAGCAACCCAGGACGCGATGGCTTCCCTTGTGTTGATGACCGTTG 645
Db 212 CysThrHisMetGluProThrAspAlaArgLeuMetValProCysPheAspGluProThr 231
Qy 646 TTCAAAGCCCAACTTTTCAATCAAGATACGAAGAGAGAGAGGAGGCATATTGCACTATCAAC 705
Db 232 PheLysAlaAsnTrpThrValThrValIleHisProLysGlyThrSerAlaValSerAsn 251
Qy 706 ATGCCAAAGGTTAAGACAATTTGAACCTTGAAGAGGCTTTTGGGAAGATCACTTTGAAACT 765
Db 252 GlyIleGluLysGlyGluGlyGluValSerGlyAspTrpValThrThrArgPheAspPro 271
Qy 766 ACTGTAAATAGTAGTACATACCTTGTAGCCTACATAGTTTGTGATTTCCACTCTCTGAGT 825
Db 272 ThrProArgMetProSerTyrLeuIleAlaLeuValIleSerGluPheLysTyrIleGlu 291
Qy 826 GGCTTCACTTCATCAGGGGTCAAAGGTGTCATCTATGCATCCCGACACAAACCGAATCAA 885
Db 292 AsnTyrThrLysSerGlyValArgPheArgIleProAlaArgProGluAlaMetLysMet 311
Qy 886 ACACATTATGCTTTGACAGGCATCATGAAGCTACTTGAATTTTATGAAAAGTACTTTGAT 945
Db 312 ThrGluTyrAlaMetIleAlaGlyIleLysCysLeuAspTyrTyrGluAspPheGly 331
Qy 946 ATCTACTATCCACTCTCCAAACTGGATTAAATTGCTATTCTCTGACTTTGACCTGGAGCC 1005
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Db 352 MetGluAsnTrpGlyLeuIleThrTyrArgGluGlySerValLeuTyrAspGluAsnLeu 371
Qy 1066 TCTTCTGCTTCCGATAAACTGTGGGTCAACAGAGTCAAGCCCATGAACTGAGCCACAG 1125
Db 372 TyrGlyProMetAsnLysGluArgValAlaGluValIleAlaHisGluLeuAlaHisGln 391
Qy 1126 TGGTTGGCACTGGTTCACAATGGAATGGTGGATGATATTGGCTTAAGGAGGGTTTT 1185

Db 392 TrpPheGlyAsnLeuValThrMetLysTrpTrpAspAsnLeuTrpLeuAsnGluGlyPhe 411
Qy 1186 GCAAAATCATGGAATCTATCCCTGTTAAATGCTACATATCCAGAGCTG---CAATTGAT 1242
Db 412 AlaserPheValGluTyriIleGlyAlaAspPheIleSerAspGlyLeuTrpGluMetLys 431
Qy 1243 GACTATTTTGAAGTGTGTTT---GAAGTAATTTACAAAGATTCATTGNAATCATCC 1299
Db 432 AspPhePheLeuLeuAlaProTyThrSerGlyIleThrAlaAspAlaValAlaSerSer 451
Qy 1300 CCCCCTATCTCCAAACCGAGCGCAACCCGACTCAAAATACAGGAATGTTTGATCAAGTT 1359
Db 452 HisProLeuSerPheArgIleAspLysAlaAlaAspValSerGluAlaPheAspIle 471
Qy 1360 TCCTATACAAAGGAGCTGTATTTGAATATGCTCAAGGATTTTCTCGGTGAGGAGAA 1419
Db 472 ThrTyArgLysGlyAlaSerValLeuGluMetLeuLeuAsnLeuValGlyAspGluAsn 491
Qy 1420 TTCAGAAAGGAATATTCAGTACTTAAGAGTTTCAGTATAGAAATGCTAAGNATGAT 1479
Db 492 PheLysGlnSerValSerArgTyLeuLysLysPheSerTyAspAsnAlaAlaGlu 511
Qy 1480 GACTTGTGGAGAGCTGTGCAATAGTTGTTAGAAAGTGATTTTACATCTGGTGGAGTT 1539
Db 512 AspLeuTrpAlaAlaPhe-----AspGluThrValGlnGlyIle 524
Qy 1540 TGTCAATCCGATCCCAAGATGCAAGTAAACATGCTCGCTTCTCGGGGAAATGACAG 1599
Db 525 -----ThrGlyProAsn-----GlyGlyProLeuLys 533
Qy 1600 GTCAAGAGATGATCATACATGAGTCTCCAGAAAGGAATCCCTCTGCTGTTAA 1659
Db 534 MetSerGluPheAlaProGlnTrpThrGlnMetGlyPheProValLeuThrValGlu 553
Qy 1660 CAA---GACGGTGTCTACCTCGAGCTCAACAGAGCGCTTCTCCAGGGGGTTTCCAG 1716
Db 554 SerValAsnAlaThrThrLeuLysValThrGlnLysArgTyArgGlnAsnLysAspAla 573
Qy 1717 GAAGACCTGAA---TGGAGGCGCTCGCAGGAGGTACCTGTGCTATATCCCATTTGACC 1773
Db 574 LysGluProGluLysTyArgHisProThrTyGlyPheLysTrpAspValProLeuTrp 593
Qy 1774 TACTCCAGAGTCTTCTAATGTGATCCACAGACATCTTAAATCAACAGACATACT 1833
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Qy 1834 CTGGATCTACCTGAAACAGACCATGTTGGTGAATTTAATGTGGACTCAATGTTACTAC 1893
Db 614 PheHisValSerAsnSerAspSerValValValAsnAlaGluArgAlaPheCys 633
Qy 1894 ATCGTTCACTATGAGGTCATGGATGGGACCACTATTACACAGCTGAATCAGAACCCAC 1953
Db 634 ArgSerAsnTyAspAlaAsnGlyTrpArgAsnIleMetArgArgLeuLysGlnAsnHis 653
Qy 1954 ACATTTCTCAGACCTAAGACAGATAGTGTGATCATGATGTGTTTTCAGCTAGTTGGT 2013
Db 654 LysValTyGlyProArgThrArgAsnAlaLeuIleSerAspAlaPheAlaAlaAla 673
Qy 2014 GCAGGAGACGTGACCTAGACAAAGCTCTTCACATGACTTACTACTCCACATGAACA 2073
Db 674 ValGluGluMetAsnTyGluThrValPheGluMetLeuLysTyThrValLysGluGlu 693
Qy 2074 AGCAGCCCGCAGCTTCTCGAAGGTCTGATGTTTGAATCGTTTACCACATGATGAC 2133
Db 694 AspTyLeuProTrpLysGluAlaIleSer-----GlyPheAsnThrIleLeuAsp 710
Qy 2134 AGAAGGATATTTAGATATCTCTGAAACCTCAAGCGTTTACCTTCTTCAGTATTTAAG 2193
Db 711 PhePheGlySerGluProGluSerGlnTrpAlaSerGluTyMetArgLysLeuMetLys 730
Qy 2194 CCAGTGATTTGACAGCAAGC-----TGGAGTGACAGGGCTCA 2232
Db 731 ProIleTyAspLysSerIleLysPheIleAlaGluAsnTyLysLysAspSerLeu 750

Qy 2233 GTCTGGGACAGGATGCTCCGCTCTCTTTGAAGCTGGCTGTGACCTGAACCATGCT 2292
Db 751 PhePheLysAsnAsnLeuGlnIleAlaValIleAspThrTyCysGlyLeuGlyGlyLys 770
Qy 2293 CCTTGATCCAGAAAGCTGCTGAACTCTTCTCCAG-----TGG 2331
Db 771 GluCysLeuGluMetLysLeuPheAspLysGluValMetLysCysGlnProGly 790
Qy 2332 ATGGAATCCAGTGAATAATATACCAACAGATGTTTAAAGATTTGTGTTCTGTG 2391
Db 791 GlnGlnAlaThrAspCysValLysValThrAlaProLeuArgLysThrValTyCysTy 810
Qy 2392 GGTCTCAGACA-----ACAGCAGGATGGAATTTACCTTTTAGCAATATGAATGTC 2445
Db 811 GlyValGlnGluGlyGlyAspGluAlaPheAspLysValMetGluLeuTyAsnAlaGlu 830
Qy 2446 ATGTCAGTCTGCAACAAACAAATTTCTGTATCTTGTCAACGAGCAACATCAGGAA 2505
Db 831 GlnValGlnLeuGluLysAspSerLeuArgGluAlaLeuGlyCysHisLysAspValThr 850
Qy 2506 AAGTTACTGAAGTTAATTTGAATAGGAA-----GGAAAGGTTATCAAGACACAG 2559
Db 851 AlaLeuLysGlyLeuLeuMetLeuAlaLeuAspArgAsnSerSerPheValArgLeuGln 870
Qy 2560 AACTTGGCAGCTCTCTTCATGCGATTTGCCAGAGCTCCAAAGGGGCGAGCAATGATGG 2619
Db 871 AspAlaHisAspValPheAsnIleValSerArgAsnProValGlyAsnGluLeuPhe 890
Qy 2620 GATTTCTAAGAGAAATTTGACCCCATCTTCTGAAAAAATTTTGACTTGGGCTCATATGAC 2679
Db 891 AsnPheLeuThrGluArgTrpGluGluLeuLeuSerLeuSerIleArgHisArgSer 910
Qy 2680 ATAGGATGATCATCTCTGGCACAACAGCTCACATTTTCTTCCAAAGGATAAGTTGCAAG 2739
Db 911 ValAspArgValIleLysAlaCysThrArgGlyLeuArgSerArgGluGlnValGlnGln 930
Qy 2740 GTGAAATATTTTGAATCTCTTTGAGCTCAAGGATCACATCTGGATATTTTCAAACT 2799
Db 931 LeuLysAsnLeuTyLysAsn---AspLysArgAlaArgGluTyGlyAlaPheGlyGly 949
Qy 2800 GTTCTGGAACGATAACCAAAATATAAATATGCTGGAGAGAGATCTTCCGACTCTG 2856
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RESULT 12

US-08-335-844A-24

; Sequence 24, Application US/08335844A

; Patent No. 6066503

; GENERAL INFORMATION:

; APPLICANT: GRAHAM, MARGARET

; APPLICANT: SMITH, TREVOR STANLEY

; APPLICANT: MUNN, EDWARD ALBERT

; APPLICANT: KNOX, DAVID PATRICK

; APPLICANT: OLIVER, JOHANNA JANE

; APPLICANT: NEWTON, SUSAN ELIZABETH

; TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING

; TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE PREPARATION OF

; NUMBER OF SEQUENCES: 73

; CORRESPONDENCE ADDRESS:

; ADDRESS: Rothwell, Figg, Ernst & Kurz

; STREET: Suite 701-E, 555 Thirteenth St., N.W

; CITY: Washington

; STATE: D. C.

; COUNTRY: U.S.A.

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/335,844A
FILING DATE: 09-JAN-1995
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
PCT/GB93/00943
FILING DATE: 06-MAY-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9209936
FILING DATE: 08-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: WALKER, Barbara W.
REGISTRATION NUMBER: 35,400
REFERENCE/DOCKET NUMBER: 1181-223A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)783-6040
TELEFAX: (202)783-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 972 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-335-844A-24

Alignment Scores:
Pred. No.: 6.88e-103 Length: 972
Score: 1117.00 Matches: 279
Percent Similarity: 48.93% Conservative: 199
Best Local Similarity: 28.56% Mismatches: 391
Query Match: 22.07% Indels: 108
DB: 3 Gaps: 25

US-10-039-073-3 (1-2883) x US-08-335-844A-24 (1-972)

Qy 115 TCAGTGCATCTAGTTACTTCACT-----GAGGATCCTGGG 153
Db 32 SerileGlyLeuThrTyrThrArglySalPheAspThrSerGluLysProGly 51
Qy 154 GCT-----TTCCAGTAGCCACTAATGGGAACGA 183
Db 52 LysAspAspThrGlyGlyLysAspLysAspAsnSerProSerAlaAla----- 67
Qy 184 TTCTCTGGCAGGAGCTTAAGGCTCCCGAGTGTGTCATCTCTCCATTATGACCTTTT 243
Db 68 -----GluLeuLeuLeuProSerAsnileLysProLeuSerTyrAspLeuThr 83
Qy 244 GTC-----CACCCCAATCTCACCCTCTCTGGACTTTGTT 276
Db 84 IleLysThrTyrLeuProGlyTyrValAspPheProGluLysAsnLeuThrPheAsp 103
Qy 277 GCATCTGAGAAGATCGAAGTCTTGGTCAGCAATGCTACCCAGTTTATCATCTTGCACAGC 336
Db 104 GlyArgValGluIleSerMetValIleGluProThrLysSerIleValLeuAsnSer 123
Qy 337 AAAGATCTTGAATCAGCAATGCCACCTTCCAGTCAGAGGAAGATTCAGATACATGAAA 396
Db 124 LysLysIleSerValIle-----ProGlnGluCysGluLeuValSer 137
Qy 397 CCAGAAAGACTGAAGTTTGAAGT-----TACCTGTCTCATGACAAATGCA 447
Db 138 GlyAspLysLysLeuGluIleGluSerValLysGluHisProArgLeuGluLysValGlu 157
Qy 448 CTGCTGGTTCCAGAGAATTTACGCTCACCTGAATACTATGTGGCTATGGACTTCCAA 507
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Qy 508 GCCAAGTGTAGTGGCTTGAAGGTTTTATAAAGCACATACAGAACTCTTGGTGGT 567
Db 178 GlyLeuIleSerAsnSerPheGlyGlyIleTyrGlnThrThrTyrThrProAspGly 197
Qy 568 GAAACAGAAATCTTGCAGTAAAGATTTGAGCCCAACCCAGGCGCATGGCTTCCCT 627
Db 198 ThrProLysIleAlaAlaValSerGlnAsnGluProIleAspAlaAlaArgMetValPro 217

Qy 628 TGCTTTGATGAACCGTTGTTCAAAGCCAACTTTTCAATCAAGATACGAAAGAGAGCAGG 687
Db 218 CysMetAspGluProLysTyrLysAlaAsnThrThrValThrValIleHisProLysGly 237
Qy 688 CATATTGCATATCCCAACATGCCAAAGGTTAAG---ACAATTGAACCTTGAAGAGGCTCTT 744
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Qy 745 TTGGAAGATCATTTCGAACTACTGTAAATAAGTACATACCTGTAGCTACATAGTT 804
Db 258 IleThrSerLysPheLeuThrThrProArgMetSerSerTyrLeuLeuAlaValMetVal 277
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Db 398 LeuTrpLeuAsnGluGlyPheAlaArgPheThrGluPheIleGlyAlaGlyGlnIleThr 417
Qy 1222 TATCCAGAGTCGAATTTGATGACTATTTTGTG---AATGTGTGTTTTGAAGTAATTACA 1278
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Qy 1279 AAAGATTCATGAATTCATCCCGCTCTACTCTCCAAACCCGCGGAAACCCGACTCAATA 1338
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Qy 1339 CAGAAATGTTTGAAGTTTCTCTATAACAAGGAGCTTGTATTTTGAATATGCTCAAG 1398
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Db 478 AlaLeuIleGlyGluLysHisLysHisAlaValSerGlnTyrLeuLysLysPheSer 497
Qy 1459 TATAGAAATGCTAAGATGATGATGCTGTGGAGCAGTCTGTCAAAATAGTCTTTAGAAAGT 1518
Db 498 TyrSerAsnAlaGluAlaThrAspLeuTrpAlaValPheAspGluValValThrAspVal 517
Qy 1519 GATTTTACATCTGCTGGAGTTTGTCTCATTCGGATCCCAAGATGACAAAGTACATGCTGCC 1578
Db 518 GluGlyProAspGly-----LysProMetLysThrThr----- 528
Qy 1579 TTTCTGGGGAAATCGAGAGTCAAGAGATGATGACTACATGGAAGTCTCCGAAAGGA 1638
Db 529 -----GluPheAlaSerGlnTrpThrThrGlnMetGly 539
Qy 1639 ATCCCTCTGCTGCTGCTTAAACAA---GACGGGTGTTCTACCTCCGACTGCAACAGGAGCGC 1695
Db 540 PheProValIleSerValAlaGluPheAsnSerThrThrLeuLysLeuThrGlnSerArg 559


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US-10-039-073-3 (1-2883) x US-09-129-366-24 (1-972)
QY 115 TCAGTGCATCTAGTTATCACTTCACT-----GAGGATCCTGGG 153
Db 32 SerIleGlyLeuThrTyrTyrPheThrArgLysAlaPheAspThrSerGluLysProGly 51
QY 154 GCT-----TTCCAGTAGGACCACTAATGGGAACGA 183
Db 52 LysAspAspThrGlyGlyLysAspLysAspAsnSerProSerAlaAla----- 67
QY 184 TTTCCTTGGCAGGAGCTAAGGCTCCCGAGTGTGTCATCTCTCCATTATGACCTTTT 243
Db 68 -----GluLeuLeuLeuProSerAsnIleLysProLeuSerTyrAspLeuThr 83
QY 244 GTC-----CACCCCAATCTCACCTCTCTGGACTTTGTT 276
Db 84 IleLysThrTyrLeuProGlyTyrValAspPheProGluLysAsnLeuThrPheAsp 103
QY 277 GCATCTGAGAAGATCGAAGTCTTGGTCAGCAATGCTACCCAGATTATCATCTTGCACAGC 336
Db 104 GlyArgValGluIleSerMetValIleGluProThrLysSerIleValLeuAsnSer 123
QY 337 AAGATCTTGAATACGAATGCCACCCTTCAGTCAGAGGAAGATTCAAGATACATAA 396
Db 124 LysLysIleSerValIle-----ProGlnGluCysGluLeuValSer 137
QY 397 CCAGAAAGAACTGAAGTTTTCAGT-----TACCCTGCTCATGAACAATTGCA 447
Db 138 GlyAspLysLysLeuGluIleGluSerValLysGluHisProArgLeuLysValGlu 157
QY 448 CTGCTGGTTCCAGAGAATCTTACGCCCTCACCTGAATACTATGTGGCTATGGACTTCCAA 507
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QY 508 GCCAAGTTCAGTGGCTTTGAAGGTTTTPATAAAGCACATACAGAATCTTTGGTGGT 567
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QY 568 GAAACAAGAAATCTTCGAGTAAACAGATTTTGAGCCACACCCAGCCATGGCTTCCCT 627
Db 198 ThrProLysIleAlaAlaValSerGlnAsnGluProIleAspAlaArgMetValPro 217
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QY 805 TGTGATTTCCACTCTCTGAGTGGCTTCACTTCATCAGGGGTCAAGGTGTCATCTATGCA 864
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QY 925 TTTTATGAAAGTACTTTGATATCTACTATCCACTCTCCAACTGGATTTAATGCTATT 984
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QY 985 CCTGACTTTGACCTGGAGCCATGAAATTTGGGGCTCATTTACATATAGGAGACGTCA 1044
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QY 1045 CTGCTTTTGGACCCCAAGACCTCTTCTGCTTCCGATAAACTGTGGGTCCACAGAGTCATA 1104
Db 1104
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QY 1165 ATTGGCTTTAAGGAGGGTTTTCAAAATACATCGAACTTATC---GCTGTTAATGTACA 1221
Db 398 LeuTrpLeuAsnGluGlyPheAlaArgPheThrGluPheIleGlyAlaGlyGlnIleThr 417
QY 1222 TATCCAGAGCTGCAATTTGATGACTATTTTTTG---AATGTGTGTTTTGAAGTAATTACA 1278
Db 418 GlnAspAlaArgMetArgAsnTyrPheLeuIleAspValLeuGluArgAlaLeuLys 437
QY 1279 AAGATTCATTGAATTCATCCGCCCTATCTCCAAACACCGCGGAAACCCGACTCAATA 1338
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QY 1459 TATAGAAATGCTAAGAATGATGACTTGTGAGCAGTCTGCAAAATAGTTGTTTAGAAAGT 1518
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QY 1696 TTC---CTCCAGGGGGTTTTTCCAGGAAGACCCCTGAATGGAGGGCCCTCGAGAGAGGTAC 1752
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QY 1813 CTAAAATCAAAGACATATCTCTGGATCTACCTGAAAGACACAGTGGGTGAAATTT--- 1869
Db 600 LeuArg---ArgAspGluProLeuTyrLeuHisValSerAspAlaGlyAlaProPheVal 618
QY 1870 ---AATGTGGACTCAAATGGTTACTACTCGTTTCACTATGAGGCTCATGATGGAGCAAA 1926
Db 619 ValAsnAlaAspArgTyrGlyPheTyrArgGlnAsnHisAspAlaAsnGlyTyrLysLys 638
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QY 1987 ATTCAATGATGTGTTTCAGCTAGTTGTTGGTCAGGGAGACTGACCCCTAGACAAAGCTCTTGAC 2046
Db 659 IleSerAspAlaPheAlaAlaAlaThrAspAlaIleGluTyrGluThrValPheGlu 678
QY 2047 ATGACTTACTACTCCAAACATGAAACAGCAGCCCGCACTT-----CTCGAAGGT 2097
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QY 2098 CTGAGTTACTTGAATCGTTTATCCACATGATGACAGAGGAATATTTTCAGATATCTCT 2157
Db 699 IleSerSerIleLeuLysTyrPheProThrGluProGlu-----Ala 712
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   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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RESULT 14
US-08-335-844A-23
; Sequence 23, Application US/08335844A
; Patent No. 6066503
; GENERAL INFORMATION:
; APPLICANT: GRAHAM, MARGARET
; APPLICANT: SMITH, TREVOR STANLEY
; APPLICANT: MUNN, EDWARD ALBERT
; APPLICANT: KNOX, DAVID PATRICK
; APPLICANT: OLIVER, JOANNA JANE
; APPLICANT: NEWTON, SUSAN ELIZABETH
; TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING
; TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE PREPARATION OF
; TITLE OF INVENTION: VACCINES AGAINST HELMINTH INFECTIONS
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Rothwell, Figg, Ernst & Kurz
; STREET: Suite 701-E, 555 Thirteenth St., N.W
; CITY: Washington
; STATE: D. C.
```

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; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/335,844A
; FILING DATE: 09-JAN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB PCT/GB93/00943
; FILING DATE: 06-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9209936
; FILING DATE: 08-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: WALKER, Barbara W.
; REGISTRATION NUMBER: 35,400
; REFERENCE/DOCKET NUMBER: 1181-223A
; TELEPHONE: (202)783-6040
; TELEFAX: (202)783-6031
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 972 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-335-844A-23

Alignment Scores:
Pred. No.: 3,51e-101 Length: 972
Score: 1100.00 Matches: 284
Percent Similarity: 47.02% Conservative: 190
Best Local Similarity: 28.17% Mismatches: 390
Query Match: 21.73% Indels: 144
DB: 26

US-10-039-073-3 (1-2883) x US-08-335-844A-23 (1-972)

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QY 124 TCTAGTTATCACTTCACCT-----GAGGAT 147
   : : : : : : : : : : : : : : : : : : : : : : : :
Db 35 LeuThrTyrTyrPheThrArgLysAlaPheAspThrThrGlnLysGluGlnLysAsp 54
   : : : : : : : : : : : : : : : : : : : : : : : :
QY 148 CTTGGGCT-----TTCCAGTAGCCACTAATGGGGAACGATTTCTTTGG 192
   ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 55 SerGlyGlyLysGluLysAspAsnSerProSerAla----- 66
   : : : : : : : : : : : : : : : : : : : : : : : :
QY 193 CAGGAGCTAAGCTCCCGAGTGGTCACTCTCTCCATTATGACCTTTTGTGTC----- 246
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QY 286 AAGATCGAAGTCTTGGTGCAGCAATGCTACCCAGTTTATCATCTTGCACAGCAAGATCTT 345
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Db 107 GluIleAlaMetValValGluProThrAsnSerIleValLeuAsnSerLysLysIle 126
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Db 281 GluTyrIleGluGlyPheThrLysThrGlyValArgPheArgIleTrpSerArgProGlu 300
Qy 874 AAACGGAAATCAACACATATTTGCTTGCAGGCATCACTGAAGCTACTTGTATTTATGAA 933
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Qy 934 AAGTACTTTGATATCTACTATCTCACTCTCCAACTGGATTTAATGTCTATCTCGACTTT 993
Db 321 LysPhePheAspIleLysPheProLeuGluLysGlnAspMetIleAlaLeuProAspPhe 340
Qy 994 GCACCTCGAGCCATGGAAATTTGGGCTCATATACATATAGGAGAGCTCACTGCTTTT 1053
Db 341 ThrAlaGlyAlaMetGluAsnTrpGlyLeuIleThrTyrArgGluAspSerLeuLeuTyr 360
Qy 1054 GACCCCAAGACCTCTTCTGCTTCGATAAACTGTGGGTCCACGAGTCAATAGCCCATGAA 1113
Db 361 AspGluLysIleTyrAlaProMetAsnLysGlnArgValAlaLeuValAlaHisGlu 380
Qy 1114 CTGGCGCACCGTGGTTGGCACTCGTCACATGGAATGGTGAATGATATTTGGCTT 1173
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Qy 1231 CTGCAATTTGATGACTATTTT---TTGAATGTGTGTTTTGAAGTAATTTACAAAGATTCA 1287
Db 421 PheArgThrGlnAspPhePheLeuLeuAspGlyMetAspArgGlyMetArgAlaAspSer 440
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Db 481 GlyLysAspAsnTyrArgAsnAlaValGlnTyrLeuLysLysPheSerTyrSerAsn 500
Qy 1468 GCTAAGAAATGATGACTTGTGGAGCAGTCTGCAATAGTTGTTAGAAAGTATTTACA 1527
Db 501 AlaGlnAlaAlaAspLeuTrp---AsnValPheAsnGluValValLys----- 515
Qy 1528 TCTGGTGGAGTTTGTCTATTCGATCCCAAGATGACAAGTAACATGCTCGCTTCTGGGG 1587
Db 516 -----GlyValLysGlyProAsp-----Gly 522
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Db 523 AsnValMetLysIleAspGlnPheThrAspGlnTrpThrTyrGlnMetGlyTyrProVal 542
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Db 543 ValLysValGluGluPheAsnAlaThrAlaLysValThrGlnSerArgTyrLysThr 562
Qy 1705 GGGGTTTTCCAGGAAGACCTGAA---TGGAGGGCCCTGCGAGAGAGTACCTGTGGCAT 1761
Db 563 AsnLysAspAlaLeuGluProGluLysTyrArgAsnProLysTyrGlyPheLysTrpAsp 582
Qy 1762 ATCCCATGACCTACTCCACGAGTCTTCTAATGTGATCCACACACATTTCTAAATCA 1821
Db 583 ValProLeuTrpTyrGlnGluGlyAsnSerLysGluValLysArgThrTrpLeuLysArg 602
Qy 1822 AAGCACATACT---CTGGATCTACCTGAAAGACAGTGGGTGAAATTTAATGTGGAC 1878
Db 603 AspGluProLeuTyrLeuAsnValAsnAsnArgAspThrSerLeuValValAsnAlaAsp 622

Qy 1879 TCAAAATGGTTACTACATCGTTCACTATGAGGGTTCATGATGGACCACTCATTTACACAG 1938
Db 623 ArgHisGlyPheTyrArgGlnAsnTyrAspAlaAsnGlyTrpLysLysIleLeuLysGln 642
Qy 1939 CTGAATCAAGAACACACACTTCTCAGACCTAAGACAGAGTAGGTCTGATTCATGATGTG 1998
Db 643 LeuLysLysAspHisLysValPheGlyProArgThrArgAsnAlaIleIleSerAspAla 662
Qy 1999 TTTCAGCTAGTTGGTCCAGGAGACTGACCCCTAGACAAAGCTCTTGACACTGACTTACTAC 2058
Db 663 PheAlaAlaAlaThrIleAspAlaIleAspTyrGluThrValPheGluLeuLeuGluTyr 682
Qy 2059 CTCACCACTGAA----- 2070
Db 683 AlaLysAsnGluGluGluPheLeuProTrpLysGluAlaLeuSerGlyMetPheAlaVal 702
Qy 2071 -----ACAAGCAGCCCGCAGCTTCTCGAAGGTCTGAGTTTAC 2106
Db 703 LeuLysPhePheGlyAsnGluProGluThrLysProAlaArgAlaTyrMetMetSerIle 722
Qy 2107 TTGGAATCGTTTACCACATGATGGACAGAGAATATTTTCAGATATCTCTGAAACCTC 2166
Db 723 LeuGluProMetTyr-----AsnLysSerSerIleAspTyrIleVal 736
Qy 2167 AAGCGTTACTCTTCTTCAAGTATTTTAAAGCAGTCAATTCAGAGGCAAGCTGGAGTGAAG 2226
Db 737 LysAsnTyrLeuAspAspThrLeuPheThrLysIleAsnThrGln----- 751
Qy 2227 GGCTCAGTCTGGACAGGATGCTCCGCTCGCTCTTGAAGCTGCGCTGTGACCTGGAAC 2286
Db 752 -----LysAspIleIleAspAlaTyrCysSerLeuGly 762
Qy 2287 CATGCTCTTCGATCCAGAAAGCTGCTGAACCTTTC---TCCCAGTGGATGGAATCCAGT 2343
Db 763 SerLysAspCysIleLysGlnTyrLysAspIlePheTyrAspGluValMetProLysCys 782
Qy 2344 GGAATAATTAATATACCAACAGATGTTTAAAGATT-----GTG 2382
Db 783 LysAlaGlyGluAlaAlaThrLysCysValLysValSerAlaProLeuArgAlaAsnVal 802
Qy 2383 TATTCGTGGTGTCTCAGACACAGCAGAGATGGAAT----- 2418
Db 803 TyrCysTyrGlyValGln---GluGlyGlyGluGluAlaPheGluLysValMetGlyLeu 821
Qy 2419 TACCTTTTAGACAAATATCACTGTCAATGCTCAAGTGTCAAGTGTGAACAAACAAATTTCTGAT 2478
Db 822 TyrLeuAlaGluAspValGlnLeu-----GluLysGlyIleLeuPheLys 836
Qy 2479 GCTTTTCTCAACGAGCAAGCATCAGGAAAAGTTTACTGAAGTTAATT-----GAACCTAGGA 2532
Db 837 AlaLeuAlaCysHisLysAspValThrAlaLeuLysGluLeuLeuArgAlaLeuAsp 856
Qy 2533 ATGGAAGGAAAGTTATCAAGACACAGAACTTGGCAGCTCTCTTCATCGGATGCCAGA 2592
Db 857 ArgLysSerSerPheValArgLeuGlnAspValProThrAlaPheArgAlaValSerGlu 876
Qy 2593 CGTCCAAAGGGCAGCAACTAGCATGGGATTTTGAAGAGAAAATTTGGACCCATCTTCTG 2652
Db 877 AsnProValGlyGluGluPheMetPheAsnPheLeuMetGluArgTrpGluIleThr 896
Qy 2653 AAAAAATTTGACTTGGGCTCATATGACATAAGGATGATCTCTCTGGCACACAGCTCAC 2712
Db 897 AlaSerLeuGluThrGluHisArgAlaValAspLysValValGlyAlaCysCysThrGly 916
Qy 2713 TTTTCTTCCAAGATAAGTTGCAAGAGGTGAACATATTTTGAATCTCTTGGGCTCAA 2772
Db 917 IleArgSerGlnGlnGlnIleAspGlnLeuLys---AsnLeuGlnLysAsnAlaGln 935
Qy 2773 GGATCACATCTGGATATTTTCAAACTGTTCTGGAAACCGATACCAACAAAATATAAATGG 2832
Db 936 AlaLysLysPheGlySerPheThrGlnGluIleGluLysGlyGluHisLysIleAlaTrp 955

QY 2833 CTGGAGAGATCTTCCGACTCTG 2856
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Db 956 ILeYsLYsHIsPheHIsArgLeu 963

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Job time : 188.818 secs

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